

CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE.
 XX

SO Sequence 15 AA;

Query Match 100.0%; Score 81; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNDSPICQDYTTTG 15
 |||||
 1 RNDSPICQDYTTTG 15

Db

RESULT 2

ADRI0607
 ID ADRI0607 standard; peptide; 15 AA.

AC ADRI0607;

DT 21-OCT-2004 (first entry)

DE Pig IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 KM pig.

XX Sue scrofa.

OS WO2004065936-A2.

PN 05-AUG-2004.

PD 15-JAN-2004; 2004WO-US003566.

PE 16-JAN-2003; 2003US-0440472P.

PR (UYNC-) UNIV NORTH CAROLINA STATE.

PA Hammerberg B;

PI WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.
 XX

PS Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC pig IGE 5.91 recognition site.
 CC

SO Sequence 15 AA;

Query Match 65.4%; Score 53; DB 8; Length 15;
 Best Local Similarity 57.1%; Pred. No. 0.042; 1; Indels 0; Gaps 0;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNDSPICQDYTTT 14
 |||||
 1 RNDAPVQADRHSTT 14

Db

RESULT 3

ADRI0602
 ID ADRI0602 standard; peptide; 15 AA.

AC ADRI0602;

DT 21-OCT-2004 (first entry)

DE Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 KM cat.

XX Felis catus.

OS WO2004065936-A2.

PN 05-AUG-2004.

PD 15-JAN-2004; 2004WO-US003566.

PE 16-JAN-2003; 2003US-0440472P.

PR (UYNC-) UNIV NORTH CAROLINA STATE.

PA Hammerberg B;

PI WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.
 XX

PS Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC cat IGE 5.91 recognition site.
 CC

SO Sequence 15 AA;

Query Match 59.3%; Score 48; DB 8; Length 15;
 Best Local Similarity 61.5%; Pred. No. 0.31;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDSPIQDYTTT 14
 |||||
 2 NDSPIQDYTTT 14

Db

RESULT 4

ADRI0603
 ID ADRI0603 standard; peptide; 15 AA.


```

XX AC ADR10603;
XX XX
XX DT 21-OCT-2004 (first entry)
XX XX
DE Horse IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 3.
XX
XX Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
XX Anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX horse.
XX
XX OS Equus caballus.
XX
XX PN WO2004065936-A2.
XX
XX PD 05-AUG-2004.
XX
XX PF 15-JAN-2004; 2004WO-US003566.
XX
XX PR 16-JAN-2003; 2003US-0440472P.
XX
XX PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX PI Hammerberg B;
XX
XX DR WPI; 2004-593545/57.
XX
XX PT Novel antibody that specifically binds to mammalian IGE epitope, useful
XX for testing an allergen reactivity of IGE sample, detecting mammalian IGE
XX or treating asthma or anaphylactic shock.
XX
XX PS Example 6; Page 9; 14pp; English.
XX
XX CC The present invention relates to a novel monoclonal antibody (I) that
XX specifically binds to a mammalian IGE epitope, where the epitope is
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX (I) is useful for testing an allergen reactivity of an IGE sample. The
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX and corn allergens. The sample is a biological sample collected from a
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX antibodies recognise epitopes on canine IGE corresponding to amino acid
XX residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
XX cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
XX 3.76 were observed to have good cross-reactivity with the epsilon-chain
XX of IGE from cat and horse, but did not exhibit cross-reactivity with
XX either pig or human epsilon-chains of IGE. The present sequence is the
XX horse IGE 5.91 recognition site.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 50.6%; Score 41; DB 8; Length 15;
XX Best Local Similarity 64.3%; Pred. No. 5.1;
XX Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 RNDSPQTQDYTTT 14
XX ||:|||||
XX 1 RNNVLTQDQOATT 14
XX
XX RESULT 5
XX ADR10603 standard; peptide; 15 AA.
XX
XX AC ADR10603;
XX
XX DT 18-DEC-2003 (first entry)
XX
XX DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P4.
XX
XX XX Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.
XX
XX KW

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OS OS Equus caballus.
XX
XX PN US2003087314-A1.
XX
XX PD 08-MAY-2003.
XX
XX PF 08-NOV-2001; 2001US-00052788.
XX
XX PR 08-NOV-2001; 2001US-00052788.
XX
XX PA (RBGC ) UNIV CALIFORNIA.
XX
XX PI Gershwin LJ, Pettigrew HD, Kalina WV;
XX
XX DR WPI; 2003-765437/72.
XX
XX PT Immunogenic composition comprising an isolated equine immunoglobulin E
XX polypeptide that induces production of antibodies which specifically bind
XX to equine immunoglobulin E.
XX
XX PS Example 1; Page 8; 14pp; English.
XX
XX CC The invention relates to an immunogenic composition comprising an
XX isolated polypeptide having an amino acid sequence that is at least 80%
XX identical to 6 (SI-S6), 15 amino acid peptide sequences derived from
XX equine immunoglobulin E (the composition induces production of an
XX antibody that specifically binds to equine immunoglobulin (IgE), the six
XX polypeptides are not explicitly identified in the specification. Also
XX included are a composition comprising an antibody that specifically binds
XX to a polypeptide at least 80% identical to (SI)-(S6), an antibody that
XX specifically binds to equine IGE made by the process of immunising an
XX animal with a polypeptide at least 80% identical to (SI)-(S6), making an
XX antibody that specifically binds to equine IGE (involving immunising an
XX animal with a composition further comprising an isolated polypeptide (the
XX amino acid sequence of the polypeptide is at least 80% identical to (SI)-
XX (S6)), and collecting antiserum from the animal) and a kit for detection
XX of equine IGE in a biological sample comprising the antibody and means
XX for detecting specific binding of the antibody to equine IGE. The
XX antibody is useful for detecting equine IGE protein in a biological
XX sample (serum) which involves contacting the sample with the antibody,
XX thus forming an antigen/antibody complex, and detecting the presence or
XX absence of the antigen/antibody complex. The antibody and antigen are
XX immobilised on a solid surface. The antibody is labelled such that the
XX complex can be detected. The complex is detected using a second labelled
XX antibody. The peptides are useful for generating antibodies specific for
XX IGE which can serve as a diagnostic test for allergy. The present
XX sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic
XX peptide from the early portion of the C4 region.
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 42.0%; Score 34; DB 7; Length 15;
XX Best Local Similarity 77.8%; Pred. No. 85;
XX Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 6 IOTDQYTTT 14
XX |||||
XX 1 IOTDQOATT 9
XX
XX RESULT 6
XX ABG98754
XX
XX ID ABG98754 standard; peptide; 10 AA.
XX
XX AC ABG98754;
XX
XX DT 13-JAN-2003 (first entry)
XX
XX DE F protein decapetide #241.
XX
XX XX F protein; RSV; decapetide; negative sense single stranded RNA virus;
XX viral F protein; F protein mediated host cell virion fusion; virucide;
XX F protein mediated host cell virion budding.
XX
XX KW

```

[illegible]

XX	PD		30-MAY-2002.	
XX	PF	22-NOV-2001;	2001WO-AU001517.	
XX	PR	22-NOV-2000;	2000US-0252767P.	
XX	PA	(BIOT-) BIOTA SCT MANAGEMENT PTY LTD.		
XX	PI	Mason AJ, Tucker SP, Young PR;		
XX	DR	WPI, 2002-599372/64.		
XX	PT	Facilitating production of a protein for analyzing, designing and/or		
XX	PT	modifying an agent that can interact with a viral F protein, comprises		
XX	PT	expressing a nucleic acid optimized for expression of the protein, using		
XX	PS	a eukaryotic cell.		
XX	PS	Claim 42; Page 102; 367bp; English.		
XX	CC	The invention relates to a method for facilitating production of a		
XX	CC	protein or its derivative from a negative sense single stranded RNA		
XX	CC	virus, by expressing a nucleic acid molecule encoding the protein in a		
XX	CC	host cell, where the nucleic acid is optimised for expression by a		
XX	CC	eukaryotic cell. The protein, especially F protein, is useful for		
XX	CC	analysing, designing and/or modifying an agent capable of interacting		
XX	CC	with a viral F protein or its derivative and modulating a functional		
XX	CC	activity associated with the protein, by contacting the protein with a		
XX	CC	putative agent and assessing the degree of interactive complementarity of		
XX	CC	the agent with the protein. An optimised nucleic acid or its derivative,		
XX	CC	equivalent, analogue or mimetic is useful for interacting with a viral F		
XX	CC	protein and modulating a functional activity associated with the viral		
XX	CC	protein, for use in the manufacture of a medicament utilised in the		
XX	CC	therapeutic and/or prophylactic treatment of conditions characterised by		
XX	CC	infection with a negative sense single stranded RNA virus, and for		
XX	CC	modulating a functional activity associated with a viral F protein in a		
XX	CC	subject, preferably a mammal, especially a human, where the functional		
XX	CC	activity is F protein mediated host cell virion fusion and/or virion		
XX	CC	budding and the modulating is down regulation. Sequences ABG98514-		
XX	CC	ABG99058 represent F protein decapeptides of the invention		
XX	SQ	Sequence 10 AA;		
	Query Match	39.5%; Score 32; DB 5; Length 10;		
	Best Local Similarity	66.7%; Pred. No. 1.2e+02;		
	Matches	6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
OY	2 NDSPIQTNDQ 10			
Db	1 NDMPITNDQ 9			
RESULT 8				
AAR79898	AAR79898 standard; peptide; 13 AA.			
AC	AAR79898;			
DT	25-MAR-2003 (revised)			
DT	25-APR-1996 (first entry)			
DE	Fusion protein syntehtic fragment SP4.			
KM	Respiratory syncytiallial virus; RS virus; fusion protein; antibody; vaccine;			
KM	human; therapy; diagnosis; immunosasey.			
OS	Synthetic.			
PN	CA1336955-C.			
PD	12-SEP-1995.			
PF	20-SEP-1989; 89CA-00612111.			

XX 20-SEP-1988; 88US-00247017.
 PR 20-SEP-1989; 89US-00409915.
 XX
 PA (PRAK-) PRAKIS BIOLOGICS INC.
 XX
 PI Paradise PR, Hu BT, Arumugham R, Hildreth SW, Martin-Gallardo A,
 PI Walsh BE;
 XX
 DR WPI; 1995-328674/43.
 XX
 PT Sub-unit vaccine against respiratory syncytial virus - contains
 PT polypeptide related to neutralising epitope on G protein, opt. also
 PT polypeptide from F protein.
 XX
 PS Disclosure; Fig 3; 119pp; English.
 XX
 CC The sequences represented by AAR79895-R79899 are synthetic peptides
 CC corresponding to regions of the respiratory syncytial (RS) virus fusion
 CC protein (see AAR79894). This sequence corresponds to residues 261-273.
 CC These fragments were used to create antibodies. The DNA encoding these
 CC fragments is inserted into expression vectors and used to transform cell
 CC cultures, the expressed protein is then isolated and purified. These
 CC peptide fragments are then used in a vaccine. Alternatively, the
 CC antibodies against these fragments could be used to confer short-term
 CC protection against the RS virus. The vaccine can then be used to protect
 CC humans and animals (for animals, the RS sequence used is from the RS
 CC virus of that species). The dose of the vaccine is 0.1-100 micro grammes
 CC per kg body weight. The vaccine can also be used in diagnosis, such as
 CC immunoassays. The DNA encoding this sequence can be used in hybridisation
 CC tests to detect RS virus in blood. The antibodies can be used to identify
 CC viral epitopes. The advantage with using this methodology is that there
 CC is no enhancement/potentiation of the disease seen with current
 CC treatments. (Updated on 25-MAR-2003 to correct PF field.)
 CC
 XX
 SQ Sequence 13 AA;
 XX
 Query Match 39.5%; Score 32; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 NDSPIQTQD 10
 DB 2 NDMPTINDQ 10
 XX
 RESULT 9
 AAW35339
 ID AAW35339 standard; peptide; 14 AA.
 XX
 AC AAW35339;
 XX
 DT 01-MAY-1998 (first entry)
 XX
 DE Rat GDNF receptor residues 356-369.
 XX
 KW Rat; glial cell line-derived neurotrophic factor; GDNF; receptor;
 KW treatment; dopaminergic nerve cell disorder; Parkinson's disease;
 KW Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
 KW Huntington's disease; glaucoma; retinal degeneration; hearing loss;
 KW gene therapy.
 XX
 OS Rattus sp.
 XX
 PN WO9740152-A1.
 XX
 PD 30-OCT-1997.
 XX
 PF 15-APR-1997; 97WO-US006281.
 XX
 PR 22-APR-1996; 96US-0015907P.
 PR 09-MAY-1996; 96US-0017221P.
 PR 14-APR-1997; 97US-00837199.
 XX

XX (AMGE-) AMGEN INC.
 PA
 XX
 PI Fox GM, Wen D, Jing S;
 XX
 DR WPI; 1997-535836/49.
 XX
 PT Glial cell line derived neurotrophic factor receptor - useful to treat
 PT dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
 PT disease.
 XX
 PS Disclosure; Page 21; 196pp; English.
 XX
 CC The present peptide is derived from rat glial cell line-derived
 CC neurotrophic factor (GDNF) receptor, which can be used to treat
 CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
 CC disease or amyotrophic lateral sclerosis, complications of diabetes and
 CC Huntington's disease and (optionally in combination with GDNF) glaucoma,
 CC retinal degeneration and hearing loss caused by injury to inner ear
 CC sensory neurons. The receptor can also be used to block unwanted GDNF
 CC activity, analyse GDNF related molecules and stabilise GDNF in
 CC pharmaceutical formulations. Receptor expressing cells, preferably
 CC transfected ex vivo, can be used similarly by implantation, and the use
 CC of the receptor cDNA in gene therapy is also contemplated. Probes based
 CC on the cDNA can be used to identify GDNF responsive cells and tissues,
 CC e.g. to identify patients who would benefit from GDNF therapy, and
 CC abnormalities in receptor expression, and to isolate molecules that form
 CC a complex with the cDNA or are homologous/cross-reactive with the cDNA.
 CC Anti-receptor antibodies, oligonucleotides derived from the cDNA and
 CC animal models that overexpress the receptor can be used to study the
 CC biological function of GDNF, knockout transgenic animals can be used to
 CC detect GDNF dependent neurons or processes and the antibody can be used
 CC in immunoassays for the receptor. The receptor binds GDNF specifically
 CC and with high affinity, acting as part of a complex that
 CC mediates/enhances signal transduction by GDNF, i.e. increasing dopamine
 CC uptake in dopaminergic cells
 CC
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 38.3%; Score 31; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.6e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 5 PIQTDQYTTT 14
 DB 4 PVIQTATT 13
 XX
 RESULT 10
 AAW84178
 ID AAW84178 standard; peptide; 14 AA.
 XX
 AC AAW84178;
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE Rat GDNFR-alpha derived peptide.
 XX
 KW Rat; glial cell-line derived neurotrophic factor receptor-alpha;
 KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
 KW neurotrophin; signal transduction; dopaminergic nerve cell;
 KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KW neurological disorder; diabetes; glaucoma; sensory neuron;
 KW retinal ganglion cell degeneration; sensory neuropathy; retinopathy;
 KW gene therapy.
 XX
 OS Synthetic.
 XX
 PN WO9854213-A2.
 XX
 PD 03-DEC-1998.
 XX

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PF 27-APR-1998; 98WO-US008486.
PR 30-MAY-1997; 97US-00866354.
XX (AMGE-) AMGEN INC.
XX
XX PI Fox GM, Jing S, Wen D;
XX WPI; 1999-080806/07.
DR
XX New isolated glial cell line-derived neurotrophic factor receptors - used
PT to develop products for treating e.g. improperly functioning dopaminergic
PT nerve cells, Parkinson's disease, Alzheimer's disease or amyotrophic
PT lateral sclerosis.
XX
XX Disclosure; Page 24; 318pp; English.
PS
XX The present peptide is derived from rat glial cell-line derived
CC neurotrophic factor receptor-alpha (GDNFR-alpha) amino acids 356-369. It
CC is used to raise antibodies against GDNFR-alpha. The peptide may also
CC possess an activity of GDNFR-alpha. The GDNFR-alpha protein is capable of
CC complexing with glial cell line-derived neurotrophic factor (GDNF) and
CC mediating cell response to GDNF. GDNFR-alpha proteins are functionally
CC characterised by the ability to bind GDNF and/or neurturin specifically,
CC and to act as part of a molecular complex which mediates or enhances the
CC signal transduction affects of GDNF and/or neurturin. The proteins can be
CC used for treating improperly functioning dopaminergic nerve cells,
CC Parkinson's disease, Alzheimer's disease or amyotrophic lateral
CC sclerosis. They can also be used for treating neurological disorders
CC associated with diabetes, glaucoma or other diseases and conditions
CC involving retinal ganglion cell degeneration, sensory neuropathy caused
CC by injury to, insults to, or degeneration of, sensory neurons,
CC pathological conditions, or disease or injury-related retinopathies. The
CC products can also be used for detection, diagnosis, drug screening and
CC gene therapy
CC
XX Sequence 14 AA;
SQ
Query Match 38.3%; Score 31; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 5 PLOTDOYTTT 14
|:|:|:|:|
DB 4 PVQTTATTT 13

RESULT 11
AAM98177
ID AAM98177 standard; peptide; 14 AA.
XX
XX AAM98177;
AC
XX
XX 24-JAN-2002 (first entry)
DE
XX Human peptide #1452 encoded by a SNP oligonucleotide.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX
XX Homo sapiens.
OS
XX
XX WO200147944-A2.
PN
XX
XX 05-JUL-2001.
PD
XX
XX 28-DEC-2000; 2000WO-US035498.
PF

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XX 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach M;
XX WPI; 2001-465210/50.
DR
XX Polymorphic nucleic acids encoding e.g. amylases, cyclin, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
XX Disclosure; Page 3986; 4143pp; English.
PS
XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms
CC
XX Sequence 14 AA;
SQ
Query Match 37.0%; Score 30; DB 4; Length 14;
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
OY 6 IOTDOYTTT 14
|:|:|:|:|
DB 5 VQTDKVTST 13

RESULT 12
AAY51451
ID AAY51451 standard; peptide; 10 AA.
XX
XX AAY51451;
AC
XX
XX 11-MAY-2000 (first entry)
DE
XX AAV VP3 derived peptide fragment #6.
XX
XX VP3; structural protein; capsid; tropism; diagnosis; gene therapy.
KW
XX Adeno-associated virus.
OS
XX
XX WO9967393-A2.
PN
XX
XX 29-DEC-1999.
PD
XX
XX 21-JUN-1999; 99WO-EP004288.
PR 19-JUN-1998; 98DE-01027457.
XX
XX (MEDI-) MEDIGENE AG.
PA
XX
XX Haliek M, Ried M, Deleage G, Girod A;
PI
XX
XX WPI; 2000-160586/14.
DR
XX
XX Structure proteins of adeno-associated virus with at least one mutation
PF

```

PT have increased infectiveness.
XX
PS
XX Example 2; Page 42; 43pp; German.
XX
CC This invention describes novel structural proteins of adeno-associated virus (AAV) especially AAV-capsids with at least one mutation and which have an increased infectiveness. The structural proteins are used to alter the tropism of AAV, to transform cells, for diagnosis and for effectivity studies for gene therapy and/or for genomic targeting.
CC AAY51446-V51467 represent AAV derived peptides used to illustrate the method of the invention
CC
XX
SQ Sequence 10 AA;
XX
Query Match 35.8%; Score 29; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
QY 4 SPIQTDQY 11
:|:|:|
DB 1 NPVATEQY 8
XX
RESULT 13
AAB46909
ID AAB46909 standard; peptide; 10 AA.
XX
XX AAB46909;
XX
XX 04-MAY-2001 (first entry)
XX
XX AAV mutant VP3 derived peptide SEQ ID 14.
DE
XX
XX
XX VP3 protein; structural protein; chromatography; tropism; antigenicity;
XX genomic targeting; gene therapy; purification; affinity tag.
OS Adeno associated virus.
XX
XX DE19933719-A1.
XX
XX 25-JAN-2001.
PD
XX
XX 19-JUL-1999; 99DE-01033719.
PF
XX
XX 19-JUL-1999; 99DE-01033719.
PR
XX
XX (MEDI-) MEDIGENE AG.
PA
XX
XX Hallek M, Girod A, Ried M, Koerner C;
PI
XX
XX WPI; 2001-203661/21.
DR
XX
XX
XX New mutant adeno-associated virus structural protein with altered
PT chromatographic properties, useful in preparation of gene therapy
PT vectors.
XX
XX Example 1; Page 15; 20pp; German.
PS
XX
XX This invention describes a novel structural protein (I) of adeno-associated virus (AAV) which has at least one mutation that alters the
CC chromatographic properties of the virus. The invention also describes (1)
CC a nucleic acid (II) that encodes (1); (2) a cell (III) containing (II);
CC and (3) producing (I) comprising culturing (III). (I), (II) and (III) are
CC used to purify AAV and its particles, to alter the tropism or
CC antigenicity of AAV, to transform cells, for genomic targeting, for
CC diagnosis, for examination of activity and/or gene therapy. Altering the
CC chromatographic properties improves purification, especially
CC concentration of virus and produces viral particles to a higher titre or
CC higher purity and/or provides more efficient purification (fewer steps,
CC and a quicker and less expensive process). Particularly, mutated (I)
CC result in viruses that are eluted at a different (higher or lower) salt
CC concentration than the wild type, which tends to co-elute with other
CC viruses, serum proteins and cellular debris, or that include a specific

CC affinity tag. Mutation may also allow targeting of cells, e.g.
CC hematopoietic cells, that are not normally targets for AAV
XX
XX
SQ Sequence 10 AA;
XX
Query Match 35.8%; Score 29; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
QY 4 SPIQTDQY 11
:|:|:|
DB 1 NPVATEQY 8
XX
RESULT 14
ADG94454
ID ADG94454 standard; peptide; 10 AA.
XX
XX ADG94454;
XX
XX 25-MAR-2004 (first entry)
XX
XX
XX Human JAM-1 permeabilising peptide SEQ ID NO:433.
DE
XX
XX human; permeabilising; interferon-beta; IFN-beta; mucosal delivery;
XX immunosuppressive; virucide; autoimmune disease; viral disease;
XX multiple sclerosis; chronic hepatitis B; condyloma acuminata;
XX papilloma virus; childhood viral encephalitis; wart.
OS Homo sapiens.
XX
XX WO2004002404-A2.
PN
XX
XX 08-JAN-2004.
PD
XX
XX 18-JUN-2003; 2003WO-US019261.
PF
XX
XX 28-JUN-2002; 2002US-0393066P.
PR
XX
XX (MAST-) NASTECH PHARM CO INC.
PA
XX
XX Quay SC, Gupta M, De Weireles JC, Abd El- Shafy M;
PI
XX
XX WPI; 2004-122360/12.
DR
XX
XX
XX Stable pharmaceutical composition comprising interferon compound(s)
PT formulated for mucosal delivery to mammalian subjects in combination with
PT mucosal delivery-enhancing agent(s).
XX
XX
XX Disclosure; SEQ ID NO 433; 353pp; English.
PS
XX
XX The invention relates to a novel stable pharmaceutical composition
CC comprising one or more interferon (IFN)-beta compound(s) formulated for
CC mucosal delivery to a mammalian subject in combination with one or more
CC mucosal delivery-enhancing agent(s), where the composition following
CC mucosal administration to the subject yields enhanced mucosal delivery of
CC the one or more IFN-beta compound(s). A composition of the invention has
CC immunosuppressive and virucide activity. The composition is useful for
CC treating autoimmune diseases, viral disease, for alleviating one or more
CC symptom(s) of multiple sclerosis (MS), chronic hepatitis B, condyloma
CC acuminata, papilloma virus warts of the larynx or skin or childhood viral
CC encephalitis in the subject without unacceptable adverse side effects.
CC The composition can be delivered intranasally which reduces or eliminates
CC compliance problems and side effects that attend delivery by injection.
CC The sequences shown in ADG94022-ADG94810 represent permeabilising
CC peptides used in a composition of the invention.
XX
XX
SQ Sequence 10 AA;
XX
Query Match 35.8%; Score 29; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDSPIQTD 9
|||:
Db 1 NDVPLPTD 8

RESULT 15

AD146852
ID AD146852 standard; peptide; 10 AA.

XX
AC AD146852;

XX
DT 06-MAY-2004 (first entry)

XX
DE Permeabilising peptide of human JAM-2 SegID561.

XX
KW mucosal delivery; permeabilising peptide;

KW mucosal epithelial paracellular transport; epithelial junction;

KW epithelial membrane adhesive protein; junctional adhesion molecule; JAM;

KW occludin; claudin; sexual dysfunction; male erectile sexual dysfunction;

XX
OS female sexual dysfunction; human.

XX
OS Homo sapiens.

XX
PN WO2004003145-A2.

XX
PD 08-JAN-2004.

XX
PF 24-JUN-2003; 2003WO-US019994.

XX
PR 28-JUN-2002; 2002US-0392512P.

XX
PA (NAST-) NASTECH PHARM CO INC.

XX
PI Quay SC;

XX
DR WPI; 2004-091087/09.

XX
PT Composition comprising biologically active agent and permeabilizing

PT peptide that reversibly enhances mucosal epithelial paracellular

PT transport by modulating epithelial junctional structure and/or physiology

XX
PS in mammal.

XX
PS Disclosure; SEQ ID NO 561; 426bp; English.

XX
CC This invention relates to a novel composition comprising a biologically

CC active agent and mucosal delivery-enhancing effective amount of

CC permeabilising peptide that reversibly enhances mucosal epithelial

CC paracellular transport by modulating epithelial junctional structure

CC and/or physiology in a mammal. The agent of the invention inhibits

CC homotypic binding of epithelial membrane adhesive protein chosen

CC junctional adhesion molecule (JAM), occludin and claudin. The

CC biologically active agent is effective for treatment of sexual

CC dysfunction, for example male erectile sexual dysfunction or female

CC sexual dysfunction. The present sequence is that of a permeabilising

CC peptide of human JAM-2 which may be used during the production of the

CC composition of the invention.

XX
SQ Sequence 10 AA;

OY Query Match 35.8%; Score 29; DB 8; Length 10;

Best Local Similarity 62.5%; Pred. No. 4.1e+02;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 2 NDSPIQTD 9
|||:
1 NDVPLPTD 8

Search completed: December 12, 2005, 21:11:34

Job time : 114.667 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:30:45 / Search time 92.6667 Seconds
(without alignments)
67.634 Million cell updates/sec

Title: US-10-758-165A-1
Perfect score: 81
Sequence: 1 RNDSPIQDTQYTTTG 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 324073

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	US-10-758-165-1	Sequence 1, Appl1
2	53	65.4	15	US-10-758-165-7	Sequence 7, Appl1
3	48	59.3	15	US-10-758-165-2	Sequence 2, Appl1
4	41	50.6	15	US-10-758-165-3	Sequence 3, Appl1
5	34	42.0	15	US-10-052-788-4	Sequence 4, Appl1
6	32	33.5	10	US-10-432-234A-249	Sequence 249, App
7	32	33.5	10	US-10-432-234A-250	Sequence 250, App
8	31	38.3	14	US-10-155-693-29	Sequence 29, Appl
9	31	38.3	14	US-10-872-161-29	Sequence 29, Appl
10	29	35.8	10	US-10-462-452-433	Sequence 433, App
11	29	35.8	10	US-10-601-953-561	Sequence 561, App
12	29	35.8	10	US-10-322-266-434	Sequence 434, App
13	29	35.8	12	US-09-990-832C-108	Sequence 108, Appl
14	29	35.8	15	US-10-758-165-4	Sequence 4, Appl1
15	28	34.6	8	US-10-462-452-457	Sequence 457, App
16	28	34.6	8	US-10-601-953-566	Sequence 566, App
17	28	34.6	8	US-10-322-266-458	Sequence 458, App
18	28	34.6	10	US-10-475-045A-24	Sequence 24, Appl
19	28	34.6	11	US-10-936-237-18	Sequence 18, Appl
20	28	34.6	10	US-10-378-173-28	Sequence 28, Appl
21	27	33.3	10	US-10-281-479A-27	Sequence 27, Appl
22	27	33.3	10	US-10-275-180A-27	Sequence 27, Appl
23	27	33.3	10	US-10-286-132A-27	Sequence 27, Appl
24	27	33.3	10	US-10-432-234A-248	Sequence 248, App
25	27	33.3	13	US-10-948-707-846	Sequence 846, App
26	27	33.3	13	US-10-948-707-949	Sequence 949, App
27	27	33.3	4	US-10-080-608A-161	Sequence 161, App

28	27	33.3	15	4	US-10-370-685-70	Sequence 70, Appl
29	26	32.1	10	3	US-10-428-335-103	Sequence 103, App
30	26	32.1	10	4	US-09-572-404B-1728	Sequence 1728, App
31	26	32.1	10	4	US-10-149-138-543	Sequence 543, App
32	26	32.1	10	4	US-10-149-138-1265	Sequence 1265, App
33	26	32.1	10	4	US-10-149-138-1502	Sequence 1502, App
34	26	32.1	10	4	US-10-149-138-543	Sequence 543, App
35	26	32.1	10	4	US-10-149-138-1265	Sequence 1265, App
36	26	32.1	10	4	US-10-149-138-1502	Sequence 1502, App
37	26	32.1	10	4	US-10-432-234A-251	Sequence 251, App
38	26	32.1	10	5	US-10-475-045A-15	Sequence 15, Appl
39	26	32.1	12	4	US-10-078-968-5	Sequence 5, Appl1
40	26	32.1	12	4	US-10-279-991-13	Sequence 13, Appl1
41	26	32.1	13	5	US-10-948-707-1324	Sequence 1324, App
42	26	32.1	14	4	US-09-826-290-126	Sequence 126, App
43	26	32.1	14	4	US-10-264-302-71	Sequence 71, Appl
44	26	32.1	14	5	US-10-264-309-71	Sequence 71, Appl
45	26	32.1	15	3	US-09-903-327A-19	Sequence 19, Appl

ALIGNMENTS

```

RESULT 1
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1

Query Match      100.0%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RNDSPIQDTQYTTTG 15
Db      1 RNDSPIQDTQYTTTG 15

RESULT 2
US-10-758-165-7
; Sequence 7, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-7

Query Match      65.4%; Score 53; DB 5; Length 15;

```

Best Local Similarity 57.1%; Pred. No. 0.035;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 RNDSP1QTDQYTTT 14
|||:|:|:|:
Db 1 RNDAPVQADRHSTT 14

RESULT 3
US-10-758-165-2
; Sequence 2, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758.165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-2

Query Match 59.3%; Score 48; DB 5; Length 15;
Best Local Similarity 61.5%; Pred. No. 0.26;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSP1QTDQYTTT 14
|||:|:|:|:
Db 2 NDSPVREQQAAT 14

RESULT 4
US-10-758-165-3
; Sequence 3, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758.165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-3

Query Match 50.6%; Score 41; DB 5; Length 15;
Best Local Similarity 64.3%; Pred. No. 4.2;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNDSP1QTDQYTTT 14
|||:|:|:|:
Db 1 RNNVLIQTDQQAAT 14

RESULT 5
US-10-052-788-4
; Sequence 4, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
; APPLICANT: Gerahwin, Laurel J.
; APPLICANT: Pettigrew, Howard David

; APPLICANT: Kalina, Warren V.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; TITLE OF INVENTION: Induction of Anti-IGF Antibodies
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052.788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:epitope peptide
; OTHER INFORMATION: P4, early portion of C4 of equine IGF epsilon
US-10-052-788-4

Query Match 42.0%; Score 34; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 IQTDQYTTT 14
|||:|:|:|:
Db 1 IQTDQQAAT 9

RESULT 6
US-10-432-234A-249
; Sequence 249, Application US/10432234A
; Publication No. US20040161846A1
; GENERAL INFORMATION:
; APPLICANT: Bioca Scientific Management Pty Ltd
; TITLE OF INVENTION: A method of expression and agents identified thereby
; FILE REFERENCE: 12084720/TDO
; CURRENT APPLICATION NUMBER: US/10/432.234A
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US 60/252767
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 574
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 249
; LENGTH: 10
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-10-432-234A-249

Query Match 39.5%; Score 32; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSP1QTDQ 10
|||:|:|:|:
Db 2 NDMPITNDQ 10

RESULT 7
US-10-432-234A-250
; Sequence 250, Application US/10432234A
; Publication No. US20040161846A1
; GENERAL INFORMATION:
; APPLICANT: Bioca Scientific Management Pty Ltd
; TITLE OF INVENTION: A method of expression and agents identified thereby
; FILE REFERENCE: 12084720/TDO
; CURRENT APPLICATION NUMBER: US/10/432.234A
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US 60/252767
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 574
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 250
; LENGTH: 10

TYPE: PRT
ORGANISM: respiratory syncytial virus
US-10-432-234A-250

Query Match 39.5%; Score 32; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTDQ 10
|||
1 NDMPITNDQ 9

RESULT 8
US-10-155-693-29
Sequence 29, Application US/10155693
Publication No. US20030175876A1
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUQIAN
APPLICANT: MEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/10/155,693
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US/08/837,199
PRIOR FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 14
TYPE: PRT
ORGANISM: RAT
US-10-155-693-29

Query Match 38.3%; Score 31; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PIQTDQYTTT 14
|||
4 PVQTTTATTT 13

RESULT 9
US-10-872-161-29
Sequence 29, Application US/10872161
Publication No. US20040235714A1
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUQIAN
APPLICANT: MEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401D
CURRENT APPLICATION NUMBER: US/10/872,161
CURRENT FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: US/08/866,354
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
PRIOR APPLICATION NUMBER: US 08/837,199
PRIOR FILING DATE: 1997-04-14
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.2
SEQ ID NO 29
LENGTH: 14
TYPE: PRT

ORGANISM: RAT
US-10-872-161-29

Query Match 38.3%; Score 31; DB 5; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PIQTDQYTTT 14
|||
4 PVQTTTATTT 13

RESULT 10
US-10-462-452-433
Sequence 433, Application US/10462452
Publication No. US20040037809A1
GENERAL INFORMATION:
APPLICANT: Quay, Steven
APPLICANT: El Shafy, Mohammed Abd
APPLICANT: Gupta, Malini
APPLICANT: de Meireles, Jorge
TITLE OF INVENTION: Compositions and Methods for Enhanced
TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
FILE REFERENCE: 02-0205
CURRENT APPLICATION NUMBER: US/10/462,452
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/393,066
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 790
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 433
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-462-452-433

Query Match 35.8%; Score 29; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTD 9
|||
1 NDVPLPTD 8

RESULT 11
US-10-601-953-561
Sequence 561, Application US/10601953
Publication No. US2004007540A1
GENERAL INFORMATION:
APPLICANT: Quay, Steven C.
TITLE OF INVENTION: Compositions and Methods For Modulating Physiology Of Epithelial
TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
FILE REFERENCE: 02-0305
CURRENT APPLICATION NUMBER: US/10/601,953
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: 60/392,512
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 900
SOFTWARE: PatentIn version 3.2
SEQ ID NO 561
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-601-953-561

Query Match 35.8%; Score 29; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDSPIQTD 9
|| : ||
Db 1 NDVPLPTD 8

RESULT 12
US-10-322-266-434
; Sequence 434, Application US/10322266
; Publication No. US20040115135A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide
; TITLE OF INVENTION: YY And Methods For Treating And Preventing Obesity
; FILE REFERENCE: NPEI0567
; CURRENT APPLICATION NUMBER: US/10/322,266
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 797
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 434
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-322-266-434

Query Match 35.8%; Score 29; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDSPIQTD 9
|| : ||
Db 1 NDVPLPTD 8

RESULT 13
US-09-990-832C-108
; Sequence 108, Application US/09990832C
; Publication No. US20030149235A1
; GENERAL INFORMATION:
; APPLICANT: University Court of the University of Glasgow
; TITLE OF INVENTION: Targeting peptides
; FILE REFERENCE: PC/MC/JM/F11910US
; CURRENT APPLICATION NUMBER: US/09/990,832C
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting peptide sequence
US-09-990-832C-108

Query Match 35.8%; Score 29; DB 3; Length 12;
Best Local Similarity 62.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 SPIOTDQY 11
: || : ||
Db 2 TPIDSTQY 9

RESULT 14
US-10-758-165-4
; Sequence 4, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165

; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Ovis aries
US-10-758-165-4

Query Match 35.8%; Score 29; DB 5; Length 15;
Best Local Similarity 42.9%; Pred. No. 5e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 RNDSPIDQYTTT 14
|| : || : ||
Db 1 RNKELMREGQHTTT 14

RESULT 15
US-10-462-452-457
; Sequence 457, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-020US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-457

Query Match 34.6%; Score 28; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNDSPIDQY 8
|| : || : ||
Db 1 RNDVPLPT 8

Search completed: December 12, 2005, 21:05:28
Job time : 93.6667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 20:20:00 ; Search time 27 Seconds
(without alignments)
45.931 Million cell updates/sec

Title: US-10-758-165a-1
Perfect score: 81
Sequence: 1 RNDSPQDTQYTTTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 186887

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5 COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/6 COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/7 COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/8 COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/9 COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/10 COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	39.5	13	6	5223254-6
2	31	38.3	14	2	US-08-837-199A-29
3	27	33.3	9	2	US-09-341-982-75
4	27	33.3	12	1	US-08-479-233-8
5	27	33.3	12	4	PCT-US93-00643-8
6	27	33.3	13	1	US-08-209-525-50
7	27	33.3	15	2	US-09-914-259-161
8	26	32.1	12	1	US-08-423-441-4
9	26	32.1	12	2	US-09-514-739-5
10	26	32.1	12	2	US-09-517-866-13
11	26	32.1	15	2	US-10-378-707-1
12	25	30.9	8	1	US-08-413-708B-4
13	25	30.9	11	1	US-08-077-939-2
14	25	30.9	11	1	US-08-461-599-2
15	25	30.9	11	1	US-07-949-812-24
16	25	30.9	11	1	US-08-461-621-2
17	25	30.9	11	1	US-08-465-334-2
18	25	30.9	12	1	US-07-756-230-12
19	25	30.9	12	1	US-08-634-060-37
20	25	30.9	12	2	US-09-534-717-212
21	25	30.9	13	1	US-08-218-608-5
22	25	30.9	13	1	US-08-162-081B-7
23	25	30.9	13	1	US-08-780-872-7
24	25	30.9	13	1	US-08-747-137-23
25	25	30.9	13	2	US-09-205-680A-9
26	25	30.9	13	2	US-09-085-957-7
27	25	30.9	13	2	US-09-623-548A-1363

28	25	30.9	13	2	US-09-657-276-1363	Sequence 1363, App1
29	25	30.9	14	2	US-09-252-404A-15	Sequence 15, App1
30	25	30.9	14	2	US-08-851-567B-4	Sequence 4, App1
31	25	30.9	15	1	US-08-945-168-117	Sequence 117, App1
32	25	30.9	15	2	US-08-743-168B-17	Sequence 17, App1
33	25	30.9	15	2	US-09-306-998-4	Sequence 4, App1
34	25	30.9	15	2	US-09-233-086-6	Sequence 6, App1
35	25	30.9	15	2	US-09-117-860-11	Sequence 11, App1
36	25	30.9	15	4	PCT-US96-10435-17	Sequence 17, App1
37	24.5	30.2	14	1	US-08-162-403B-26	Sequence 26, App1
38	24.5	30.2	15	6	5204326-74	Patent No. 5204326
39	24	29.6	7	2	US-09-147-993-15	Sequence 15, App1
40	24	29.6	9	2	US-09-341-982-73	Sequence 73, App1
41	24	29.6	9	2	US-09-341-982-74	Sequence 74, App1
42	24	29.6	10	2	US-08-986-659B-16	Sequence 16, App1
43	24	29.6	12	2	US-09-349-661-4	Sequence 4, App1
44	24	29.6	12	2	US-09-341-982-79	Sequence 79, App1
45	24	29.6	13	2	US-09-680-728-9	Sequence 9, App1

ALIGNMENTS

RESULT 1
5223254-6
Patent No. 5223254
APPLICANT: PARADISO, PETER R.; HILDBRETH, STEPHEN W.; HU, BRANDA T.; MARTIN-GALLARDO, ANTONIA; ARUMUGHAM, RASAPPA
TITLE OF INVENTION: RESPIRATORY SYNCTIAL VIRUS VACCINES
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/247,017
FILING DATE: 20-SEP-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 102,180
FILING DATE: 29-SEP-1987
SEQ ID NO: 6
LENGTH: 13
5223254-6

Query Match 39.5%; Score 32; DB 6; Length 13;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQDTQ 10
DB 2 NDMPIITNDQ 10

RESULT 2
US-08-837-199A-29
Sequence 29, Application US/08837199A
Patent No. 6455277
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUOJIAN
APPLICANT: MEN, DUNZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/08/837,199A
CURRENT FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.1
SEQ ID NO 29
LENGTH: 14
TYPE: PRT
ORGANISM: RAT
US-08-837-199A-29

Query Match 38.3%; Score 31; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 5 PLOTQDTT 14
:|:|:|
DB 4 PVQTTATT 13

RESULT 3
US-09-341-982-75
; Sequence 75, Application US/09341982
; Patent No. 6558671
; GENERAL INFORMATION:
; APPLICANT: SLINGLUFF, Craig L.
; APPLICANT: HUNT, Donald F.
; APPLICANT: ENGELHARD, Victor H.
; APPLICANT: KITTELSEN, David
; TITLE OF INVENTION: CYSTEINE-DEPLETED PEPTIDES RECOGNIZED BY A3-RESTRICTED
; TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES THEREFOR
; FILE REFERENCE: SLINGLUFF=3B
; CURRENT FILING DATE: 1999-09-20
; EARLIER FILING DATE: 1998-01-29
; EARLIER FILING DATE: 1997-01-31
; EARLIER FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 75
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fragment of
US-09-341-982-75

Query Match 33.3%; Score 27; DB 2; Length 9;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 SPIQTDQY 11
:|:|:|
DB 2 SDISTDEY 9

RESULT 4
US-08-479-233-8
; Sequence 8, Application US/08479233
; Patent No. 559679
; GENERAL INFORMATION:
; APPLICANT: Baylink, David J.
; APPLICANT: Linkhart, Susan
; TITLE OF INVENTION: AMINO PROCOLLAGEN 1(I) PEPTIDE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Stuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,233
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/829,142
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14508-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-479-233-8

Query Match 33.3%; Score 27; DB 1; Length 12;
Best Local Similarity 58.3%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 2 NDSPIQTDQY 13
:|:|:|
DB 3 SESE--TDQETT 12

RESULT 5
PCT-US93-00643-8
; Sequence 8, Application PC/TUS9300643
; GENERAL INFORMATION:
; APPLICANT: Baylink, David J.
; APPLICANT: Linkhart, Susan
; TITLE OF INVENTION: AMINO PROCOLLAGEN 1(I) PEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Stuart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/00643
; FILING DATE: 19930125
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14508-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-00643-8

Query Match 33.3%; Score 27; DB 4; Length 12;
Best Local Similarity 58.3%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 2 NDSPIQTDQY 13
:|:|:|

Db 3 SESP--TDOETT 12

RESULT 6

US-08-209-525-50
; Sequence 50, Application US/08209525

; Patent No. 5571681

; GENERAL INFORMATION:

; APPLICANT: Janda, Kim D.

; TITLE OF INVENTION: Chemical Event Selection By Suicide
; Substrate Conjugates

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute
; STREET: 10666 No. 5571681th Torrey Pines Road, TPC-8

; CITY: La Jolla

; STATE: California

; COUNTRY: US

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/209,525

; FILING DATE: 10-MAR-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Lewis, Donald G.

; REGISTRATION NUMBER: 28,636

; REFERENCE/DOCKET NUMBER: SCRF 408.0

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-554-2937

; TELEFAX: 619-554-6312

; INFORMATION FOR SEQ ID NO: 50:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

US-08-209-525-50

Query Match 33.3%; Score 27; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 10 QYTTT 14
| | | | |
| | | | |
Db 2 QYTTT 6

RESULT 7

US-09-914-259-161
; Sequence 161, Application US/09914259

; Patent No. 6495336

; GENERAL INFORMATION:

; APPLICANT: Makowski, Lee

; APPLICANT: Hyman, Paul
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES

; FILE REFERENCE: 8471-010-999

; CURRENT APPLICATION NUMBER: US/09/914,259

; NUMBER OF SEQ ID NOS: 180

; SOFTWARE: FaestSeq for Windows Version 4.0

; SEQ ID NO 161

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Murine sarcoma virus

US-09-914-259-161

Query Match 33.3%; Score 27; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;Qy 9 DQYTTG 15
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| | | | |
Db 8 DQYRTG 14

RESULT 8

US-08-423-441-4
; Sequence 4, Application US/08423441

; Patent No. 5529926

; GENERAL INFORMATION:

; APPLICANT: MAAT, JAN

; APPLICANT: MUSTERS, WOUTER

; APPLICANT: STAM, HEIN

; APPLICANT: SCHAP, PETER J.

; APPLICANT: VAN DE VONDERVOORT, PETER J.

; APPLICANT: VISSER, JACOB

; TITLE OF INVENTION: CLONING AND EXPRESSION OF DNA ENCODING A

; TITLE OF INVENTION: RIPENING FORM OF A POLYPEPTIDE HAVING SULFHYDRYL OXIDASE

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

; STREET: 1100 NEW YORK AVENUE, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/423,441

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/044,620

; FILING DATE: 09-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: KOKULIS, PAUL N.

; REGISTRATION NUMBER: 16773

; REFERENCE/DOCKET NUMBER: 202744/T7019(V)

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3000

; TELEFAX: 202-822-0944

; TELEEX: 248453CUSH

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

US-08-423-441-4

Query Match 32.1%; Score 26; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;Qy 3 DSPQTDQYT 12
| : | | | |
| : | | | |
Db 2 DNKIDTDTYT 11

RESULT 9

US-09-514-739-5
; Sequence 5, Application US/09514739

FILING DATE: 16-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: GOES-3A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-413-708B-4

Query Match 30.9%; Score 25; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 IQDPQYT 12
:|:|:|:
Db 2 VTIDNYT 8

RESULT 13
US-08-077-939-2
Sequence 2, Application US/08077939
Patent No. 5521088
GENERAL INFORMATION:
APPLICANT: FUJII, Toshio
APPLICANT: IWAMATSU, Akihiro
APPLICANT: YOSHIMOTO, Hiroyuki
APPLICANT: MINETOKI, Toshitaka
APPLICANT: BOGAKI, Takayuki
APPLICANT: NAGASAWA, Naoshi
TITLE OF INVENTION: ALCOHOL ACETYLTTRANSFERASE GENES AND USE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,939
FILING DATE: 18-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: JP 184328/1992
FILING DATE: 18-JUN-1992
APPLICATION DATA:
PRIOR APPLICATION NUMBER: JP 62997/1993
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/101 KYPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid

TOPOLOGY: linear
US-08-077-939-2
Query Match 30.9%; Score 25; DB 1; Length 11;
Best Local Similarity 33.3%; Pred. No. 4.4e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNDSPIQTD 9
:|:|:|:
Db 1 KNQAPVQGE 9

RESULT 14
US-08-461-599-2
Sequence 2, Application US/08461599
Patent No. 5558777
GENERAL INFORMATION:
APPLICANT: FUJII, Toshio
APPLICANT: IWAMATSU, Akihiro
APPLICANT: YOSHIMOTO, Hiroyuki
APPLICANT: MINETOKI, Toshitaka
APPLICANT: BOGAKI, Takayuki
APPLICANT: NAGASAWA, Naoshi
TITLE OF INVENTION: ALCOHOL ACETYLTTRANSFERASE GENES AND USE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,599
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,939
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 62997/1993
FILING DATE: 26-FEB-1993
APPLICATION DATA:
PRIOR APPLICATION NUMBER: JP 184328/1992
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/105 KYPA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-461-599-2

Query Match 30.9%; Score 25; DB 1; Length 11;
Best Local Similarity 33.3%; Pred. No. 4.4e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNDSPIQTD 9
:|:|:|:
Db 1 KNQAPVQGE 9

RESULT 15
US-07-949-812-24
; Sequence 24, Application US/07949812
; Patent No. 5668007
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: RECOMBINANT 21KD COCOA PROTEIN AND PRECURSOR
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/949,812
; FILING DATE: 27-JAN-1993
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-949-812-24

Query Match 30.9%; Score 25; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 4.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 DSPIC1D 9
: ||: ||
Db 2 NSPLD1D 8

Search completed: December 12, 2005, 21:00:45
Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:00:56 ; Search time 4.66667 Seconds
(without alignments)
17.950 Million cell updates/sec

Title: US-10-758-165A-1

Perfect score: 81

Sequence: 1 RNDSPICQDTTGTG 15

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqe, 5584426 residues

Total number of hits satisfying chosen parameters: 8641

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA New:*
1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	30.9	13	6	US-10-969-314-9
2	23	28.4	15	6	US-10-503-575-78
3	22	27.2	6	7	US-11-176-868-2
4	22	27.2	7	7	US-11-056-825-11
5	22	27.2	12	6	US-10-997-066-26
6	21	25.9	10	7	US-11-105-268-1
7	21	25.9	12	6	US-10-467-657-8983
8	21	25.9	14	6	US-10-524-643-51
9	21	25.9	15	7	US-11-022-562-119
10	20	24.7	7	7	US-11-096-706-58
11	20	24.7	8	6	US-10-989-226-49
12	20	24.7	9	6	US-10-989-226-50
13	20	24.7	9	6	US-10-491-096-94
14	20	24.7	9	7	US-11-010-748A-473
15	20	24.7	9	7	US-11-010-748A-479
16	20	24.7	10	6	US-10-491-096-95
17	20	24.7	12	7	US-11-016-706-14
18	20	24.7	13	6	US-10-511-559-117
19	20	24.7	13	6	US-10-511-559-118
20	20	24.7	13	6	US-10-511-559-104
21	20	24.7	13	6	US-10-511-559-305
22	20	24.7	13	6	US-10-511-559-628
23	20	24.7	15	6	US-10-511-559-77
24	20	24.7	15	7	US-11-022-562-120
25	19	23.5	9	7	US-11-010-748A-482

26	19	23.5	9	7	US-11-097-864-17	Sequence 17, Appl
27	19	23.5	9	7	US-11-097-912-17	Sequence 17, Appl
28	19	23.5	10	7	US-11-097-864-53	Sequence 53, Appl
29	19	23.5	10	7	US-11-097-912-53	Sequence 53, Appl
30	19	23.5	13	6	US-10-511-559-429	Sequence 429, Appl
31	19	23.5	13	6	US-10-511-559-430	Sequence 430, Appl
32	19	23.5	13	6	US-10-511-559-700	Sequence 700, Appl
33	19	23.5	13	6	US-10-511-559-702	Sequence 702, Appl
34	19	23.5	13	6	US-10-511-559-802	Sequence 802, Appl
35	19	23.5	13	6	US-10-511-559-803	Sequence 803, Appl
36	19	23.5	13	6	US-10-511-559-1080	Sequence 1080, Appl
37	19	23.5	13	6	US-10-989-226-22	Sequence 22, Appl
38	19	23.5	13	7	US-11-054-515-3054	Sequence 3054, Appl
39	19	23.5	14	6	US-10-494-781-12	Sequence 12, Appl
40	19	23.5	14	6	US-10-939-890-65	Sequence 65, Appl
41	19	23.5	14	7	US-11-054-515-2445	Sequence 2445, Appl
42	19	23.5	15	6	US-10-614-559-19	Sequence 19, Appl
43	19	23.5	15	6	US-10-989-226-54	Sequence 54, Appl
44	18.5	22.8	11	6	US-10-467-657-8862	Sequence 8862, Appl
45	18	22.2	7	6	US-10-467-657-7712	Sequence 7712, Appl

ALIGNMENTS

RESULT 1
US-10-969-314-9
; Sequence 9, Application US/10969314
; Publication No. US20050249719A1
; GENERAL INFORMATION:
; APPLICANT: SHAN, LU
; APPLICANT: BETHUNE, MICHAEL
; APPLICANT: KHOSLA, CHARITAN
; APPLICANT: GASS, JONATHAN
; APPLICANT: PYLE, GAIL G.
; APPLICANT: ISAACS, INDU
; APPLICANT: STROHMEIER, GREGG
; APPLICANT: STROHMEIER, GREGG
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR
; FILE REFERENCE: STAN-361
; CURRENT APPLICATION NUMBER: US/10/969,314
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: 60/565,668
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 10/367,405
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Trifolium aestivum
US-10-969-314-9

Query Match 30.9%; Score 25; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 27;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 IQDQYTTG 15
|:|:|:|:|
Db 4 IEDNEYTARG 13

RESULT 2

US-10-503-575-78
; Sequence 78, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Drifhout, Jan Mouter
; APPLICANT: van Veele, Petrus Antonius
; APPLICANT: Koning, Rits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-78

Query Match 28.4%; Score 23; DB 6; Length 15;
Best Local Similarity 57.1%; Pred. No. 75;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 PLOTDOY 11
|||
|:
Db 3 PLOTDOF 9

RESULT 3
US-11-176-868-2
; Sequence 2, Application US/11176868
; Publication No. US20050245454A1
; GENERAL INFORMATION:
; APPLICANT: Goldstein, Gideon
; TITLE OF INVENTION: Methods and Compositions for Impairing Multiplication of HIV-1
; FILE REFERENCE: GGP3USA
; CURRENT APPLICATION NUMBER: US/11/176,868
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: US/10/323,013
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/10/114,176
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-176-868-2

Query Match 27.2%; Score 22; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNDSP 5
|||
|:
Db 2 RGDSP 6

RESULT 4
US-11-056-825-11
; Sequence 11, Application US/11056825
; Publication No. US20050255109A1
; GENERAL INFORMATION:
; APPLICANT: Felding-Habermann, Brunhilde
; APPLICANT: Janda, Kim D.
; APPLICANT: Saven, Alan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS

; FILE REFERENCE: SGRP-0042
; CURRENT APPLICATION NUMBER: US/11/056,825
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/626,726
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/544,807
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-056-825-11

Query Match 27.2%; Score 22; DB 7; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNDSP 5
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|:
Db 2 RGDSP 6

RESULT 5
US-10-997-066-26
; Sequence 26, Application US/10997066
; Publication No. US20050244891A1
; GENERAL INFORMATION:
; APPLICANT: GRAHAM, RONALD J.
; APPLICANT: LEE, HONGYE
; APPLICANT: SUN, LINDA G.
; TITLE OF INVENTION: LIGAND-CONTAINING MICELLES AND USES THEREOF
; FILE REFERENCE: 375461-011US
; CURRENT APPLICATION NUMBER: US/10/997,066
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/525,492
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/628,509
; PRIOR FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 26
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: Ser(PO4)
US-10-997-066-26

Query Match 27.2%; Score 22; DB 6; Length 12;
Best Local Similarity 44.4%; Pred. No. 89;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNDSP1QTD 9
|||
|:
Db 1 RHSSPFOSE 9

RESULT 6
US-11-105-268-1
; Sequence 1, Application US/11105268
; Publication No. US20050260204A1
; GENERAL INFORMATION:
; APPLICANT: Allan, Christian
; TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF

```

; FILE REFERENCE: 10271-126-999
; CURRENT APPLICATION NUMBER: US/11/105,268
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: 60/561,845
; PRIOR FILING DATE: 2004-04-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PR
; ORGANISM: Homo sapiens
; US-11-105-268-1

Query Match
Best Local Similarity 25.9%; Score 21; DB 7; Length 10;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YTTTG 15
DB 2 YTTTG 6

RESULT 7
US-10-467-657-8983
; Sequence 8983, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8983
; LENGTH: 12
; TYPE: PR
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-8983

Query Match
Best Local Similarity 25.9%; Score 21; DB 6; Length 12;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 OTDOYTTT 14
DB 4 RTQYTTT 11

RESULT 8
US-10-524-643-51
; Sequence 51, Application US/10524643
; Publication No. US20050261215A1
; GENERAL INFORMATION:
; APPLICANT: GARREN, Heidi
; APPLICANT: HO, Peggy P.
; APPLICANT: STEINMAN, Lawrence
; TITLE OF INVENTION: METHODS AND IMMUNE MODULATORY NUCLEIC ACID COMPOSITIONS FOR
; TITLE OF INVENTION: PREVENTING AND TREATING DISEASE
; FILE REFERENCE: 022259-001010US
; CURRENT APPLICATION NUMBER: US/10/524,643
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: PCT/US2003/037157
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 296
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 51
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; LENGTH: 14
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide antigen
; US-10-524-643-51

Query Match
Best Local Similarity 25.9%; Score 21; DB 6; Length 14;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 IQTDQYT 12
DB 7 IETDKAT 13

RESULT 9
US-11-022-562-119
; Sequence 119, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Rupprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 15
; TYPE: PR
; ORGANISM: Human Immunodeficiency Virus
; US-11-022-562-119

Query Match
Best Local Similarity 25.9%; Score 21; DB 7; Length 15;
Matches 4; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 RNDSPIQTDQYTT 14
DB 2 QKQEPIDKELYPLT 15

RESULT 10
US-11-096-706-58
; Sequence 58, Application US/11096706
; Publication No. US20050245476A1
; GENERAL INFORMATION:
; APPLICANT: Sangamo Biosciences, Inc.
; APPLICANT: Collingwood, Trevor
; TITLE OF INVENTION: Treatment of Neuropathic Pain with Zinc Finger Proteins
; FILE REFERENCE: 019496-008220US
; CURRENT APPLICATION NUMBER: US/11/096,706
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 60/560,535
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/576,757
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 7
; TYPE: PR
; ORGANISM: Artificial
; OTHER INFORMATION: Chemically synthesized peptide (zinc finger protein recognition
; OTHER INFORMATION: Region)
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US-11-096-706-58

Query Match 24.7%; Score 20; DB 7; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNDSP1 6
Db 1 RNDNR1 6

RESULT 11

US-10-989-226-49
; Sequence 49, Application US/10989226
; Publication No. US20050255491A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank D.
; APPLICANT: Meng, Xun
; APPLICANT: Afeyan, Noubar B.
; TITLE OF INVENTION: SMALL MOLECULE AND PEPTIDE ARRAYS AND
; FILE REFERENCE: EPTM-P01-005
; CURRENT APPLICATION NUMBER: US/10/989,226
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,530
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/532,687
; PRIOR FILING DATE: 2003-12-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-989-226-49

Query Match 24.7%; Score 20; DB 6; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NDSP 5
Db 2 NDAP 5

RESULT 12

US-10-989-226-50
; Sequence 50, Application US/10989226
; Publication No. US20050255491A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank D.
; APPLICANT: Meng, Xun
; APPLICANT: Afeyan, Noubar B.
; TITLE OF INVENTION: SMALL MOLECULE AND PEPTIDE ARRAYS AND
; FILE REFERENCE: EPTM-P01-005
; CURRENT APPLICATION NUMBER: US/10/989,226
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,530
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/532,687
; PRIOR FILING DATE: 2003-12-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-989-226-50

Query Match 24.7%; Score 20; DB 6; Length 8;

Best Local Similarity 75.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NDSP 5
Db 2 NDAP 5

RESULT 13

US-10-491-096-94
; Sequence 94, Application US/10491096
; Publication No. US20050267020A1
; GENERAL INFORMATION:
; APPLICANT: FAURE, OLIVIER
; APPLICANT: KOSMATOPOULOS, KONSTANTINOS
; TITLE OF INVENTION: POLYPEPTIDES DERIVED FROM INDUCIBLE HSP70 AND PHARMACEUTICAL
; FILE REFERENCE: 0508-1098
; CURRENT APPLICATION NUMBER: US/10/491,096
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: PCT/EP02/10821
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: FR 01402496.2
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-491-096-94

Query Match 24.7%; Score 20; DB 6; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+04;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 DSPICDT 9
Db 1 DAVQSD 7

RESULT 14

US-11-010-748A-473
; Sequence 473, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: WOLZ, Heidrun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 473
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 471
US-11-010-748A-473

Query Match 24.7%; Score 20; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 10 QYTTG 15

Db :||:|
3 RYTSAG 8

RESULT 15
US-11-010-748A-479

; Sequence 479, Application US/11010748A
; Publication No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOHL, Heidrun
; APPLICANT: SCHARF, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 479
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 471
US-11-010-748A-479

Query Match 24.7%; Score 20; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. NO. 2.8e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 QYTTTG 15
:||:|
Db 3 RYTSAG 8

Search completed: December 12, 2005, 21:17:40
Job time : 4.66667 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:05:42 / Search time 18 Seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-10-758-165A-1
Perfect score: 81
Sequence: 1 RNDSPRQDQYTTTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	34.6	14	2 PH1306	Ig heavy chain DJ
2	26	32.1	11	2 S71304	amine oxidase (cop
3	24	29.6	14	2 PS0249	porin - rice (stra
4	22	27.2	14	2 PH1305	Ig heavy chain DJ
5	21	25.9	11	2 PS0259	39k protein 3225 -
6	21	25.9	13	2 H56046	urinary tract ston
7	20.5	25.3	13	2 S47376	T-cell antigen rec
8	20	24.7	11	2 S04875	nifs protein - Bra
9	20	24.7	11	2 A26120	6-phosphofructokin
10	20	24.7	11	2 S05002	corazonin - Americ
11	20	24.7	12	2 PH0771	T-cell receptor be
12	20	24.7	13	2 PN0125	serine proteinase
13	20	24.7	14	2 PH1347	Ig heavy chain DJ
14	19	23.5	10	1 GMROL2	leucosulfakinin-II
15	19	23.5	10	2 B60656	leucosulfakinin II
16	19	23.5	11	2 S58244	pyrrolquinoline q
17	19	23.5	13	2 B61458	Ig kappa chain V-I
18	19	23.5	13	2 A61458	Ig kappa chain V-I
19	19	23.5	14	2 PH1705	Ig heavy chain V r
20	19	23.5	14	2 S50900	chlorophyll a/b-bl
21	19	23.5	15	2 S42741	ubiquinol-cytochro
22	19	23.5	7	2 I48086	Ig H chain V-D-J r
23	18	22.2	10	2 S43625	DNA topoisomerase
24	18	22.2	12	2 A61332	cytochrome-c oxida
25	18	22.2	12	2 B58502	Na+/K+-exchanging
26	18	22.2	12	2 A61503	43.2K bile stome p
27	18	22.2	12	2 A33660	sterol carrier pro
28	18	22.2	13	2 A33660	osteoclast functio
29	18	22.2	13	2 PT0331	Ig heavy chain CRD

30	18	22.2	14	2 PT0232	Ig heavy chain CRD
31	18	22.2	15	2 S32677	nitrogenase cofact
32	18	22.2	15	2 PA0097	starch phosphoryla
33	18	22.2	15	2 S29485	GTP-binding protei
34	18	22.2	15	2 S72432	epoxypropan isomer
35	17	21.0	8	2 I57018	gene C1tr protein
36	17	21.0	9	2 PT0247	Ig heavy chain CRD
37	17	21.0	9	2 PL0139	carbon-monoxide de
38	17	21.0	10	2 B61512	variant surface gl
39	17	21.0	11	2 C53652	rh1r protein - pre
40	17	21.0	11	2 A28806	acidic prolina-ric
41	17	21.0	11	2 S42449	anti protein - pha
42	17	21.0	12	2 S25485	transcription fact
43	17	21.0	12	2 PT0228	Ig heavy chain CDR
44	17	21.0	12	2 JU0356	cycloleounrulin -
45	17	21.0	12	2 PN0170	alcohol dehydrogen

ALIGNMENTS

RESULT 1

PH1306
Ig heavy chain DJ region (clone C96-100) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1306
R:Masserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1306
A:Molecule type: DNA
A:Residues: 1-14 <WAS>
A:Cross-references: UNIPARC:UPI000017C253
C:Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 14;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YTTTG 15
DB 6 YTTTG 10

RESULT 2

S71304
amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragment)
C:Species: Aspergillus niger
C:Date: 12-Feb-1998 #sequence_revision 01-May-1998 #text_change 09-Jul-2004
C:Accession: S71304
R:Frederic, I.; Tamaki, H.; Ichida, H.; Pec, P.; Luhova, L.; Tsuno, H.; Halata, M.; Asanc
Eur. J. Biochem. 237, 255-265, 1996
A:Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the myc
A:Reference number: S71303; MUID:96203933; PMID:8620882
A:Accession: S71304

A:Molecule type: protein

A:Residues: 1-11 <PRE>

A:Cross-references: UNIPROT:Q7M504; UNIPARC:UPI000017B3B7

C:Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquinine

Query Match
Best Local Similarity 32.1%; Score 26; DB 2; Length 11;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTD 9
DB 1 NDSPIALND 8

RESULT 3

PS0249

porin - rice (strain Nihonbare) (fragment)
C/Species: Oryza sativa (rice)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C/Accession: PS0249
R/Tsugita, A.
submitted to JIPID, April 1993
A/Reference number: PS0206
A/Accession: PS0249
A/Molecule type: protein
A/Residues: 1-14 <TSU>
A/Cross-references: UNIPROT:Q7M1U8; UNIPARC:UPI000017B118
A/Experimental source: callus

Query Match 29.6%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 8 TDQYTTG 15
DB 5 TDDHTANG 12

RESULT 4
PH1305
IG heavy chain DJ region (clone C85-1B) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1305
R/Maserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Royera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1305
A/Molecule type: DNA
A/Residues: 1-14 <MAS>
A/Cross-references: UNIPARC:UPI000017C252
C/Keywords: heterotrimer; Immunoglobulin

Query Match 27.2%; Score 22; DB 2; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 6 IQTDQYTT 13
DB 2 ILTGYYTT 9

RESULT 5
PS0259
39K protein 3225 - rice (strain Nihonbare) (fragment)
C/Species: Oryza sativa (rice)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C/Accession: PS0259
R/Tsugita, A.; Kamo, M.
submitted to JIPID, April 1993
A/Reference number: PS0209
A/Accession: PS0259
A/Molecule type: protein
A/Residues: 1-11 <TSU>
A/Cross-references: UNIPARC:UPI000017B102
A/Experimental source: callus
C/Comment: molecular weight 39K, pI 5.7.

Query Match 25.9%; Score 21; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 3 DSPIQTD 9
DB 5 DGPIVAD 11

RESULT 6

H56046
urinary tract stone matrix protein 10, 42K - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C/Accession: H56046
R/Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.
submitted to the Protein Sequence Database, February 1995
A/Description: Isolation, Characterization and sequence of stone proteins.
A/Reference number: A56046
A/Accession: H56046
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-13 <BIN>
A/Cross-references: UNIPROT:Q7M4P7; UNIPARC:UPI000017C406

Query Match 25.9%; Score 21; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 2 NDSPIQTD 9
DB 6 NDLAETD 13

RESULT 7
S47376
T-cell antigen receptor VJ junction beta chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C/Accession: S47376
R/Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A/Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce
A/Reference number: S47355
A/Accession: S47376
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-13 <LEH>
A/Cross-references: UNIPARC:UPI0000116687; EMBL:Z35702; NID:G527497; PIDN:CMA84771.1; PII
C/Keywords: T-cell receptor

Query Match 25.3%; Score 20.5; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
OY 4 SPIQTD-QY 11
DB 4 SPRSTDYQY 12

RESULT 8
S04875
nifs protein - Bradyrhizobium japonicum (fragment)
C/Species: Bradyrhizobium japonicum
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: S04875
R/Beiling, S.
submitted to the EMBL Data Library, December 1988
A/Reference number: S04873
A/Accession: S04875
A/Molecule type: DNA
A/Residues: 1-11 <EBE>
A/Cross-references: UNIPROT:P37030; UNIPARC:UPI000016E719; EMBL:X13691; NID:G39544; PIDN
A/Genetics: nifs
A/Start codon: GTG

Query Match 24.7%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 2 NDSPIQTD 9

Db 4 NRAPYLID 11

RESULT 9

A26120 6-phosphofructokinase (EC 2.7.1.11) - pig roundworm (fragment)

N:Alternate names: phosphofructokinase; phosphohexokinase

C:Species: Ascaris suum (pig roundworm)

C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004

C:Accession: A26120

R:Kulkarni, G.; Rao, G.S.V.; Srinivasan, N.G.; Hofer, H.W.; Yuan, P.M.; Harris, B.G.

J. Biol. Chem. 262, 32-34, 1987

A:Title: Ascaris suum phosphofructokinase. Phosphorylation by protein kinase and sequencing

A:Reference number: A26120; PMID:87083467; PMID:3025208

A:Accession: A26120

A:Molecule type: protein

A:Residues: 1-11 <KUL>

A:Cross-references: UNIPROT:Q7M4U2; UNIPARC:UPI000017B699

C:Keywords: glycolysis; phosphotransferase

Query Match

Best Local Similarity 24.7%; Score 20; DB 2; Length 11;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNDSPROT 8

Db 4 RSDSIVPT 11

RESULT 10

S05002 corazonin - American cockroach

C:Species: Periplaneta americana (American cockroach)

C>Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004

C:Accession: S05002

R:Veenastra, J.A.

FEBS Lett. 250, 231-234, 1989

A:Title: Isolation and structure of corazonin, a cardioactive peptide from the american

A:Reference number: S05002; PMID:8935572; PMID:2753132

A:Accession: S05002

A:Molecule type: protein

A:Residues: 1-11 <VEE>

A:Cross-references: UNIPROT:P11496; UNIPARC:UPI0000127F28

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

P:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

P:1/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match

Best Local Similarity 24.7%; Score 20; DB 2; Length 11;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 QTDQYT 12

Db 1 QTFQYS 6

RESULT 11

PH0771 T-cell receptor beta chain (P55.1.1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C:Accession: PH0771

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-II

A:Reference number: PH0746; PMID:9207846; PMID:1836010

A:Accession: PH0771

A:Molecule type: mRNA

A:Residues: 1-12 <CMS>

A:Cross-references: UNIPARC:UPI0000115FBE; EMBL:X60865; NID:G53624; PIDD:CAA43255.1; PIDD

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 24.7%; Score 20; DB 2; Length 12;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 SPIQTDQY 11

Db 3 SSFOYEQY 10

RESULT 12

PN0125 serine proteinase (EC 3.4.21.-) - Actinomyces sp. (fragment)

C:Species: Actinomyces sp.

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: PN0125

R:Mosolova, O.V.; Rudenskaya, G.N.; Stepanov, V.M.; Khodova, O.M.; Tsaplina, I.A.

Biochimika 52, 414-422, 1987

A:Title: Glu, Asp-specific proteinase from Actinomyces.

A:Reference number: PN0125

A:Accession: PN0125

A:Molecule type: protein

A:Residues: 1-13 <MOS>

A:Cross-references: UNIPROT:Q7M107; UNIPARC:UPI000017AD24

A:Note: article in Russian with English abstract

C:Keywords: hydrolase; serine proteinase

Query Match

Best Local Similarity 24.7%; Score 20; DB 2; Length 13;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 SPIQTDQY 11

Db 1 SVICIDVY 8

RESULT 13

PH1347 Ig heavy chain DJ region (clone C100-103A) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PH1347

R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A:Reference number: PH1302; PMID:93094761; PMID:1460419

A:Accession: PH1347

A:Molecule type: DNA

A:Residues: 1-14 <WAS>

A:Cross-references: UNIPARC:UPI000017C21C

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 24.7%; Score 20; DB 2; Length 14;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 DQYTTG 15

Db 4 EDFLTG 10

RESULT 14

GM0012 Leucosulfakinin-II - Madeira cockroach

N:Alternate names: LSK-II

C:Species: Leucophaea maderae (Madeira cockroach)

C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004

C:Accession: A26335

R:Nachman, R.J.; Holman, G.M.; Cook, B.J.; Haddon, W.F.; Ling, N.

Biochem. Biophys. Res. Commun. 140, 357-364, 1986

A:Title: Leucosulfakinin-II, a blocked sulfated insect neuropeptide with homology to ch

A:Reference number: A26335; PMID:87048769; PMID:3778455

A:Accession: A26335

A:Molecule type: protein
A:Residues: 1-10 <NAC>
A:Cross-references: UNIPROT:P09039; UNIPARC:UPI000012B961
C:Comment: This peptide was isolated from head extracts. It stimulates muscle contracti
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; sulfoprotein
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:5/Binding site: sulfate (Tyr) (covalent) #status experimental
F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 23.5%; Score 19; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 QTDQY 11
|:|
Db 1 QSDDY 5

RESULT 15

B60656
leucosulfakinin II, non-sulfated - American cockroach
C:Species: Periplaneta americana (American cockroach)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C:Accession: B60656
R:Veestra, J.A.
Neuropeptides 14, 145-149, 1989
A:Title: Isolation and structure of two gastrin/CK-1like neuropeptides from the American
A:Reference number: A60656; MUID:90137190; PMID:2615921
A:Accession: B60656
A:Molecule type: protein
A:Residues: 1-10 <VEE>
A:Cross-references: UNIPROT:P09039; UNIPARC:UPI000012B961
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 23.5%; Score 19; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 QTDQY 11
|:|
Db 1 QSDDY 5

Search completed: December 12, 2005, 21:18:41
Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:59:31 ; Search time 114 Seconds
(without alignments)
92.833 Million cell updates/sec

Title: US-10-758-165A-1
Perfect score: 81
Sequence: 1 RNDSPICQDQYTTTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 7855

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trernbl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	32.1	11	Q7M504 ASPNG	Q7M504 aspergillus
2	24	29.6	13	Q804K2 FICPA	Q804K2 ficedula pa
3	24	29.6	14	Q7M1U8 ORYSA	Q7M1U8 oryza sativ
4	24	29.6	15	Q9S929 SOYBN	Q9S929 glycine max
5	23	28.4	13	PLMS LAMNA	P83009 lamna nasus
6	22	27.2	9	Q9TVF1 TRYCR	Q9TVF1 trypanosoma
7	22	27.2	14	Q7IGS6 9HYME	Q7IGS6 andrena n.
8	22	27.2	15	Q54394 STRLI	Q54394 streptomyces
9	22	27.2	15	UC19 MALIZ	P80625 zea mays (m
10	22	27.2	15	Q7IGV6 9HYME	Q7IGV6 andrena sim
11	22	27.2	15	Q7IH38 9HYME	Q7IH38 andrena aur
12	21	25.9	8	Q15893 HUMAN	Q15893 homo sapien
13	21	25.9	13	Q7M4P7 HUMAN	Q7M4P7 homo sapien
14	21	25.9	14	Q7ZC22 CYPCA	Q7ZC22 cyprinus ca
15	21	25.9	15	Q7IGT0 9HYME	Q7IGT0 andrena aff
16	20	24.7	8	Q7LIH2 YEAST	Q7LIH2 saccharomyc
17	20	24.7	10	ODP2 BOVIN	P11801 bos taurus
18	20	24.7	11	COR2 PERAM	P11966 periplaneta
19	20	24.7	11	Q7M4J2 ASCSU	Q7M4J2 ascaris suu
20	20	24.7	11	Q9TRR7 RABIT	Q9TRR7 oryctolagus
21	20	24.7	12	Q6SR12 CVHSA	Q6SR12 sars corona
22	20	24.7	12	Q6SR16 CVHSA	Q6SR16 sars corona
23	20	24.7	12	Q6SRJ0 CVHSA	Q6SRJ0 sars corona
24	20	24.7	12	Q6SRJ4 CVHSA	Q6SRJ4 sars corona
25	20	24.7	12	Q6SRJ8 CVHSA	Q6SRJ8 sars corona
26	20	24.7	12	Q6SRK2 CVHSA	Q6SRK2 sars corona
27	20	24.7	12	Q6SRK6 CVHSA	Q6SRK6 sars corona
28	20	24.7	12	Q6SRLO CVHSA	Q6SRLO sars corona
29	20	24.7	12	Q6SRL4 CVHSA	Q6SRL4 sars corona
30	20	24.7	12	Q6SRL8 CVHSA	Q6SRL8 sars corona
31	20	24.7	2	Q6SRM2 CVHSA	Q6SRM2 sars corona

32	20	24.7	12	2	Q6SRM6 CVHSA	Q6SRM6 sars corona
33	20	24.7	12	2	Q6SRN0 CVHSA	Q6SRN0 sars corona
34	20	24.7	12	2	Q6SRN4 CVHSA	Q6SRN4 sars corona
35	20	24.7	12	2	Q6SRN8 CVHSA	Q6SRN8 sars corona
36	20	24.7	12	2	Q6SRP2 CVHSA	Q6SRP2 sars corona
37	20	24.7	12	2	Q6SRP6 CVHSA	Q6SRP6 sars corona
38	20	24.7	12	2	Q6SRQ0 CVHSA	Q6SRQ0 sars corona
39	20	24.7	13	1	EP65 HUMAN	P54963 homo sapien
40	20	24.7	13	2	Q7M107 9ACTO	Q7M107 actinomyces
41	20	24.7	13	2	P90442 NPVSL	P90442 spodoptera
42	20	24.7	14	2	Q70L16 HUMAN	Q70L16 homo sapien
43	20	24.7	14	2	Q9P2X4 HUMAN	Q9P2X4 homo sapien
44	20	24.7	14	2	Q7IGI7 9HYME	Q7IGI7 macrotera t
45	20	24.7	14	2	Q7IGL2 9HYME	Q7IGL2 andrena fla

ALIGNMENTS

RESULT 1

Q7M504 ASPNG PRELIMINARY; PRT; 11 AA.
AC Q7M504;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Amine oxidase (Copper-containing) (EC 1.4.3.6) II (Fragment).
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_Taxid=5061;
RN [1]
RP PROTEIN SEQUENCE.
RA Freibort I., Tamaki H., Ishida H., Pec P., Luhova L., Tsuno H.,
RA Hata M., Asano Y., Kato Y., Matsushita K., Toyama H., Kumagai H.,
RA Adachi O.;
RT "Two distinct quinoprotein amine oxidases are induced by n-butylamine
in the mycelia of Aspergillus niger AKU 3302: purification,
RT characterization, cDNA cloning and sequencing.";
RL Eur. J. Biochem. 237:255-265(1996).
DR PIR; S71304; S71304.
DR GO; GO:0008131; F:amine oxidase activity; IEA.
FT NON_TER 1 11
FT NON_TER 1 11
SQ SEQUENCE 11 AA; 1158 MM; 21BBPDC4472DC7 CRC64;

Query Match 32.1%; Score 26; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 2

Q804K2 FICPA PRELIMINARY; PRT; 13 AA.
ID Q804K2;
AC Q804K2;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Aldolase B (Fragment).
GN Name=Aldob;
OS Ficedula parva (Red-breasted flycatcher).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_Taxid=126711;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Saetre G.-P., Borje T., Lindroos K., Haavie J., Sheldon B.C.,
RA Primer C.R., Svanen A.-C.;
RT "Sex chromosome evolution and speciation in Ficedula flycatchers.";

RL Proc. R. Soc. Lond., B, Biol. Sci. 0:0-0(2003).
 DR EMBL; AY154343; AAO17275.1; -, Genomic_DNA.
 FT NON TER 1
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1635 MW; 7D3029BDE712DEA4 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 13;
 Best Local Similarity 45.5%; Pred. No. 3.1e+03;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 3 DSPIGTDQYTT 13
 Db 1 DHDLRRCQYVT 11

RESULT 3
 Q7MIU8 ORYSA
 ID Q7MIU8_ORYSA PRELIMINARY; PRT; 14 AA.

AC Q7MIU8; 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Porin (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocarpaceae; Eriocarpaceae; Oryzaeae; Oryza.
 NCBI_TaxID=4530;

RP PROTEIN SEQUENCE.
 RA Tsugita A.;
 RL Submitted (APR-1993) to the PIR data bank.
 DR PIR; PS0249; PS0249.
 DR Gramene; Q7MIU8; -.

FT NON TER 1
 FT NON TER 14
 SQ SEQUENCE 14 AA; 1490 MW; 83240AEOB1FAEA CRC64;

Query Match 29.6%; Score 24; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 8 TDQYTTTG 15
 Db 5 TDDHTANG 12

RESULT 4
 Q9S929 SOYBN
 ID Q9S929 SOYBN PRELIMINARY; PRT; 15 AA.

AC Q9S929;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Pyroline-5-carboxylate reductase, PSOR (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eustersids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 NCBI_TaxID=38477;

RP PROTEIN SEQUENCE.
 RA MEDLINE=91378472; PubMed=1898034;
 RA Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;
 RT "Pyroline-5-carboxylate reductase in soybean nodules:
 RT isolation/partial primary structure/evidence for isozymes";
 RL Arch. Biochem. Biophys. 288:350-357(1991).
 FT NON TER 15
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1715 MW; D9821F73F3DF524 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 5 PIQTDQYTT 12
 Db 5 PIPAESYTT 12

RESULT 5
 PLMS_LAMNA
 ID PLMS_LAMNA STANDARD; PRT; 13 AA.

AC P83009;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Phospholemman-like protein (PLMS) (Fragment).
 OS Lama nasus (Pitheciops) (Squalus nasus).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeidae; Lamniformes; Alopiidae;
 OC Lama.
 NCBI_TaxID=7849;

RP PROTEIN SEQUENCE.
 RC TISSUE=Rectal gland;
 RX MEDLINE=21514268; PubMed=11676495; DOI=10.1006/bbrc.2001.5826;
 RA Schumman Stekhoven F.M.A.H., Plik G., Wendelaar Bonga S.E.;
 RT "N-terminal sequences of small ion channels in rectal glands of
 RT shark: a biochemical hallmark for classification and phylogeny?";
 RL Biochem. Biophys. Res. Commun. 288:670-675(2001).
 CC -1 FUNCTION: Induces a hyperpolarization-activated chloride current
 CC when expressed in Xenopus oocytes. May have a functional role in
 CC muscle contraction.

CC -1 SUBCELLULAR LOCATION: Type I membrane protein. Mitochondrial
 CC membrane.
 CC -1 PTM: Major plasma membrane substrate for camp-dependent protein
 CC kinase (PK-A) and protein kinase C (PK-C) in several different
 CC tissues. Phosphorylated in response to insulin and adrenergic
 CC stimulation (By similarity)

CC -1 SIMILARITY: Belongs to the FYXD family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC GO: GO:0005792; C:microsome; IDA.
 DR InterPro; IPR000272; FYXD.
 DR PROSITE; PS01310; FYXD; PARTIAL.
 KW Chloride; Chloride channel; Direct protein sequencing;
 KW Endoplasmic reticulum; Ion transport; Ionic channel; Microsome;
 KW Phosphorylation; Transmembrane; Transport.
 FT NON TER 13
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1542 MW; 081373C69724A444 CRC64;

Query Match 28.4%; Score 23; DB 1; Length 13;
 Best Local Similarity 36.4%; Pred. No. 4.7e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 2 NDSPIGTDQYTT 12
 Db 2 SDVPNDRFT 12

RESULT 6
 O9TVF1 TRYCR
 ID O9TVF1 TRYCR PRELIMINARY; PRT; 9 AA.

AC O9TVF1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE Mucin-like protein (Fragment).

GN Name=EMUC-19c8;
 OS Trypanosoma cruzi.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;

```

OC Schizotrypanum.
OX NCBI_TaxID=5693;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CL-Brenner.
RX MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
RA Di Nola J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.;
RT "The Trypanosoma cruzi mucin family is transcribed from hundreds of
RT genes having hypervariable regions."
RU J. Biol. Chem. 273:10843-10850(1998).
DR EMBL AF036447; AAC14246.1; -, mRNA.
FT NON_TER
SQ SEQUENCE 9 AA; 896 MW; DBA831B1B85DD72D CRC64;

Query Match
Best Local Similarity 27.2%; Score 22; DB 2; Length 9;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YTTTG 15
DB 5 YTTTG 9

RESULT 7
Q7IGS6_9HYME PRELIMINARY; PRT; 14 AA.
ID Q7IGS6_9HYME PRELIMINARY; PRT; 14 AA.
AC Q7IGS6_9HYME PRELIMINARY; PRT; 14 AA.
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena n. sp. 'goth'.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena; Callandrena.
OX NCBI_TaxID=205171;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Larkin L.L., Neff J.L., Simpson B.B.;
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL AF504376; AAQ07723.1; -, Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 14 AA; 1692 MW; 79E3B922A4E7B5B CRC64;

Query Match
Best Local Similarity 27.2%; Score 22; DB 2; Length 14;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPQT 8
DB 6 NDSPQT 12

RESULT 8
Q54394_STRLI PRELIMINARY; PRT; 14 AA.
ID Q54394_STRLI PRELIMINARY; PRT; 14 AA.
AC Q54394_STRLI PRELIMINARY; PRT; 14 AA.
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE S-adenosyl-L-homocysteine hydrolase (Fragment).
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TK21;
RA Romero N.M., Meliado R.P.;
RT "Activation of the actinorhodin biosynthetic pathway in Streptomyces

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RT lividans."
RL FEMS Microbiol. Lett. 1217:79-84(1995).
DR EMBL X79814; CA56211.1; -, Genomic DNA.
DR GO; GO:0004013; F:adenosylhomocysteine activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR00043; Ad_hcy_hydrolase.
DR Pfam; PF05221; AdhCysase; 1.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 14 AA; 1725 MW; 1303D5023C485D2B CRC64;

Query Match
Best Local Similarity 27.2%; Score 22; DB 2; Length 14;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 DSPIQTDT 11
DB 4 EGPYRADHY 12

RESULT 9
UC19_MAIZE STANDARD; PRT; 15 AA.
ID UC19_MAIZE STANDARD; PRT; 15 AA.
AC P80625;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 406)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP PROTEIN SEQUENCE.
RA Trousier P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RC TISSUE=Coleoptile;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.6, its MW is: 18.4 kDa.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Maize-2DPAGE; P80625; COLEOPTILE.
DR Gramene; P80625; -.
DR MaizeDB; 123951; -.
KW Direct protein sequencing.
FT NON_TER
SQ SEQUENCE 15 AA; 1672 MW; 1CF69D4DA873F9D CRC64;

Query Match
Best Local Similarity 27.2%; Score 22; DB 1; Length 15;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 QYTTTG 15
DB 4 RYTTTG 9

RESULT 10
Q7IGV6_9HYME PRELIMINARY; PRT; 15 AA.
ID Q7IGV6_9HYME PRELIMINARY; PRT; 15 AA.
AC Q7IGV6_9HYME PRELIMINARY; PRT; 15 AA.

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DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena simulata.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena.
OX NCBI_TaxID=205253;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Larkin L., Neff J.L., Simpson B.B.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF504361; AAC07693.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON TER
SQ SEQUENCE 15 AA; 1744 MW; 181B812922A4F3EE CRC64;

Query Match 27.2%; Score 22; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 8.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQT 8
DB 6 NEIPIMT 12

RESULT 11
071H38_9HYME PRELIMINARY; PRT; 15 AA.
ID 071H38_9HYME PRELIMINARY; PRT; 15 AA.
AC 071H38;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena auripes.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena.
OX NCBI_TaxID=205215;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Larkin L., Neff J.L., Simpson B.B.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF504330; AAC07611.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON TER
SQ SEQUENCE 15 AA; 1776 MW; 09EE90D922A4EE59 CRC64;

Query Match 27.2%; Score 22; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 8.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQT 8
DB 6 NEIPIMT 12

RESULT 12
015893_HUMAN PRELIMINARY; PRT; 8 AA.
ID 015893_HUMAN PRELIMINARY; PRT; 8 AA.
AC 015893;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Homo sapiens (clone XP587A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

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OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh W.L., Chinnault C.A., Baldini A., Lindsey E.A., Zhao Z.-Y.,
RA Gaeky C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32073; AAA73883.1; -; mRNA.
FT NON TER
FT NON TER
SQ SEQUENCE 8 AA; 874 MW; DAA1B6D7376456C5 CRC64;

Query Match 25.9%; Score 21; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 2.2e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 NDSPIQT 8
DB 1 SQNPLOT 7

RESULT 13
07M4P7_HUMAN PRELIMINARY; PRT; 13 AA.
ID 07M4P7_HUMAN PRELIMINARY; PRT; 13 AA.
AC 07M4P7;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Urinary tract stone matrix protein 10, 42K (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RA Binette J.P., Binette M.B., Gawinowicz M.A., Kendrick N.;
RL Submitted (FEB-1995) to the PIR data bank.
DR PIR; H56046; H56046.1
FT NON TER
FT NON TER
SQ SEQUENCE 13 AA; 1483 MW; 0A219099F5D32A4 CRC64;

Query Match 25.9%; Score 21; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQT 9
DB 6 NDLAERTD 13

RESULT 14
07ZC2_CYPCA PRELIMINARY; PRT; 14 AA.
ID 07ZC2_CYPCA PRELIMINARY; PRT; 14 AA.
AC 07ZC2;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Transcription factor Pit-1 (Fragment).
OS Cypripus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kausel G., Salazar M.F., Castro L.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AY273789; AAP33497.1; -; Genomic_DNA.
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1557 MW; 883F8C975EA8B5 CRC64;

Query Match 25.9%; Score 21; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 1.2e+04;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 TDQYTT 13
 ||:|
 Db 9 TDCFTT 14

RESULT 15
 071GTO_9HWE
 ID 071GTO_9HWE PRELIMINARY; PRT; 15 AA.

AC 071GTO; 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Cytochrome oxidase subunit I.
 OS Andrena aff. manifesta LIL-2002.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 OC Andrenidae; Andreninae; Andrena.
 OX NCBI_TaxID=205242;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Larkin L.L., Neff J.L., Simpson B.B.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF504374; AA007719.1; -; Genomic_DNA.
 DR GO: GO:0005739; Mitochondrion; IEA.
 KW Mitochondrion.
 SQ SEQUENCE 15 AA; 1840 MW; 118E961922A39E59 CRC64;

Query Match 25.9%; Score 21; DB 2; Length 15;
 Best Local Similarity 30.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 NDSPITDQY 11
 |:|:|:
 Db 6 NEIPLMTMKF 15

Search completed: December 12, 2005, 21:17:21
 Job time : 116 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:20:50 ; Search time 109.333 Seconds
(without alignments)
72.337 Million cell updates/sec

Title: US-10-758-165A-10
Perfect score: 97
Sequence: 1 VDCQKATNIPFYTAFGKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 827869

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	18	ADRI0610	Cat IGE e
2	87	89.7	18	ADRI0609	Dog IGE e
3	55	56.7	18	ADRI0612	Sheep IGE
4	37	38.1	18	ADCS6890	Peptide f
5	35	36.1	18	ADRI0611	Horse IGE
6	34	35.1	15	ADCS64569	Horse imm
7	33.5	34.5	15	ADJ38597	HSV-4 Gly
8	32.5	33.5	15	ADJ38596	HSV-4 Gly
9	32.5	33.5	15	ADJ38596	HSV-4 Gly
10	32	33.0	9	ADW78189	Human met
11	32	33.0	9	AAU76520	Anti-Inte
12	32	33.0	11	ADT40399	Human mab
13	32	33.0	11	ADT40399	Human mab
14	32	33.0	11	ADT40399	Human mab
15	32	33.0	15	ADT40399	Human mab
16	32	33.0	15	ADT40399	Human mab
17	32	33.0	15	ADT40399	Human mab
18	32	33.0	15	ADT40399	Human mab
19	32	33.0	15	ADT40399	Human mab
20	32	33.0	15	ADT40399	Human mab
21	32	33.0	15	ADT40399	Human mab
22	32	33.0	15	ADT40399	Human mab
23	32	33.0	15	ADT40399	Human mab
24	32	33.0	15	ADT40399	Human mab

25	30	30.9	9	6	ABJ19961	AbJ19961 MHC bindi
26	30	30.9	9	7	ADD94584	Add94584 Human SIM
27	30	30.9	10	7	ADD94584	Add94584 Human SIM
28	30	30.9	11	9	ABJ17405	AbJ17405 Type II P
29	30	30.9	12	2	AAK49911	AaK49911 Glutamin
30	30	30.9	13	2	AAK49912	AaK49912 Glutamin
31	30	30.9	13	2	AAK49913	AaK49913 Glutamin
32	30	30.9	14	2	AAK49914	AaK49914 Glutamin
33	30	30.9	14	3	AAK49915	AaK49915 Glutamin
34	30	30.9	14	3	AAK49916	AaK49916 Glutamin
35	30	30.9	15	2	AAK49917	AaK49917 Glutamin
36	30	30.9	15	9	ADU70842	AdU70842 Human hep
37	30	30.9	16	2	AAK53562	AaK53562 Birch pol
38	30	30.9	16	8	ADQ90450	AdQ90450 RANTES re
39	30	30.9	17	2	AAK95159	AaK95159 bcl-x(L)/
40	30	30.9	18	9	ADV22975	AdV22975 HCV H77 i
41	29	29.9	9	2	AAW24775	AaW24775 Human imm
42	29	29.9	9	2	AAW80144	AaW80144 Light cha
43	29	29.9	9	2	AAW80142	AaW80142 Light cha
44	29	29.9	9	2	AAW40427	AaW40427 Amino aci
45	29	29.9	9	5	ABP62411	AbP62411 Human imm

ALIGNMENTS

RESULT 1	ADRI0610	standard; peptide; 18 AA.
ADRI0610	ADRI0610	standard; peptide; 18 AA.
AC	ADRI0610	
XX	ADRI0610	
XX	ADRI0610	
DT	21-OCT-2004	(first entry)
DE	Cat IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.	
KW	Antiaesthetic; Antiallergic; Immunosuppressive; IGF; dog; asthma; anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;	
KW	cat.	
XX		
OS	Felis catus.	
XX		
PN	WO2004065936-A2.	
XX		
PD	05-AUG-2004.	
XX		
PF	15-JAN-2004; 2004WO-US003566.	
XX		
PR	16-JAN-2003; 2003US-0440472P.	
XX		
PA	(UNNC-) UNIV NORTH CAROLINA STATE.	
XX		
PI	Hammerberg B;	
XX		
DR	WPI; 2004-593545/57.	
XX		
PT	Novel antibody that specifically binds to mammalian IGE epitope, useful for testing an allergen reactivity of IGE sample, detecting mammalian IGE or treating asthma or anaphylactic shock.	
PT		
XX		
XX	Example 6; Page 9; 14pp; English.	
CC	The present invention relates to a novel monoclonal antibody (I) that specifically binds to a mammalian IGE epitope, where the epitope is between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.	
CC	(I) is useful for testing an allergen reactivity of an IGE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (I) is also useful for detecting mammalian IGE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine IGE corresponding to amino acid residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from	

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE. The present sequence is the
 CC cat IgE 3.76 recognition site.

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.4e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGGKATNIFPYTAPGKQ 18
 |||||
 Db 1 VDGGKATNIFPYTAPGKQ 18

RESULT 2
 ADR10609

ID ADR10609 standard; peptide; 18 AA.

XX ADR10609;

XX 21-OCT-2004 (first entry)

XX Dog IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IgE; dog; asthma;

KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.

XX Canis familiaris.

XX MO2004065936-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

DR WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IgE epitope, useful
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IgE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE.

XX Sequence 18 AA;

Query Match 89.7%; Score 87; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGGKATNIFPYTAPG 16
 |||||
 Db 1 VDGGKATNIFPYTAPG 16

RESULT 3
 ADR10612

ID ADR10612 standard; peptide; 18 AA.

XX ADR10612;

XX 21-OCT-2004 (first entry)

XX Sheep IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 12.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IgE; dog; asthma;

KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;

XX sheep.

XX Ovis aries.

XX MO2004065936-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

DR WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IgE epitope, useful
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IgE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE. The present sequence is the
 CC sheep IgE 3.76 recognition site.

XX Sequence 18 AA;

Query Match 56.7%; Score 55; DB 8; Length 18;
 Best Local Similarity 66.7%; Pred. No. 0.063;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDGGKATNIFPYTAP 15
 |||||
 Db 1 VDGGQEDRNLFPSYAP 15

RESULT 4

ADCS6890
 ID ADCS6890 standard; peptide; 15 AA.

```

XX AC ADC56890;
XX PI 18-DEC-2003 (first entry)
XX DT
XX DE Peptide fragment Seq ID7 related to human protein 36-41.
XX KW human; protein 36-41; arrhythmia; asthma; dementia.
XX OS Homo sapiens.
XX PN CN1382718-A.
XX PD 04-DEC-2002.
XX PE 26-APR-2001; 2001CN-00112751.
XX PR 26-APR-2001; 2001CN-00112751.
XX PA (BIOM-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2003-269480/27.
XX PT New human macroprotein-36-41, encoding polynucleotide, antagonist and
XX PT recombinant production, useful for treating dementia, arrhythmia, asthma
XX PT and digestive ulcers.
XX PS Example 6; SEQ ID NO 7, 33pp; Chinese.
XX CC This invention relates to a novel protein, human protein 36-41, and the
XX CC DNA sequence encoding it. The protein of the invention may be useful for
XX CC the treatment of diseases such as arrhythmia, asthma and dementia. The
XX CC present sequence is the amino acid sequence of a peptide fragment of
XX CC human protein 36-41 which was used in the exemplification of the
XX CC invention.
XX SQ Sequence 15 AA;

Query Match      38.1%; Score 37; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 56;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 VDGQKATNIFPYTAP 15
      :|||: |||:
Db      1 MDGKMQPNSEFPWQSP 15

RESULT 5
ADRI0611
ID ADRI0611 standard; peptide; 18 AA.
XX
XX ADR10611;
XX
XX DT 21-OCT-2004 (first entry)
XX DE Horse IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 11.
XX KW Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
XX KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX KW horse.
XX OS Equus caballus.
XX PN WO2004065936-A2.
XX PD 05-AUG-2004.
XX PF 15-JAN-2004; 2004WO-US003566.
XX PR 16-JAN-2003; 2003US-0440472P.
XX PS

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PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hammerberg B;
XX WPI; 2004-593545/57.
XX
XX PT Novel antibody that specifically binds to mammalian IGE epitope, useful
XX PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
XX PT or treating asthma or anaphylactic shock.
XX PS Example 6; Page 9; 14pp; English.
XX
XX CC The present invention relates to a novel monoclonal antibody (1) that
XX CC specifically binds to a mammalian IGE epitope, where the epitope is
XX CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX CC (1) is useful for testing an allergen reactivity of an IGE sample. The
XX CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX CC and corn allergens. The sample is a biological sample collected from a
XX CC dog, cat or horse. (1) is also useful for detecting mammalian IGE and for
XX CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX CC antibodies recognise epitopes on canine IGE corresponding to amino acid
XX CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
XX CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
XX CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
XX CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
XX CC of IGE from cat and horse, but did not exhibit cross-reactivity with
XX CC either pig or human epsilon-chains of IGE. The present sequence is the
XX CC horse IGE 3.76 recognition site.
XX SQ Sequence 18 AA;

Query Match      36.1%; Score 35; DB 8; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.5e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY      1 VDGQKATNIFPYTAPGKQ 18
      :|||: |||:
Db      1 IDGQKVDEQFPGHGLVKQ 18

RESULT 6
ADC64569
ID ADC64569 standard; peptide; 15 AA.
XX
XX ADC64569;
XX
XX DT 18-DEC-2003 (first entry)
XX DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P5.
XX KW Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.
XX OS Equus caballus.
XX PN US2003087314-A1.
XX PD 08-MAY-2003.
XX PF 08-NOV-2001; 2001US-00052788.
XX PR 08-NOV-2001; 2001US-00052788.
XX PA (REGC ) UNIV CALIFORNIA.
XX Gershwin LJ, Pettigrew HD, Kalina WV;
XX WPI; 2003-765437/72.
XX
XX PT Immunogenic composition comprising an isolated equine immunoglobulin E
XX PT polypeptide that induces production of antibodies which specifically bind
XX PT to equine immunoglobulin E.
XX PS Example 1; Page 8; 14pp; English.

```

XX The invention relates to an immunogenic composition comprising an
 CC isolated polypeptide having an amino acid sequence that is at least 80%
 CC identical to 6 (SI-86), 15 amino acid peptide sequences derived from
 CC equine immunoglobulin E (the composition induces production of an
 CC antibody that specifically binds to equine immunoglobulin (Ig)E, the six
 CC polypeptides are not explicitly identified in the specification. Also
 CC included are a composition comprising an antibody that specifically binds
 CC to a polypeptide at least 80% identical to (SI)-86), an antibody that
 CC specifically binds to equine IgE made by the process of immunising an
 CC animal with a polypeptide at least 80% identical to (SI)-86), making an
 CC antibody that specifically binds to equine IgE (involving immunising an
 CC animal with a composition further comprising an isolated polypeptide (the
 CC amino acid sequence of the polypeptide is at least 80% identical to (SI)-
 CC (86)), and collecting antiserum from the animal) and a kit for detection
 CC of equine IgE in a biological sample comprising the antibody and means
 CC for detecting specific binding of the antibody to equine IgE. The
 CC antibody is useful for detecting equine IgE protein in a biological
 CC sample (serum) which involves contacting the sample with the antibody,
 CC thus forming an antigen/antibody complex, and detecting the presence or
 CC absence of the antigen/antibody complex. The antibody and antigen are
 CC immobilised on a solid surface. The antibody is labelled such that the
 CC complex can be detected. The complex is detected using a second labelled
 CC antibody. The peptides are useful for generating antibodies specific for
 CC IgE which can serve as a diagnostic test for allergy. The present
 CC sequence is a Horse immunoglobulin E, IgE, heavy chain immunogenic
 CC peptide from the middle portion of the C2 region.

XX Sequence 15 AA;
 SQ

Query Match 35.1%; Score 34; DB 7; Length 15;
 Best Local Similarity 54.5%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VDGKATNIEP 11
 | : | | | | |
 Db 2 IDGKVDQDFP 12

RESULT 7
 ADJ38597
 ID ADJ38597 standard; peptide; 15 AA.
 XX
 AC ADJ38597;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE HSV-4 Glycoprotein B late domain motif mutant peptide #1.
 XX
 KM Vitucide; HSV infection; antiviral; late domain motif; mutein; mutant.
 XX
 OS Human herpesvirus 4.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 6 /note= "Wild-type residue replaced with Ala"
 FT
 PN WO2004009027-A2.
 XX
 PD 29-JAN-2004.
 PD
 PF 21-JUL-2003; 2003WO-US022828.
 PF
 PR 19-JUL-2002; 2002US-0397265P.
 PR 19-JUL-2002; 2002US-0397477P.
 PR 19-JUL-2002; 2002US-0397479P.
 PR 03-MAR-2003; 2003US-0451903P.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 XX
 PI Morham S, Zavitz K, Hobden A;
 XX

DR WPI; 2004-123282/12.
 XX
 XX Use of cells displaying herpes simplex virus (HSV) altered budding
 PT phenotype for the manufacture of a medicament for treating HSV infection.
 XX
 PS Example 13; Page 66; 74pp; English.

XX The present invention relates to cells displaying herpes simplex virus
 CC (HSV) altered budding phenotype which are useful for the manufacture of a
 CC medicament for treating HSV infection. The medicament further comprises
 CC an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL
 CC -4, IL-12, IL-18 or gamma-interferon. The cells are human cells and
 CC contain a nucleic acid encoding a mutant HSV protein or a nucleic acid
 CC encoding the polypeptide sufficient for virus-like particle assembly but
 CC devoid of late-domain motifs. The nucleic acid is within an HSV genome.
 CC The genome is devoid of late domain motifs capable of effecting viral
 CC budding. The composition also comprises a compound capable of interfering
 CC with the protein-protein interaction between a host cell protein capable
 CC of binding a late domain motif and a HSV protein containing a late domain
 CC motif. The composition further comprises another HSV protein or its
 CC immunogenic fragment, and/or a nucleic acid encoding the other HSV
 CC protein or the immunogenic fragment. The present sequence is a mutant HSV
 CC peptide, derived from the wild-type peptide ADJ38596, used to illustrate
 CC the invention.

XX Sequence 15 AA;
 SQ

Query Match 34.5%; Score 33.5; DB 8; Length 15;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 6 ATNIFPYTAPGX 17
 | : | | | | |
 Db 1 ATTV-PATAPGX 11

RESULT 8
 ADJ38596
 ID ADJ38596 standard; peptide; 15 AA.
 XX
 AC ADJ38596;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE HSV-4 Glycoprotein B late domain motif wild-type peptide.
 XX
 KM Vitucide; HSV infection; antiviral; late domain motif.
 XX
 OS Human herpesvirus 4.
 OS
 PN WO2004009027-A2.
 XX
 PD 29-JAN-2004.
 PD
 PF 21-JUL-2003; 2003WO-US022828.
 PF
 PR 19-JUL-2002; 2002US-0397265P.
 PR 19-JUL-2002; 2002US-0397477P.
 PR 19-JUL-2002; 2002US-0397479P.
 PR 03-MAR-2003; 2003US-0451903P.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 XX
 PI Morham S, Zavitz K, Hobden A;
 XX
 DR WPI; 2004-123282/12.
 XX
 XX Use of cells displaying herpes simplex virus (HSV) altered budding
 PT phenotype for the manufacture of a medicament for treating HSV infection.
 XX
 PS Example 13; Page 66; 74pp; English.
 PS
 CC The present invention relates to cells displaying herpes simplex virus

CC (HSV) altered budding phenotype which are useful for the manufacture of a
 CC medicament for treating HSV infection. The medicament further comprises
 CC an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL
 CC -4, IL-12, IL-18 or gamma-interferon. The cells are human cells and
 CC contain a nucleic acid encoding a mutant HSV protein or a nucleic acid
 CC encoding the polypeptide sufficient for virus-like particle assembly but
 CC devoid of late-domain motifs. The nucleic acid is within an HSV genome.
 CC The genome is devoid of late domain motifs capable of effecting viral
 CC budding. The composition also comprises a compound capable of interfering
 CC with the protein-protein interaction between a host cell protein capable
 CC of binding a late domain motif and a HSV protein containing a late domain
 CC motif. The composition further comprises another HSV protein or its
 CC immunogenic fragment, and/or a nucleic acid encoding the other HSV
 CC protein or the immunogenic fragment. The present sequence is a wild-type
 CC HSV peptide, from which mutant sequences (ADJ38597-ADJ38600) were
 CC generated for use in the invention.

XX Sequence 15 AA;

Query Match 33.5%; Score 32.5; DB 8; Length 15;
 Best Local Similarity 66.7%; Pred. No. 3.2e+02;
 Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 6 ATNIPPYAPGK 17
 ||: |||||
 DB 1 ATTV-PTAPGK 11

RESULT 9
 ADM78189

ID ADM78189 standard; peptide; 15 AA.

XX ADM78189;

DT 07-APR-2005 (first entry)

XX Human metabolic therapy target peptide PACT.

XX DEF domain; MAP kinase; cytosolic; cardiovascular-gen.; cardiac;
 XX anastrotic; hypotensive; antiarteriosclerotic; antiinflammatory;
 XX antiallergic; immunosuppressive; antibacterial; antiaesthetic;
 XX dermatological; antidiabetic; gastrointestinal-gen.; antitumor;
 XX thrombolytic; neuroprotective; ophthalmological; antineumatic;
 XX antipyretic; uterine; antipsoriatic; hepatotropic; antianemic;
 XX muscular-gen.; thymic; antihypertensive; hepatotropic; antianemic;
 XX hepatotropic; virucide; anti-HIV; anabolic; hypertensive; anorectic;
 XX endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;
 XX antidiabetic; antidiabetic; sedative; hypnotic; CNS-gen.;
 XX antinfertility; cancer; cardiovascular disease; inflammation;
 XX metabolic disorder; neuropathy; sleep disorder.

XX Homo sapiens.

XX WO2005007090-A2.

XX 27-JAN-2005.

XX 02-JUL-2004; 2004WO-US021514.

XX 03-JUL-2003; 2003US-0484761P.

XX (HARD) HARVARD COLLEGE.

XX Blenis J, Murphy LO;

XX WPI; 2005-112720/12.

XX Identification of compound for treating e.g. cancer by culturing cells
 PT expressing target protein in the presence of growth factor, cytokine,
 PT tumor promoter or oncogene and assessing binding after contacting with
 PT the compound.

XX Claim 14; Page 64; 104pp; English.

XX The invention relates to a novel method for the identification of a
 CC therapeutic compound. The method involves providing test cells that
 CC express a target protein containing a DEF domain and MAP kinase;
 CC culturing the cells in the presence of growth factor, cytokine, tumor
 CC promoter or oncogene; contacting the cells with a candidate compound; and
 CC assessing the binding of the MAP kinase to the DEF domain relative to the
 CC binding in the absence of the candidate compound. The invention further
 CC comprises a method for the identification of a therapeutic compound; a
 CC method for treatment of cancer, which involves administering a compound
 CC that inhibits the binding of a MAP kinase to the DEF domain of a target
 CC protein; and an antibody that specifically binds to phospho-T-325 c-Fos
 CC (preferably polyclonal or monoclonal). The novel therapeutic compounds
 CC have the following activities: cytosolic, cardiovascular-gen., cardiac,
 CC vasotropic, hypotensive, antiarteriosclerotic, antiinflammatory,
 CC antiallergic, immunosuppressive, antibacterial, antiaesthetic,
 CC dermatological, antidiabetic, gastrointestinal-gen., antitumor,
 CC thrombolytic, neuroprotective, ophthalmological, antineumatic,
 CC antipyretic, uterine, antipsoriatic, hepatotropic, antianemic,
 CC -gen., thymic, antihypertensive, hepatotropic, nephrotropic;
 CC hepatotropic; virucide; anti-HIV; anabolic; hypertensive; anorectic;
 CC endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;
 CC antidiabetic; antidiabetic; sedative; hypnotic; CNS-gen.; and
 CC antinfertility. The therapeutic compound may be used in the treatment
 CC of: cancer, cardiovascular disorders, inflammatory disorders, metabolic
 CC disorders, neuropathy or a behavioural disorder, and a sleep disorder.
 CC This sequence represents a metabolic therapy target peptide of the
 CC invention.

XX Sequence 15 AA;

Query Match 33.5%; Score 32.5; DB 9; Length 15;
 Best Local Similarity 66.7%; Pred. No. 3.2e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 5 KATNIPPYAPG 16
 ||| |||||
 DB 1 KAT---PYTPFG 9

RESULT 10
 AAU76520

ID AAU76520 standard; peptide; 9 AA.

XX AAU76520;

XX 05-JUN-2002 (first entry)

XX Anti-Interleukin-12 (IL-12) antibody CDR3 light chain.

XX Human; antibody; anti-interleukin-12; CDR3 light chain; circulatory;
 KW complementarity determining region; neuroprotective; antipsoriatic;
 KW immunostimulant; cytosolic; anti-microbial; psoriasis; infection;
 KW multiple sclerosis; immune disorder; cardiovascular; malignant disease;
 KW neurological disorder.

XX Homo sapiens.

XX WO200212500-A2.

XX 14-FEB-2002.

XX 07-AUG-2001; 2001WO-US024720.

XX 07-AUG-2000; 2000US-023358P.

XX 29-SEP-2000; 2000US-0236827P.

XX 01-AUG-2001; 2001US-00920262.

XX (CENZ) CENTOCOR INC.

XX Giles-Komar J, Knight DM, Peritt D, Scallon B, Shealy D;
 PI WPI; 2002-257482/30.

XX New mammalian anti-IL-12 antibodies, useful for diagnosing or treating IL
PT -12 related conditions, e.g. psoriasis or multiple sclerosis, as well as
PT other for treating immune, infectious, malignant or neurological
PT disorders.
XX
PS Claim 41; Page 93; 96pp; English.
XX
CC The invention relates to novel isolated mammalian anti-interleukin-12 (IL
CC -12) antibodies. The antibodies comprise at least one complementarity
CC determining region (CDR) of a heavy or light chain, a heavy chain or
CC light chain variable region, or a heavy chain or light chain constant
CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or
CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.
CC The antibodies are also useful for treating immune, cardiovascular,
CC infectious, malignant or neurological disorders or diseases. The present
CC sequence represents the amino acid sequence of human anti-Interleukin-12
CC (IL-12) antibody CDR3 light chain
XX
SQ Sequence 9 AA;
XX
Query Match 33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 8 NIPPYT 13
||:||||
Db 4 NIPPYT 9
XX
RESULT 11
AAE15818
ID AAE15818 standard; peptide; 9 AA.
XX
AC AAE15818;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human mAb 12B1 VK complementarity determining region (CDR) #3.
XX
XX Human: sialoadhesin factor-3; SAP-3; therapy; cancer; inflammation;
KW autoimmunity; allergy; asthma; infection; central nervous system; CNS;
KW rheumatoid arthritis; multiple sclerosis; stem cell mobilisation; AIDS;
KW haematopoietic development; anaemia; chemoprotective agent; cytostatic;
KW immunoglobulin; complementarity determining region; CDR; protozoacide;
KW antiinflammatory; immunosuppressive; anti-HIV; antibacterial; virocid;
KW fungicide; neuroprotective; light chain variable region; VK; mAb;
KW monoclonal antibody.
XX
OS Homo sapiens.
XX
PN WO200190193-A1.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US016864.
XX
PR 24-MAY-2000; 2000US-00577930.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Abrahamson JA, Kikly KK;
XX
DR WPI; 2002-083094/11.
XX
PT Novel monoclonal antibody that binds to human sialoadhesin factor-3 for
PT treating or preventing cancer, inflammation, autoimmunity, allergy,
PT asthma, rheumatoid arthritis, multiple sclerosis, AIDS and infections.
PS Claim 13; Page 67; 69pp; English.
XX
CC The invention relates to monoclonal antibodies that bind to human

CC sialoadhesin factor-3 (SAF-3). SAF-3 antibody is useful for treating or
CC preventing cancer, inflammation, autoimmunity, allergy, asthma, central
CC nervous system (CNS) inflammation, rheumatoid arthritis, multiple
CC sclerosis, AIDS and bacterial, fungal, protozoan and viral infections and
CC for modulating an immune response in a mammal, where the immune response
CC is downregulated or enhanced. SAF-3 antibody is useful as diagnostic and
CC therapeutic reagents, to subcharacterise cell populations during
CC haematopoietic development, to treat anaemia, as a diagnostic marker to
CC distinguish between different forms of cancer, to purge bone marrow ex
CC vivo of cancer cells expressing SAF-3, as a tool to aid in the ex vivo
CC expansion (proliferation and/or differentiation) of haematopoietic
CC progenitor cells expressing SAF-3, as a stimulus in vivo for stem cell
CC mobilisation into the periphery and as an vivo chemoprotective agent.
CC Protein comprising immunoglobulin complementarity determining region
CC (CDR) of SAF-3 antibody and its nucleic acid is useful to configure
CC screening methods for detecting the effect of added compounds on the
CC production of mRNA and polypeptide in cells. The present sequence is
CC complementarity determining region of human monoclonal antibody (mAb)
CC 12B1 light chain variable region (VK), which binds to SAF-3
XX
SQ Sequence 9 AA;
XX
Query Match 33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 8 NIPPYT 13
||:||||
Db 4 NIPPYT 9
XX
RESULT 12
ADT40399
ID ADT40399 standard; peptide; 11 AA.
XX
AC ADT40399;
XX
DT 30-DEC-2004 (first entry)
XX
DE hSARS virus peptide, SEQ ID 1387.
XX
XX Virocid; Severe Acute Respiratory Syndrome; SARS; vaccine.
KW
KW SARS coronavirus.
OS
PN WO2004085650-A1.
XX
PD 07-OCT-2004.
XX
PF 24-MAR-2004; 2004WO-CN000246.
XX
PR 24-MAR-2003; 2003US-0457031P.
PR 26-MAR-2003; 2003US-0457730P.
PR 02-APR-2003; 2003US-0459931P.
PR 03-APR-2003; 2003US-0460357P.
PR 08-APR-2003; 2003US-0461265P.
PR 14-APR-2003; 2003US-0462805P.
PR 23-APR-2003; 2003US-0464886P.
PR 25-APR-2003; 2003US-0465738P.
PR 14-MAY-2003; 2003US-0470935P.
XX
PA (UYHK-) UNIV HONG KONG.
XX
PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Foon L, Yuen K,
PI Leung FC;
XX
DR WPI; 2004-737326/72.
XX
PT New nucleic acid molecule encoding nucleocapsid- or spike-gene protein of
PT a human Severe Acute Respiratory Syndrome (hSARS) virus, useful for
PT diagnosing and treating SARS.
PS Example; SEQ ID NO 1387; 200pp; English.
XX

XX The present invention relates to novel human Severe Acute Respiratory
 CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a
 CC hSARS virus having China Center for Type Culture Collection Deposit
 CC Accession No. CCTCC-V200303. The present invention also relates to novel
 CC nucleic acid molecules (1; ADT41483 or ADT41485) encoding a nucleocapsid-
 CC (N) or spike (S)-gene protein of a hSARS virus. Also disclosed are
 CC methods for detecting the presence of a N- or S-gene of the hSARS virus
 CC or of the protein in a biological sample and identifying a subject
 CC infected with the hSARS virus. The hSARS virus, nucleic acid and protein
 CC sequences are useful as vaccines for diagnosing or treating SARS. They
 CC are also useful in clinical and scientific research applications. The
 CC hSARS virus genome (ADT39027) was obtained and the amino acid sequences
 CC of all three reading frames were deduced from the complementary strand.
 CC ADT40120 is the full-length protein encoded by the first reading frame of
 CC the complementary strand and ADT40121-ADT40601 are the peptides from the
 CC first reading frame protein. ADT40602 is the full-length protein encoded
 CC by the second reading frame of the complementary strand and ADT40603-
 CC ADT40976 are the peptides from the second reading frame protein. ADT40977
 CC is the full-length protein encoded by the third reading frame of the
 CC complementary strand and ADT40978-ADT41482 are the peptides from the
 CC third reading frame protein.

XX SQ Sequence 11 AA;

Query Match 33.0%; Score 32; DB 8; Length 11;
 Best Local Similarity 54.5%; Pred. No. 2.8e+02;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 GQKATNIPPYT 13
 ||:||||
 1 GQSQSNILPQT 11

Db

RESULT 13
 ADS79816
 ID ADS79816 standard; protein; 11 AA.

AC ADS79816;

XX 30-DEC-2004 (first entry)

DE SARS virus complementary DNA strand reading frame 1 protein #279.

XX

KM viroicide; vaccine; detection; severe acute respiratory syndrome;

XX real-time quantitative polymerase chain reaction; SARS.

OS SARS coronavirus.

XX WO2004085455-A1.

PN 07-OCT-2004.

PD 24-MAR-2004; 2004WO-CN000247.

PF 24-MAR-2003; 2003US-0457031P.

PR 26-MAR-2003; 2003US-0457730P.

PR 02-APR-2003; 2003US-0459931P.

PR 03-APR-2003; 2003US-0460357P.

PR 08-APR-2003; 2003US-0461265P.

PR 14-APR-2003; 2003US-0462805P.

PR 23-APR-2003; 2003US-0464886P.

PR 05-MAY-2003; 2003US-0468139P.

PR 16-MAY-2003; 2003US-0471200P.

XX (UYHK-) UNIV HONG KONG.

XX

PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;

XX WPI; 2004-737292/72.

DR

XX New isolated nucleic acid molecule useful for detecting, treating,

PT ameliorating, or preventing the virus causing severe acute respiratory

PT syndrome in humans using a real-time quantitative polymerase chain
 PT reaction assay.

XX Example; SEQ ID NO 1387; 183pp; English.

XX The invention relates to an isolated nucleic acid molecule consisting
 CC essentially of, and/or hybridizes under stringent conditions to a fully
 CC defined nucleotide sequence of 16-25 base pairs (bp; SEQ ID NO: 2471-
 CC 2476), or its complement. The methods and compositions of the present
 CC invention are useful for the detection of the virus causing Severe Acute
 CC Respiratory Syndrome (SARS) in humans using a real-time quantitative
 CC polymerase chain reaction (PCR) assay. They can also be used in treating,
 CC ameliorating, managing or preventing SARS. This sequence corresponds to a
 CC partial SARS protein sequence from the complementary reading frame 1.

XX SQ Sequence 11 AA;

Query Match 33.0%; Score 32; DB 8; Length 11;
 Best Local Similarity 54.5%; Pred. No. 2.8e+02;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 GQKATNIPPYT 13
 ||:||||
 1 GQSQSNILPQT 11

Db

RESULT 14
 ADT37929
 ID ADT37929 standard; peptide; 11 AA.

AC ADT37929;

XX 30-DEC-2004 (first entry)

DE hSARS virus peptide, SEQ ID 1387.

XX viroicide; Severe Acute Respiratory Syndrome; SARS; vaccine.

OS SARS coronavirus.

XX WO2004085633-A1.

PN 07-OCT-2004.

PD 24-MAR-2004; 2004WO-CN000248.

PF 24-MAR-2003; 2003US-0457031P.

PR 26-MAR-2003; 2003US-0457730P.

PR 02-APR-2003; 2003US-0459931P.

PR 03-APR-2003; 2003US-0460357P.

PR 08-APR-2003; 2003US-0461265P.

PR 14-APR-2003; 2003US-0462805P.

PR 23-APR-2003; 2003US-0464886P.

XX (UYHK-) UNIV HONG KONG.

XX

PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;

XX Leung PC;

XX WPI; 2004-728736/71.

DR

XX New isolated human severe acute respiratory syndrome (hSARS) virus,

PT useful as vaccine for diagnosing or treating SARS or in clinical and

PT scientific research applications.

XX Example; SEQ ID NO 1387; 176pp; English.

XX

PI The present invention relates to novel human Severe Acute Respiratory

CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a

CC hSARS virus having China Center for Type Culture Collection Deposit

CC Accession No. CCTCC-V200303. The hSARS virus, nucleic acid and protein

CC sequences are useful in clinical and scientific research applications. The

CC hSARS virus genome (ADT36557) was obtained and the amino acid sequences
 CC of all three reading frames were deduced from the complementary strand.
 CC ADT37650 is the full-length protein encoded by the first reading frame of
 CC the complementary strand and ADT37651-ADT38131 are the peptides from the
 CC first reading frame protein. ADT38132 is the full-length protein encoded
 CC by the second reading frame of the complementary strand and ADT38133-
 CC ADT38506 are the peptides from the second reading frame protein. ADT38507
 CC is the full-length protein encoded by the third reading frame of the
 CC complementary strand and ADT38508-ADT39012 are the peptides from the
 CC third reading frame protein.

XX Sequence 11 AA;

Query Match 33.0%; Score 32; DB 8; Length 11;
 Best Local Similarity 54.5%; Pred. No. 2.8e+02;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GQKATNFPYT 13
 Db 1 GQSQSNILPOT 11

RESULT 15

AA65747 ID AA65747 standard; peptide; 15 AA.

XX AC AA65747;

DT 10-FEB-2000 (first entry)

XX DE Breast cancer susceptibility (BRCA 2) mutant peptide 31.

XX KW Human; frameshift mutant; T cell response; tumour; treatment; cancer;
 XX mutcin.

OS Homo sapiens.
 OS Synthetic.

PN W0958552-A2.

PD 18-NOV-1999.

PF 03-MAY-1999; 99WO-N0000143.

PR 08-MAY-1998; 98NO-00002097.

XX (NH2D) NORSK HYDRO AS.

PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;

DR WPI; 2000-039064/03.

PT New peptides derived from genes with frameshift mutations, used to
 PT develop products for the treatment and prophylaxis of cancers.

PS Claim 13; Page 25; 166pp; English.

XX Peptides AA65684-Y66142 are fragments of mutant proteins arising from a
 CC frameshift mutation in a gene from a cancer cell. The peptides are
 CC characterised in that they: (i) are at least 8 amino acids long and a
 CC fragment of a mutant protein arising from a frameshift mutation in a gene
 CC of a cancer cell; (ii) consist of at least one amino acid of the mutant
 CC part of a protein sequence encoded by the gene; (iii) comprise 0-10 amino
 CC acid from the carboxyl terminus of the normal part of the protein
 CC sequence preceding the amino terminus of the mutant sequence and may
 CC further extend to the carboxyl terminus of the mutant part of the protein
 CC as determined by a new stop codon generated by the frameshift mutation;
 CC and (iv) induce, either in their full lengths or after processing by an
 CC antigen presenting cell (APC), T cell responses. The genes that the
 CC peptides are derived from, are characterised as susceptible to frameshift
 CC mutation by having a mono nucleoside base repeat sequence of at least 5
 CC residues, or a di-nucleoside base repeat sequence of at least 4 di-
 CC nucleoside base units. The peptides are created by the addition or

CC deletion of 1 or 2 nucleoside base residues from the repeat sequence. The
 CC novel peptides can elicit T cell responses and toxicity against tumours
 CC and cancer cells carrying genes with frameshift mutations. The novel
 CC peptides and DNA sequences can be used for the preparation of a
 CC composition for the treatment or prophylaxis of cancer

XX Sequence 15 AA;

Query Match 33.0%; Score 32; DB 3; Length 15;
 Best Local Similarity 54.5%; Pred. No. 3.9e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGKATNFP 11
 Db 4 VEDQKTLVFP 14

Search completed: December 12, 2005, 21:52:03
 Job time : 110.333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:05:57 ; Search time 27 Seconds
(without alignments)
55.117 Million cell updates/sec

Title: US-10-758-165A-10
Perfect score: 97
Sequence: 1 VDQKATNIFPYAPGKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 208455

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5 COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/6 COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/7 COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/8 COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/9 COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/10 COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	33.0	9	2	US-09-920-262A-6
2	32	33.0	15	2	US-09-674-973A-64
3	31	33.0	11	2	US-09-307-265A-14
4	31	33.0	12	1	US-08-260-582-47
5	31	32.0	12	1	US-08-260-582-48
6	31	32.0	12	4	PCT-US95-05471-47
7	31	32.0	12	4	PCT-US95-05471-48
8	30	30.9	9	2	US-09-865-548A-126
9	30	30.9	17	1	US-08-333-565-22
10	30	30.9	17	1	US-08-661-479-22
11	29	29.9	9	2	US-09-042-353-366
12	29	29.9	9	2	US-08-758-417A-214
13	29	29.9	15	2	US-08-278-774-20
14	29	29.9	18	2	US-09-856-920-1
15	28	28.9	10	2	US-09-641-803-18
16	28	28.9	10	2	US-09-641-802-18
17	28	28.9	10	2	US-09-641-801-18
18	28	28.9	10	2	US-10-281-652-18
19	28	28.9	11	1	US-07-958-903A-10
20	28	28.9	11	1	US-08-462-018-10
21	28	28.9	11	1	US-08-823-245-10
22	28	28.9	11	2	US-07-963-329A-60
23	28	28.9	11	2	US-09-318-001-10
24	28	28.9	11	2	US-09-064-159-10
25	28	28.9	11	4	PCT-US92-09443A-60
26	28	28.9	15	1	US-08-080-073-26
27	28	28.9	16	2	US-10-044-708A-3

28	28	28.9	18	1	US-08-084-718-30	Sequence 30, Appl
29	28	28.9	18	1	US-08-443-976-30	Sequence 30, Appl
30	28	28.9	18	1	US-08-443-977-30	Sequence 30, Appl
31	27	27.8	11	2	US-09-809-517A-21	Sequence 21, Appl
32	27	27.8	18	1	US-08-421-702A-100	Sequence 100, Appl
33	27	27.8	18	1	US-08-303-052A-100	Sequence 100, Appl
34	27	27.8	18	1	US-08-421-696A-100	Sequence 100, Appl
35	27	27.8	18	1	US-08-421-697A-100	Sequence 100, Appl
36	27	27.8	18	1	US-08-421-698A-100	Sequence 100, Appl
37	27	27.8	18	1	US-08-421-699A-101	Sequence 101, Appl
38	27	27.8	18	1	US-09-017-205-48	Sequence 48, Appl
39	27	27.8	18	1	US-09-017-205-49	Sequence 49, Appl
40	26	26.8	5	2	US-09-788-006-9	Sequence 9, Appl
41	26	26.8	9	2	US-09-602-812A-12	Sequence 12, Appl
42	26	26.8	10	2	US-09-914-695-24	Sequence 24, Appl
43	26	26.8	12	1	US-08-096-762-208	Sequence 208, Appl
44	26	26.8	12	2	US-09-042-353-322	Sequence 322, Appl
45	26	26.8	12	2	US-08-758-417A-170	Sequence 170, Appl

ALIGNMENTS

```

RESULT 1
US-09-920-262A-6
; Sequence 6, Application US/0920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patencin Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-6

Query Match      33.0%; Score 32; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 NIFPYT 13
      ||:|||
Db      4 NIFPYT 9

RESULT 2
US-09-674-973A-64
; Sequence 64, Application US/09674973A
; Patent No. 6759046
; GENERAL INFORMATION:
; APPLICANT: No. 6759046k Hydro ASA
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 26625-296
; CURRENT APPLICATION NUMBER: US/09/674,973A
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: Patencin version 3.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT

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ORGANISM: Homo sapiens
US-09-674-973A-64

Query Match
Best Local Similarity 33.0%; Score 32; DB 2; Length 15;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDQKATNIFP 11
|:|:|:|:
Db 4 VEDQKTLVFP 14

RESULT 3
US-09-307-265A-14
Sequence 14, Application US/09307265A

PATENT INFORMATION:
PATENT NO. 6225456
APPLICANT: Gu, Trent
APPLICANT: Orta, Satoshi
TITLE OF INVENTION: RAS SUPPRESSOR SUR-5
FILE REFERENCE: UTC-03732
CURRENT APPLICATION NUMBER: US/09/307,265A
CURRENT FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 11
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-307-265A-14

Query Match
Best Local Similarity 32.0%; Score 31; DB 2; Length 11;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAGKQ 18
|:|:|:|:
Db 1 PYTSSGKT 8

RESULT 4
US-08-260-582-47

Sequence 47, Application US/08260582
PATENT NO. 5635182
GENERAL INFORMATION:
APPLICANT: McCoy, John M.
TITLE OF INVENTION: METHOD OF DETECTING LIGAND
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,582
FILING DATE: 16-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meiner, M. C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5236
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170

TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-260-582-47

Query Match
Best Local Similarity 32.0%; Score 31; DB 1; Length 12;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAGKQ 18
|:|:|:|:
Db 4 PWLAPGEO 11

RESULT 5
US-08-260-582-48

Sequence 48, Application US/08260582
PATENT NO. 5635182
GENERAL INFORMATION:
APPLICANT: McCoy, John M.
TITLE OF INVENTION: METHOD OF DETECTING LIGAND
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,582
FILING DATE: 16-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meiner, M. C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5236
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-260-582-48

Query Match
Best Local Similarity 32.0%; Score 31; DB 1; Length 12;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAGKQ 18
|:|:|:|:
Db 4 PWLAPGEO 11

RESULT 6
PCT-US95-05471-47
; Sequence 47, Application PC/TUS9505471
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHOD OF DETECTING LIGAND INTERACTIONS
; NUMBER OF SEQUENCES: 76
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05471
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
PCT-US95-05471-47

Query Match 32.0%; Score 31; DB 4; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAGKQ 18
|:|:|:|
DB 4 PMLAPGEQ 11

RESULT 7
PCT-US95-05471-48
; Sequence 48, Application PC/TUS9505471
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHOD OF DETECTING LIGAND INTERACTIONS
; NUMBER OF SEQUENCES: 76
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05471
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
PCT-US95-05471-48

Query Match 32.0%; Score 31; DB 4; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAGKQ 18
|:|:|:|
DB 4 PMLAPGEQ 11

RESULT 8
US-09-865-548A-126
; Sequence 126, Application US/09865548A
; Patent No. 6867283

; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 126
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-126

Query Match 30.9%; Score 30; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NIFPY 12
|:|:|:|
DB 1 NIFPY 5

RESULT 9
US-08-333-565-22
; Sequence 22, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-333-565-22

Query Match 30.9%; Score 30; DB 1; Length 17;

Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYRAPG 16
|||
3 PYLAPG 8

RESULT 10
US-08-661-479-22

; Sequence 22, Application US/08661479

; Patent No. 5834209

; GENERAL INFORMATION:

; APPLICANT: KORSMEYER, Stanley J.

; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/661,479

; FILING DATE: 11-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/333,565

; FILING DATE: 31-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 15726A-000700

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-661-479-22

Query Match 30.9%; Score 30; DB 1; Length 17;

Best Local Similarity 83.3%; Pred. No. 2.3e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYRAPG 16
|||
3 PYLAPG 8

RESULT 11
US-09-042-353-366
; Sequence 366, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/042,353

; FILING DATE: 13-MAR-1998

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/810,279

; FILING DATE: 17-DEC-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/853,408

; FILING DATE: 18-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/904,068

; FILING DATE: 23-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/990,860

; FILING DATE: 16-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/053,131

; FILING DATE: 26-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/096,762

; FILING DATE: 22-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/155,301

; FILING DATE: 18-NOV-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/161,739

; FILING DATE: 03-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/165,699

; FILING DATE: 10-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/209,741

; FILING DATE: 09-MAR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/352,322

; FILING DATE: 07-DEC-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/544,404

; FILING DATE: 10-OCT-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/728,463

; FILING DATE: 10-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US96/16433

; FILING DATE: 10-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/758,417

; FILING DATE: 02-DEC-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/21803

; FILING DATE: 01-DEC-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 014643-009040US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 366:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-042-353-366

Query Match 29.9%; Score 29; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 NFFPT 13
| | | | |
Db 4 NSFPY 9

RESULT 12
US-08-758-417A-214
Sequence 214, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>

TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-08-758-417A-214

Query Match 29.9%; Score 29; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 NFFPT 13
| | | | |
Db 4 NSFPY 9

RESULT 13
US-08-278-774-20
Sequence 20, Application US/08278774
Patent No. 6653450
GENERAL INFORMATION:
APPLICANT: Berg, Richard A
Tomam, David P
APPLICANT: Wallace, Donald
TITLE OF INVENTION: MUTATED RECOMBINANT COLLAGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: COLLAGEN CORPORATION
STREET: 2500 Faber Place
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,774
FILING DATE: 22-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ralayko, Katchi L
REGISTRATION NUMBER: 36,644
REFERENCE/DOCKET NUMBER: 94-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-4642
TELEFAX: (415) 354-4752
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-278-774-20
Query Match 29.9%; Score 29; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGKATNIFPY 12
| | | | |
Db 2 IGGRKGGFAPY 13

RESULT 14
US-09-856-920-1
Sequence 1, Application US/09856920
Patent No. 6740325
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co.
TITLE OF INVENTION: Peptide-based vaccine for influenza

; FILE REFERENCE: 9822 PCT
; CURRENT APPLICATION NUMBER: US/09/856,920
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Influenza virus
US-09-856-920-1

Query Match 29.9%; Score 29; DB 2; Length 18;
Best Local Similarity 44.4%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 TNIPPYTAP 15
:|:|:|
Db 5 SNCTPYDVP 13

RESULT 15
US-09-641-803-18
; Sequence 18, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-18

Query Match 28.9%; Score 28; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.8e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 IFPYTAP 15
:|:|:|
Db 1 VYPTGP 7

Search completed: December 12, 2005, 21:20:08
Job time : 27 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:20:19 ; Search time 95 Seconds
(without alignments)
79.168 Million cell updates/sec

Title: US-10-758-165A-10
Perfect score: 97
Sequence: 1 VDQKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 356231

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	5	US-10-758-165-10 Sequence 10, Appl
2	87	89.7	18	5	US-10-758-165-9 Sequence 9, Appl
3	55	56.7	18	5	US-10-758-165-12 Sequence 12, Appl
4	37	38.1	15	5	US-10-856-118-34 Sequence 34, Appl
5	35	36.1	18	5	US-10-758-165-11 Sequence 11, Appl
6	34	35.1	15	4	US-10-052-788-5 Sequence 5, Appl
7	32	33.0	9	3	US-09-920-262A-6 Sequence 6, Appl
8	32	33.0	9	5	US-10-912-994-6 Sequence 6, Appl
9	32	33.0	9	5	US-10-975-883-6 Sequence 6, Appl
10	32	33.0	9	5	US-10-975-740A-6 Sequence 6, Appl
11	32	33.0	9	5	US-10-975-708-6 Sequence 6, Appl
12	32	33.0	11	5	US-10-808-187-1387 Sequence 1387, Ap
13	32	33.0	11	5	US-10-807-807-1387 Sequence 1387, Ap
14	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap
15	32	33.0	15	4	US-10-107-532-6124 Sequence 6124, Ap
16	32	33.0	15	5	US-10-776-224-64 Sequence 64, Appl
17	31	32.0	13	4	US-10-300-694A-64 Sequence 64, Appl
18	31	32.0	14	3	US-09-929-751A-16 Sequence 16, Appl
19	30	30.9	9	3	US-09-865-548A-126 Sequence 126, App
20	30	30.9	9	5	US-10-705-459-126 Sequence 126, App
21	29	29.9	14	5	US-10-804-772-27 Sequence 27, Appl
22	29	29.9	9	5	US-10-482-630-40 Sequence 40, Appl
23	29	29.9	12	3	US-09-813-653-26 Sequence 26, Appl
24	29	29.9	14	5	US-10-865-478-786 Sequence 786, Appl
25	29	29.9	15	5	US-10-720-831-20 Sequence 20, Appl
26	29	29.9	17	4	US-10-306-631-76 Sequence 76, Appl
27	29	29.9	18	4	US-10-654-200-28 Sequence 28, Appl

28	29	29.9	18	4	US-10-654-200-29 Sequence 29, Appl
29	29	29.9	18	5	US-10-846-548A-1 Sequence 1, Appl
30	28	28.9	9	4	US-10-160-506-34 Sequence 34, Appl
31	28	28.9	9	4	US-10-449-379-34 Sequence 34, Appl
32	28	28.9	9	4	US-10-688-015-34 Sequence 34, Appl
33	28	28.9	9	4	US-10-160-505-34 Sequence 34, Appl
34	28	28.9	9	5	US-10-482-284A-186 Sequence 186, App
35	28	28.9	10	4	US-10-281-652-18 Sequence 18, Appl
36	28	28.9	10	5	US-10-691-157-18 Sequence 18, Appl
37	28	28.9	10	5	US-10-691-330-18 Sequence 18, Appl
38	28	28.9	14	3	US-09-880-748-2653 Sequence 2653, Ap
39	28	28.9	14	4	US-10-293-418-2653 Sequence 2653, Ap
40	28	28.9	14	4	US-10-742-379-44 Sequence 44, Appl
41	28	28.9	16	3	US-09-736-959A-29 Sequence 29, Appl
42	28	28.9	16	4	US-10-044-708A-3 Sequence 3, Appl
43	28	28.9	16	4	US-10-225-567A-1478 Sequence 1478, Ap
44	28	28.9	17	4	US-10-239-313A-30 Sequence 30, Appl
45	28	28.9	18	5	US-10-758-165-13 Sequence 13, Appl

ALIGNMENTS

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RESULT 1
US-10-758-165-10
; Sequence 10, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOLOGICAL E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-10

Query Match      100.0%; Score 97; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDQKATNIFPYTAPGKQ 18
        |||||
Db       1 VDQKATNIFPYTAPGKQ 18

RESULT 2
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOLOGICAL E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-9

Query Match      89.7%; Score 87; DB 5; Length 18;
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Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAPG 16
Db 1 VDGQKATNIPFYTAPG 16

RESULT 3

US-10-758-165-12
; Sequence 12, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-12

Query Match 56.7%; Score 55; DB 5; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.055;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAP 15
Db 1 VDGQEDRNLFSYTAP 15

RESULT 4

US-10-856-118-34
; Sequence 34, Application US/10856118
; Publication No. US20050025747A1
; GENERAL INFORMATION:
; APPLICANT: Laidlaw, Stephen
; APPLICANT: Skinner, Mike
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Anderson, Richard
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 3742.1000-000
; CURRENT APPLICATION NUMBER: US/10/856,118
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: PCT/GB02/005411
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: GB0128733.3
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/334,649
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flanking sequence
US-10-856-118-34

Query Match 38.1%; Score 37; DB 5; Length 15;
Best Local Similarity 55.6%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 TNIPFYTAP 15
||:|:| |

Db 2 TNIPFYDVP 10

RESULT 5

US-10-758-165-11
; Sequence 11, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-11

Query Match 36.1%; Score 35; DB 5; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAPGKQ 18
Db 1 IDGKXVDGQFPGHGLVKGQ 18

RESULT 6

US-10-052-788-5
; Sequence 5, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
; APPLICANT: Gerethwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kalina, Warren V.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052,788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: epitope peptide
; OTHER INFORMATION: P5, middle portion of C2 of equine IgE epsilon
; OTHER INFORMATION: heavy chain
US-10-052-788-5

Query Match 35.1%; Score 34; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGQKATNIPP 11
Db 2 IDGKXVDGQFP 12

RESULT 7

US-09-920-262A-6
; Sequence 6, Application US/09920262A
; Publication No. US20030124123A1
; GENERAL INFORMATION:
; APPLICANT: Shealy, David


```
/ APPLICANT: Knight, David
/ APPLICANT: Scallion, Bernie
/ APPLICANT: Gilles-Komar, Jill
/ APPLICANT: Peritt, David
/ TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
/ FILE REFERENCE: CEN0248
/ CURRENT APPLICATION NUMBER: US/09/920,262A
/ CURRENT FILING DATE: 2002-05-06
/ PRIOR APPLICATION NUMBER: 60/223,358
/ PRIOR FILING DATE: 2000-08-07
/ PRIOR APPLICATION NUMBER: 60/236,827
/ PRIOR FILING DATE: 2000-09-29
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver 3.1
/ SEQ ID NO 6
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-920-262A-6
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Query Match          33.0%; Score 32; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      8 NIPYPT 13
        ||:||||
Db       4 NIPYPT 9
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RESULT 8
US-10-912-994-6
/ Sequence 6, Application US/10912994
/ Publication No. US20050002937A1
/ GENERAL INFORMATION:
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/ APPLICANT: Gilles-Komar, Jill
/ APPLICANT: Knight, David
/ APPLICANT: Peritt, David
/ APPLICANT: Scallion, Bernie
/ APPLICANT: Shealy, David
/ TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
/ FILE REFERENCE: CEN0248DIV1
/ CURRENT APPLICATION NUMBER: US/10/912,994
/ CURRENT FILING DATE: 2004-08-06
/ PRIOR APPLICATION NUMBER: US 60/223,358
/ PRIOR FILING DATE: 2000-08-07
/ PRIOR APPLICATION NUMBER: US 60/236,827
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: US 09/920,262
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver 3.1
/ SEQ ID NO 6
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-912-994-6
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Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
        ||:||||
Db       4 NIPYPT 9
```

```
RESULT 9
US-10-975-883-6
/ Sequence 6, Application US/10975883
/ Publication No. US20050112127A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilles-Komar, Jill
/ APPLICANT: Knight, David
```

```
/ APPLICANT: Peritt, David
/ APPLICANT: Scallion, Bernie
/ APPLICANT: Shealy, David
/ TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND USES
/ FILE REFERENCE: CEN0248DIV04
/ CURRENT APPLICATION NUMBER: US/10/975,883
/ CURRENT FILING DATE: 2004-10-28
/ PRIOR APPLICATION NUMBER: US 60/223,358
/ PRIOR FILING DATE: 2000-08-07
/ PRIOR APPLICATION NUMBER: US 60/236,827
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: US 09/920,262
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver 3.1
/ SEQ ID NO 6
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-975-883-6
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```
Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
        ||:||||
Db       4 NIPYPT 9
```

```
RESULT 10
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```
US-10-975-740A-6
/ Sequence 6, Application US/10975740A
/ Publication No. US20050196838A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilles-Komar, Jill
/ APPLICANT: Knight, David
/ APPLICANT: Peritt, David
/ APPLICANT: Scallion, Bernie
/ APPLICANT: Shealy, David
/ TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND NUCLEIC ACIDS
/ FILE REFERENCE: CEN0248DIV03
/ CURRENT APPLICATION NUMBER: US/10/975,740A
/ CURRENT FILING DATE: 2004-01-28
/ PRIOR APPLICATION NUMBER: US 60/223,358
/ PRIOR FILING DATE: 2000-08-07
/ PRIOR APPLICATION NUMBER: US 60/236,827
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: US 09/920,262
/ PRIOR FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver 3.1
/ SEQ ID NO 6
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-975-740A-6
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```
Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
        ||:||||
Db       4 NIPYPT 9
```

```
RESULT 11
US-10-975-708-6
/ Sequence 6, Application US/10975708
/ Publication No. US20050214293A1
/ GENERAL INFORMATION:
/ APPLICANT: Gilles-Komar, Jill
```

```

; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND COMPOSITIONS
; FILE REFERENCE: CEN0248DI02
; CURRENT APPLICATION NUMBER: US/10/975,708
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-708-6
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```
Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db       4 NIPYPT 9
```

```

RESULT 12
US-10-808-187-1387
; Sequence 1387, Application US/10808187
; Publication No. US200500909A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-1387
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```

Query Match          33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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```
QY      3 GOKATNIPYPT 13
      ||:||||
Db       1 GQSQSNILPQT 11
```

```

RESULT 13
US-10-807-807-1387
; Sequence 1387, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-1387
```

```
Query Match          33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      3 GOKATNIPYPT 13
      ||:||||
Db       1 GQSQSNILPQT 11
```

```

RESULT 14
US-10-107-532-5915
; Sequence 5915, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Paris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afari, Daniel E.H.
US-10-107-532-5915
```

```
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Archur
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE REFERENCE: 51158-200064.00
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US/10/107,532
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5915
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-5915
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Query Match          33.0%; Score 32; DB 4; Length 15;
Best Local Similarity 53.8%; Pred. No. 3e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
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Qy      5 KATNIPYTPGK 17
      |||:|
Db      3 KATNLAPADPNK 15
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RESULT 15
US-10-107-532-6124
; Sequence 6124, Application US/10107532
; Publication No. US20040003418A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Jakobovits, Aya
; APPLICANT: Farris, Mary
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Morrison, Robert Kendall
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel E.H.
; APPLICANT: Ge, Wangmao
; APPLICANT: Raitano, Archur
; APPLICANT: Challita-Bid, Pia M.
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; FILE REFERENCE: 51158-200064.00
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US/10/107,532
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,112
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 6321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6124
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-107-532-6124
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Query Match          33.0%; Score 32; DB 4; Length 15;
Best Local Similarity 53.8%; Pred. No. 3e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
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```
Qy      5 KATNIPYTPGK 17
      |||:|
Db      3 KATNLAPADPNK 15
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Search completed: December 12, 2005, 21:29:23
Job time : 95 secs

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OW protein - protein search, using sw model

Run on: December 12, 2005, 21:17:33 / Search time 3 seconds
(without alignments)
33.507 Million cell updates/sec

Title: US-10-758-165A-10
Perfect score: 97
Sequence: 1 VDCGKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62
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Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 9754

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published Applications AA New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	28.9	14	7	US-11-054-515-2653
2	27	27.8	14	7	US-11-054-515-2682
3	26	26.8	13	6	US-10-511-559-1085
4	25	25.8	9	7	US-11-009-939-10
5	25	25.8	9	7	US-11-009-939-40
6	25	25.8	18	6	US-10-828-033-36
7	24	24.7	8	6	US-10-999-866-57
8	24	24.7	13	6	US-10-977-334-8
9	24	24.7	16	6	US-10-507-275-17
10	24	24.7	17	7	US-11-082-381-3
11	23	23.7	9	6	US-10-952-535A-28
12	23	23.7	9	6	US-10-952-535A-43
13	23	23.7	9	7	US-11-010-748A-334
14	23	23.7	9	7	US-11-010-748A-346
15	23	23.7	9	7	US-11-158-848-41
16	23	23.7	9	7	US-11-178-639-3
17	23	23.7	9	7	US-11-137-671-4
18	23	23.7	10	6	US-10-933-025-19
19	23	23.7	10	7	US-11-093-274-16
20	23	23.7	10	7	US-11-137-671-3
21	23	23.7	11	7	US-11-137-671-2
22	23	23.7	12	6	US-10-632-150-82
23	23	23.7	12	6	US-10-507-662-9
24	23	23.7	12	6	US-10-952-535A-33
25	23	23.7	12	6	US-11-073-457-82

26	23	23.7	12	7	US-11-137-671-1	Sequence 1, Appli
27	23	23.7	13	6	US-10-511-559-719	Sequence 719, App
28	23	23.7	13	7	US-11-089-551A-8	Sequence 8, Appli
29	23	23.7	14	7	US-11-054-515-2374	Sequence 2374, Ap
30	23	23.7	14	7	US-11-054-515-2474	Sequence 2474, Ap
31	23	23.7	14	7	US-11-054-515-2655	Sequence 2655, Ap
32	23	23.7	14	7	US-11-054-515-2656	Sequence 2656, Ap
33	23	23.7	14	7	US-11-054-515-2657	Sequence 2657, Ap
34	23	23.7	14	7	US-11-054-515-2658	Sequence 2658, Ap
35	23	23.7	14	7	US-11-054-515-2670	Sequence 2670, Ap
36	23	23.7	14	7	US-11-054-515-2673	Sequence 2673, Ap
37	23	23.7	14	7	US-11-054-515-2676	Sequence 2676, Ap
38	23	23.7	14	7	US-11-054-515-2679	Sequence 2679, Ap
39	23	23.7	14	7	US-11-054-515-2710	Sequence 2710, Ap
40	23	23.7	14	7	US-11-054-515-2719	Sequence 2719, Ap
41	23	23.7	15	6	US-10-952-535A-32	Sequence 32, Appli
42	22.5	23.2	14	7	US-11-054-515-2361	Sequence 2361, Ap
43	22.5	23.2	14	7	US-11-054-515-2385	Sequence 2385, Ap
44	22.5	23.2	14	7	US-11-054-515-2608	Sequence 2608, Ap
45	22.5	23.2	14	7	US-11-054-515-2617	Sequence 2617, Ap

ALIGNMENTS

RESULT 1
US-11-054-515-2653
; Sequence 2653, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS2393
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2653
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2653
Query Match 28.9%; Score 28; DB 7; Length 14;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 IFPYTAP 15
Db 6 LFFYNP 12
RESULT 2

```
US-11-054-515-2682
; Sequence 2682, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2682
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2682

Query Match          27.8%; Score 27; DB 7; Length 14;
Best Local Similarity 80.0%; Pred. No. 30;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      9 FPPYT 13
       : |||
Db      6 LFPYT 10

RESULT 3
US-10-511-559-1085
; Sequence 1085, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Tim
; APPLICANT: Baker, Matthew
; APPLICANT: Carr, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1085
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-1085
```

```
Query Match          26.8%; Score 26; DB 6; Length 13;
Best Local Similarity 45.5%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      7 TNFFPYAPGK 17
       : |||
Db      1 TNMFATWPSK 11

RESULT 4
US-11-009-939-10
; Sequence 10, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-10

Query Match          25.8%; Score 25; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 FPYT 13
       : |||
Db      6 FPYT 9

RESULT 5
US-11-009-939-40
; Sequence 40, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-40

Query Match          25.8%; Score 25; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      8 NFPYT 13
       : |||
```

```

Db          4 NTFPWT 9

RESULT 6
US-10-828-033-36
; Sequence 36, Application US/10828033
; Publication No. US20050250206A1
; GENERAL INFORMATION:
; APPLICANT: Paul B. Fisher and Ruoguan Shen
; TITLE OF INVENTION: DEVELOPMENT OF DNA PROBES AND IMMUNOLOGICAL REAGENTS
; TITLE OF INVENTION: SPECIFIC FOR CELL
; FILE REFERENCE: SURFACE-EXPRESSED MOLECULES AND TRANSFORMATION-ASSOCIATED GENES
; CURRENT FILING DATE: 2004-04-20
; PRIOR FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: US/08/875,553
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human
US-10-828-033-36

Query Match          25.8%; Score 25; DB 6; Length 18;
Best Local Similarity 55.6%; Pred. No. 86;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY          3 GQKATNIFP 11
           ||:|:|
           10 GQEAVFYFP 18

Db

RESULT 7
US-10-999-866-57
; Sequence 57, Application US/10999866
; Publication No. US2005026004A1
; GENERAL INFORMATION:
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND
; FILE REFERENCE: CENS042NP
; CURRENT APPLICATION NUMBER: US/10/999,866
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: 60/527,794
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(8)
; OTHER INFORMATION: LC CDR3
US-10-999-866-57

Query Match          24.7%; Score 24; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY          8 NIFPYT 13
           |||
           3 NTLPYT 8

Db

RESULT 8
US-10-977-334-8
; Sequence 8, Application US/10977334
; Publication No. US20050244904A1
; GENERAL INFORMATION:
; APPLICANT: NG, LEONG

```

```

; TITLE OF INVENTION: DIAGNOSTICS BASED ON SIGNAL PEPTIDE DETECTION
; FILE REFERENCE: ISA-016.01
; CURRENT APPLICATION NUMBER: US/10/977,334
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: 60/542,647
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: GB 0325279.8
; PRIOR FILING DATE: 2003-10-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-977-334-8

Query Match          24.7%; Score 24; DB 6; Length 13;
Best Local Similarity 57.1%; Pred. No. 89;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY          11 PYTAPGK 17
           |||:|
           1 PQTAPSR 7

Db

RESULT 9
US-10-507-275-17
; Sequence 17, Application US/10507275
; Publication No. US20050250166A1
; GENERAL INFORMATION:
; APPLICANT: Masai, Hisao
; APPLICANT: Tamai, Katsuyuki
; APPLICANT: Medical and Biological Laboratories Co., Ltd.
; APPLICANT: Japan Science and Technology Agency
; APPLICANT: Ginkgo Biomedical Research Institute Co., Ltd.
; TITLE OF INVENTION: Cdc7-ASK Kinase Complex, Substrates of the Kinase Complex,
; TITLE OF INVENTION: Specific Antibodies to the Substrates, and Screening Methods
; TITLE OF INVENTION: Using the Same to Screen for Compounds Comprising Cdc7-ASK
; TITLE OF INVENTION: Kinase Inhibitory Ability
; FILE REFERENCE: 082368-001100US
; CURRENT APPLICATION NUMBER: US/10/507,275
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: JP 2002-067702
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: WO PCT/JP03/02918
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:an artificially
US-10-507-275-17

Query Match          24.7%; Score 24; DB 6; Length 16;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY          9 IFPYTAP 15
           ::|||
           1 MFDVDP 7

Db

RESULT 10
US-11-082-381-3
; Sequence 3, Application US/11082381
; Publication No. US2005024434A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, David I.
; TITLE OF INVENTION: Tat-based Tolerogen Compositions and Method of Making and Using

```

```
; TITLE OF INVENTION: Same
; FILE REFERENCE: 51311-00001
; CURRENT APPLICATION NUMBER: US/11/082.381
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: 60/553733
; PRIOR FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: 60/649021
; PRIOR FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: 10/456865
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 09/636057
; PRIOR FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-082-381-3
```

```
Query Match      24.7%; Score 24; DB 7; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      11 PYTAGSQ 18
      :|||
Db      8 PMKHGSGQ 15
```

```
RESULT 11
US-10-952-535A-28
; Sequence 28, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952.535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-952-535A-28
```

```
Query Match      23.7%; Score 23; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      10 FPYTAP 15
      :|||
Db      1 YPYDVP 6
```

```
RESULT 12
US-10-952-535A-43
; Sequence 43, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Leeceit, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
```

```
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952.535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-952-535A-43
```

```
Query Match      23.7%; Score 23; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      10 FPYTAP 15
      :|||
Db      1 YPYDVP 6
```

```
RESULT 13
US-11-010-748A-334
; Sequence 334, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOHL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010.748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 334
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 328
US-11-010-748A-334
```

```
Query Match      23.7%; Score 23; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      5 KATWIFPY 12
      :|||
Db      1 KIQEIFPP 8
```

```
RESULT 14
US-11-010-748A-346
; Sequence 346, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOHL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
```


; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 346
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 328
US-11-010-748A-346

Query Match 23.7%; Score 23; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 KATNIPY 12
|
|
|
|
Db 1 KIQEIFP 8

RESULT 15
US-11-158-848-41
; Sequence 41, Application US/1158848
; Publication No. US20050249703A1
; GENERAL INFORMATION:
; APPLICANT: Anne Dam Jensen
; TITLE OF INVENTION: Interferon gamma polypeptide variants
; FILE REFERENCE: 23us410 - INFG variants
; CURRENT APPLICATION NUMBER: US/11/158,848
; CURRENT FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: US/10/116,273
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tag
US-11-158-848-41

Query Match 23.7%; Score 23; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 10 PPYTAP 15
:|
:|
:|
|
Db 1 YPYDVP 6

Search completed: December 12, 2005, 21:20:42
Job time : 3 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:18:48 ; Search time 10.6667 Seconds
(without alignments)
162.366 Million cell updates/sec

Title: US-10-758-165a-10
Perfect score: 97
Sequence: 1 VDQKATNIPFYAPGKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	27.8	17	2 HA9048	T-cell receptor be
2	27	27.8	18	2 A59137	protein p11 - gold
3	26	26.8	18	2 A61577	24k serine protein
4	24	24.7	14	2 B58502	36K kidney stone p
5	24	24.7	17	2 S18534	hypothetical prote
6	23	23.7	12	2 P00786	NADH2 dehydrogenas
7	23	23.7	15	2 B45115	peptidylprolyl iso
8	23	23.7	18	2 S20322	gluten - wheat
9	22	22.7	13	2 PNO170	alcohol dehydrogen
10	22	22.7	12	2 S01904	H+-transporting tw
11	22	22.7	15	2 PA0056	protein QF200002 -
12	22	22.7	15	2 PA0087	cytochrome c2 - fu
13	22	22.7	15	2 PA0099	phenotypic variact
14	22	22.7	16	2 A28144	ribosomal protein
15	22	22.7	17	2 C84063	hypothetical prote
16	22	22.7	18	2 C56046	urinary tract ston
17	21	21.6	10	2 S71948	matrix metalloprot
18	21	21.6	10	2 A39745	endo-glucosylceram
19	21	21.6	11	2 A34135	DNA-binding protei
20	21	21.6	12	2 A53524	ubiquinol-cytochro
21	21	21.6	14	2 PLO142	carbon-monoxide de
22	21	21.6	15	2 S59495	formate dehydrogen
23	21	21.6	15	2 B61457	alpha-glucosidase
24	21	21.6	16	2 E53284	T-cell receptor be
25	21	21.6	16	2 S18292	30K allergen - rye
26	21	21.6	17	2 S50901	chlorophyll a/b-bi
27	21	21.6	18	2 S70612	T cell receptor be
28	21	21.6	18	2 S70612	alpha-macroglobulin
29	20.5	21.1	18	2 A28027	protein p2 - curle

30	20	20.6	9	2 S59902	glutathione transf
31	20	20.6	9	2 D48186	Arpase R1 subunit
32	20	20.6	9	2 S10784	enamelin i - bovin
33	20	20.6	13	2 B58533	CD61 homolog - cha
34	20	20.6	14	2 S22236	lipoygenase (EC 1
35	20	20.6	14	2 S19803	ubiquitin - potato
36	20	20.6	14	2 PA0109	porin por 1B - Ara
37	20	20.6	14	2 G44957	photosystem II oxy
38	20	20.6	14	2 PH1306	Ig heavy chain DJ
39	20	20.6	14	2 PA0045	porin por1 - Arabi
40	20	20.6	14	2 S12904	protein kinase (EC
41	20	20.6	15	2 PA0097	starch phosphoryla
42	20	20.6	15	2 S71300	ICU3 protein - Par
43	20	20.6	15	2 P50455	superoxide diasmu
44	20	20.6	15	2 PA0063	ubiquitin - fungus
45	20	20.6	15	2 A49177	22k protein p1, ml

ALIGNMENTS

RESULT 1
HA9048
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: HA9048
R:Stoud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
Eur. J. Immunol. 22, 2413-2418, 1992
A:Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile
A:Reference number: A49048; MUID:92387250; PMID:1387614
A:Accession: HA9048
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-17 <SIO>
A:Cross-references: UNIPARC:UPI0000176DF0
A:Experimental source: patient SS, IL-2R+ synovial T-cells
A:Note: sequence extracted from NCBI backbone (NCBIP:113270)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 27.8%; Score 27; DB 2; Length 17;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ATNIPPT 13
| | | | |
DB 8 AWTFFPYT 15

RESULT 2
A59137
protein p11 - golden needle mushroom (fragment)
C:Species: Flammulina velutipes (golden needle mushroom)
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C:Accession: A59137
R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
Submitted to the Protein Sequence Database, November 1999
A:Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr
A:Reference number: A59137
A:Accession: A59137
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <SAK>
A:Cross-references: UNIPROT:Q7M4W6; UNIPARC:UPI000017CB27

Query Match 27.8%; Score 27; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PYTAP 15
| | | | |
DB 2 PYTSP 6

RESULT 3
A61577
24k serine proteinase (EC 3.4.21.-) - Streptomyces fradiae (fragment)
C:Species: Streptomyces fradiae
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C:Accession: A61577
R:Sinha, U.; Wolz, S.A.; Lad, P.J.
Int. J. Biochem. 23, 979-984, 1991
A:Title: Two new extracellular serine proteinases from Streptomyces fradiae.
A:Reference number: A61577; MUID:92155439; PMID:1786859
A:Accession: A61577
A:Molecule type: protein
A:Residues: 1-18 <SIN>
A:Cross-references: UNIPROT:Q7M19; UNIPARC:UPI000017AE13
C:Keywords: extracellular protein; hydrolase; serine proteinase

Query Match 26.8%; Score 26; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 VDGGKATNIPY 12
| | | | | | | | | | | | | | | | | | | | | |
2 VGGTRAAQEPFW 13

RESULT 4
B58502
36k kidney stone protein - unidentified bacterium (fragment)
C:Species: unidentified bacterium
C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C:Accession: B58502
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: B58502
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <BIN>
A:Cross-references: UNIPARC:UPI000017A8D0
A:Experimental source: human kidney stone containing Ca ox.monoh dihyd, 1% struvite, CaF
A:Note: tentative identification of 8-Tyr and 9-Thr

Query Match 24.7%; Score 24; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 9.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 NIPPYT 13
| | | | | | | | | | | | | | | | | | | | | |
4 NLFGYT 9

RESULT 5
S18534
hypothetical protein 7 (eryg 3' region) - Saccharopolyspora erythraea (fragment)
C:Species: Saccharopolyspora erythraea
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-Apr-1994
C:Accession: S18534
R:Haydock, S.F.; Dowson, J.A.; Dillon, N.; Roberts, G.A.; Cortes, J.; Leadlay, P.F.
Mol. Gen. Genet. 230, 120-128, 1991
A:Title: Cloning and sequence analysis of genes involved in erythromycin biosynthesis in
methylintraferases.
A:Reference number: S18530; MUID:92079886; PMID:1840640
A:Accession: S18534
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-17 <HAY>
A:Cross-references: UNIPARC:UPI000017AD81; EMBL:X60379
A:Note: the authors translated the codon CTG for residue 12 as Gly

Query Match 24.7%; Score 24; DB 2; Length 17;

Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 9 IFPYTAP 16
| | | | | | | | | | | | | | | | | | | | | |
Db 1 IFPAVAG 8

RESULT 6
P00786
NADH2 dehydrogenase (EC 1.6.99.3) 26k chain - fava bean mitochondrion (fragment)
N:Alternate names: complex I 26k chain; NADH-ubiquinone reductase 26k chain
C:Species: mitochondrion Vicia faba (fava bean)
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: P00786
R:lesterme, S.; Boutry, M.
Plant Physiol. 102, 435-443, 1993
A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH2
A:Reference number: P00775; MUID:94151437; PMID:8108509
A:Accession: P00786
A:Molecule type: protein
A:Residues: 1-12 <LET>
A:Cross-references: UNIPROT:Q7M2G3; UNIPARC:UPI000017CDAB
C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the th
ranging from 5k to 75k.
C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by
C:Genetics:
A:Genome: mitochondrion
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 23.7%; Score 23; DB 2; Length 12;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

OY 6 ATNI-PPYTAGK 17
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ATGVPIPY-APGE 12

RESULT 7
B45115
peptidylprolyl isomerase (EC 5.2.1.8) FKBP51 - human (fragment)
N:Alternate names: FK506-binding protein FKBP51; peptidylprolyl cis-trans isomerase FKBP
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B45115
R:Wiederecht, G.; Hung, S.; Chan, H.K.; Marxy, A.; Martin, M.; Calaycay, J.; Boulton, D
J. Biol. Chem. 267, 21753-21760, 1992
A:Title: Characterization of high molecular weight FK-506 binding activities reveals a nc
A:Reference number: A45115; MUID:93016131; PMID:1383226
A:Accession: B45115
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <WIE>
A:Cross-references: UNIPROT:Q9UDK1; UNIPARC:UPI0000035473
A:Experimental source: JURKAT cells
A:Note: sequence extracted from NCBI backbone (NCBIP:116748)
C:Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match 23.7%; Score 23; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 6 ATNIPYTAGP 15
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ATESIAVLAP 10

RESULT 8
S20322
gluten - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C:Accession: S20322
R:Fukudome, S.; Yoshikawa, M.
FEBS Lett. 296, 107-111, 1992
A:Title: Opioid peptides derived from wheat gluten: their isolation and characterization
A:Reference number: S20322; PMID:92111773; PMID:1309704
A:Accession: S20322
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-18 <P>
A:Cross-references: UNIPROT:Q7M1G0; UNIPARC:UPI000017B139

Query Match 23.7%; Score 23; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 GQKATNIPY 12
DB 1 GYPTGYGYP 10

RESULT 9
PNO170
alcohol dehydrogenase (EC 1.1.1.1) - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: PNO170
R:Chow, L.P.; Sugita, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JRPID, May 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PNO160
A:Accession: PNO170
A:Molecule type: protein
A:Residues: 1-12 <P>
A:Cross-references: UNIPROT:Q7M429; UNIPARC:UPI000017B3F6
A:Experimental source: strain M-1-1
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 22.7%; Score 22; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTPGK 17
DB 6 YTVGK 11

RESULT 10
S01904
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Arabidopsis thaliana chloro
C:Species: chloroplast Arabidopsis thaliana (mouse-ear cress)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: S01904
R:Chen, H.C.; Wintz, H.; Weil, J.H.; Pillay, D.T.N.
Nucleic Acids Res. 16, 10372, 1988
A:Title: Nucleotide sequence of chloroplast CFI-ATPase epsilon-subunit and elongator rRN
A:Reference number: S01903; PMID:89057486; PMID:2904134
A:Accession: S01904
A:Status: translation not shown
A:Molecule type: DNA
A:Cross-references: UNIPROT:P19366; UNIPARC:UPI00001ED348; EMBL:X12889; NID:g11332; PIDN
C:Genetics:
A:Gene: atpB
A:Genome: chloroplast
C:Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match 22.7%; Score 22; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KATNI 9
DB 1 KATNI 5

RESULT 11
PA0056
protein QP20002 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0056
R:Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JRPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0056
A:Molecule type: protein
A:Residues: 1-15 <CHO>
A:Cross-references: UNIPARC:UPI000017B408

Query Match 22.7%; Score 22; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATNIF 10
DB 11 ATNIF 15

RESULT 12
PA0087
cytochrome c2 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: PA0087
R:Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JRPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0087
A:Molecule type: protein
A:Residues: 1-15 <CHO>
A:Cross-references: UNIPROT:Q7M427; UNIPARC:UPI000017B3F8
C:Keywords: electron transfer; heme; photosynthesis

Query Match 22.7%; Score 22; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGKATNIF 10
DB 4 DIKGANLF 12

RESULT 13
PA0099
phenolic variation protein - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: PA0099
R:Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JRPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0099
A:Molecule type: protein
A:Residues: 1-15 <CHO>
A:Cross-references: UNIPROT:Q7M4Y7; UNIPARC:UPI000017B405

Query Match 22.7%; Score 22; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PPTAPG 16
DB 7 FKYSASG 13

RESULT 14

A28144
 ribosomal protein S27a - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004
 C;Accession: A28144
 R;Reedman, K.L.; Rechsteiner, M.
 J. Biol. Chem. 263, 4926-4931, 1988
 A;Title: Extended reading frame of a ubiquitin gene encodes a stable, conserved, basic P
 A;Reference number: A28144; MUID:88169619; PMID:2832412
 A;Accession: A28144
 A;Molecule type: protein
 A;Residues: 1-16 <RED>
 A;Cross-references: UNIPROT:O97577; UNIPARC:UPI0000177161
 C;Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homology;
 C;Keywords: protein biosynthesis

Query Match 22.7%; Score 22; DB 2; Length 16;
 Best Local Similarity 66.7%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 12 YTAGK 17
 | | | | |
 Db 9 YTPPK 14

RESULT 15

C84063
 hypothetical protein BH3307 [imported] - Bacillus halodurans (strain C-125)
 C;Species: Bacillus halodurans
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C;Accession: C84063
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A;Reference number: A83650; MUID:20512582; PMID:11058132
 A;Accession: C84063
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-17 <STO>
 A;Cross-references: UNIPROT:Q9K7Q4; UNIPARC:UPI00000C4168; GB:AP001518; GB:BA000004; NIT
 A;Experimental source: strain C-125
 C;Genetics:

Query Match 22.7%; Score 22; DB 2; Length 17;
 Best Local Similarity 57.1%; Pred. No. 2.6e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 DGQKATN 8
 | : | | |
 Db 10 DNKKQTN 16

Search completed: December 12, 2005, 21:24:32
 Job time : 11.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:17:48 ; Search time 61.6667 Seconds

(without alignments)
205.938 Million cell updates/sec

Title: US-10-758-165A-10

Perfect score: 97

Sequence: 1 VDGOKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 11298

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : UniProt_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	35.1	17	2	046473_FELCA
2	33	33.0	8	2	070Y88_9LAMI
3	28.5	29.4	18	2	09TWM4_LUCCU
4	27.5	28.4	16	2	08L1Y7_PLBBO
5	27	27.8	18	2	07M4W6_FLAVE
6	26	26.8	15	2	07S007_NEUCR
7	26	26.8	18	2	07M198_STFR
8	25	25.8	15	2	09UR63_EMBNI
9	24	24.7	14	2	0714T5_9CRYP
10	24	24.7	16	2	07TRH9_PHOSU
11	24	24.7	17	2	065Y26_HORSE
12	23	23.7	10	2	09Z1B1_CLODI
13	23	23.7	14	2	07M2G3_VICFA
14	23	23.7	14	2	P78359_HUMAN
15	23	23.7	14	2	P82435_TOBAC
16	23	23.7	15	2	05D4R7_9CYAN
17	23	23.7	16	2	08L1Y8_9CYAN
18	23	23.7	16	2	089560_HHV8
19	23	23.7	17	2	09TMB9_ACACA
20	23	23.7	17	2	09PRU8_CHICK
21	23	23.7	18	2	07M1G0_WHEAT
22	22	22.7	8	2	059AB6_HUMAN
23	22	22.7	10	2	09QVE9_9MURI
24	22	22.7	10	2	071VN2_MOUSE
25	22	22.7	12	2	07M4Z9_FUSSP
26	22	22.7	14	2	070Y94_9LAMI
27	22	22.7	15	2	07M4Z7_FUSSP
28	22	22.7	15	2	07M4Z7_FUSSP
29	22	22.7	15	2	09TRES_BOVIN
30	22	22.7	15	2	09TRN8_PIG
31	22	22.7	16	2	070Y93_9LAMI

32	22	22.7	17	2	09K7Q4_BACHD	09K7Q4 bacillus ha
33	22	22.7	18	2	07M4Q7_HUMAN	07M4Q7 homo sapien
34	22	22.7	18	2	09TWM5_LUCCU	09TWM5 lucilia cup
35	22	22.7	18	2	09TRB6_PIG	09TRB6 sus scrofa
36	22	22.7	18	2	070Y99_9LAMI	070Y99 baetlicum p
37	21.5	22.2	17	1	COG2_CARMA	P81609 carcetus ma
38	21	21.6	9	2	030790_ERWAM	030790 erwina amy
39	21	21.6	9	2	065711_BEV	065711 berne virus
40	21	21.6	10	2	075SW3_ECOLI	075SW3 escherichia
41	21	21.6	10	2	07M0K7_RHOSO	07M0K7 rhodococcus
42	21	21.6	10	2	06LBT3_MOUSE	06LBT3 mus musculu
43	21	21.6	14	2	05SAP8_PEA	05SAP8 pium sativ
44	21	21.6	14	2	07M0N7_ALCEU	07M0N7 allcigense
45	21	21.6	14	2	08HGT1_GADMO	08HGT1 gadus morhu

ALIGNMENTS

RESULT 1						
ID	046473_FELCA	PRELIMINARY;	PRT;	17 AA.		
AC	046473;					
DT	01-JUN-1998	(TREMBlrel. 06, Created)				
DT	01-JUN-1998	(TREMBlrel. 06, Last sequence update)				
DT	01-DEC-2001	(TREMBlrel. 19, Last annotation update)				
DE	Lactase dehydrogenase A (Fragment).					
CN	Name=LDHA;					
OS	Felis silvestris catus (Cat).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;					
OC	Felis.					
OX	NCBI_TaxID=9685;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=domesticus;					
RX	MEDLINE=97141918; PubMed=8988168;					
RA	Lyons L.A., Laughlin T.F., Copeland N.G., Jenkins N.A., Womack J.E.,					
RA	O'Brien S.J.;					
RT	"Comparative anchor tagged sequences (CATS) for integrative mapping of					
RT	mammalian genomes."					
RT	Nat. Genet. 15:47-56(1997).					
DR	EMBL; AF012095; AAC00072.2; -; Genomic_DNA.					
FT	NON_TER	1	17			
FT	NON_TER	1	17			
SQ	SEQUENCE	17 AA;	2018 MW;	E47943B2E187C1FC	CRC64;	
Query Match						
Best Local Similarity		46.2%;	Pred. No. 1.9e+02;			
Matches		6;	Conservative	2;	Mismatches	5;
					Indels	0;
					Gaps	0;
QY	3	GOKATNIFPYTAP	15			
DB	3	GORNINIFKFIIP	15			
RESULT 2						
ID	070Y88_9LAMI	PRELIMINARY;	PRT;	8 AA.		
AC	070Y88;					
DT	05-JUL-2004	(TREMBlrel. 27, Created)				
DT	05-JUL-2004	(TREMBlrel. 27, Last sequence update)				
DT	05-JUL-2004	(TREMBlrel. 27, Last annotation update)				
DE	Ribosomal protein (Fragment).					
GN	Name=rpel6;					
OS	Platostoma fimbriatum.					
OC	Chloroplast.					
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;					
OC	lamids; Lamiales; Lamiales; Nepentales; Ocimeae; Platostoma.					
OX	NCBI_TaxID=204168;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					

RX PubMed=15019625; DOI=10.1016/j.jmpev.2003.08.002;
 RA Paton A., Spingate D.A., Sude S., Otieno D., Gray R., Hatley M.M.,
 RA Willis F., Simons M.S.J., Powell M.P., Savolainen V.;
 RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
 RT based on three plastid DNA regions."
 RL Mol. Phylogenet. Evol. 31:277-299(2004).
 DR EMBL; AJ505368; CAD5489.1; -; Genomic DNA.
 KW Ribosomal protein.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 789 MW; 86786772D1BA4772 CRC64;

Query Match 33.0%; Score 32; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.2e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAPG 16
 DB 2 PYTAPG 7

RESULT 3
 ID Q9TWA4_LUCCU PRELIMINARY; PRT; 18 AA.
 AC Q9TWA4;
 DT 01-MAY-2000 (TReMBLrel. 13; Created)
 DT 01-MAY-2000 (TReMBLrel. 13; Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26; Last annotation update)
 DE 25 kDa chymotrypsin-like enzyme (Fragment).
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Lucilia.
 NX NCBI_TaxID=7375;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95219141; PubMed=7704304;
 RA Caeu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Ridding G.A.,
 RA Tellam R.L.;
 RT "Excretory/secretory chymotrypsin from *Lucilia cuprina*: purification,
 RT enzymatic specificity and amino acid sequence deduced from mRNA."
 RL Insect Mol. Biol. 3:201-211(1994).
 SQ SEQUENCE 18 AA; 1322 MW; 352EB0729B126B11 CRC64;

Query Match 29.4%; Score 28.5; DB 2; Length 18;
 Best Local Similarity 58.3%; Pred. No. 1.8e+03;
 Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 2 DGQKAT-NIPFY 12
 DB 3 NGQKATVQGFY 14

RESULT 4
 ID Q8LIY7_PLEBO PRELIMINARY; PRT; 16 AA.
 AC Q8LIY7;
 DT 01-OCT-2002 (TReMBLrel. 22; Created)
 DT 01-OCT-2002 (TReMBLrel. 22; Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22; Last annotation update)
 DE Plectonema boryanum.
 OS Plectonema boryanum.
 OC Bacteria; Cyanobacteria; Oscillatoriales; Leptolyngbya.
 NX NCBI_TaxID=1184;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=UTEX 485;
 RA MEDLINE=21970088; PubMed=11972342; DOI=10.1093/nar/30.9.2025;
 RA Williams K.P.;
 RT "Descent of a split RNA."
 RL Nucleic Acids Res. 30:2025-2030(2002).
 DR EMBL; AY082652; AAM03311.1; -; Genomic DNA.

FT NON_TER 1
 SQ SEQUENCE 16 AA; 1640 MW; 60FE5965B9B00982 CRC64;

Query Match 28.4%; Score 27.5; DB 2; Length 16;
 Best Local Similarity 53.8%; Pred. No. 2.3e+03;
 Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 6 ATNIPY---TAP 15
 DB 1 ANNIVPARKTAP 13

RESULT 5
 ID Q7M4W6_FLAVE PRELIMINARY; PRT; 18 AA.
 AC Q7M4W6;
 DT 01-MAR-2004 (TReMBLrel. 26; Created)
 DT 01-MAR-2004 (TReMBLrel. 26; Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26; Last annotation update)
 DE Protein P11 (Fragment).
 OS Flammulina velutipes.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Tricholomataceae; Flammulina.
 NX NCBI_TaxID=38945;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Sakamoto Y., Ando A., Tamai Y., Miura K.;
 RL Submitted (NOV-1999) to the PIR data bank.
 DR PIR; A59137; A59137.
 FT NON_TER 1
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1956 MW; FB0434B0AF005AEC CRC64;

Query Match 27.8%; Score 27; DB 2; Length 18;
 Best Local Similarity 80.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PYTAP 15
 DB 2 PYTSP 6

RESULT 6
 ID Q7S007_NEUCR PRELIMINARY; PRT; 15 AA.
 AC Q7S007;
 DT 01-MAR-2004 (TReMBLrel. 26; Created)
 DT 01-MAR-2004 (TReMBLrel. 26; Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26; Last annotation update)
 DE Predicted protein.
 GN Name=NCU09752.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 NX NCBI_TaxID=5141;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=OR74A;
 RA Gajaffe D., Fitzhugh W., Ma L.-U., Smirnov S., Purcell S., Rehman B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selltrenekoff C.P., Kinsey J.A., Braun E.L., Zeller A., Schulte U.,
 RA Kohe G.O., Jedd G., Mewes W., Straben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnere S.,
 RA Kamal M., Kamyselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
 RA Krysstofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
 RA Desouza C.C., Glase L., Orbach M.J., Berglund J., Voelker R.,
 RA Yarden O., Piamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Eboho D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander B.S., Nubung C., Birren B.,
 RT "The genome sequence of the filamentous fungus *Neurospora crassa*."

RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABX01000580; FNA28619.1; -; Genomic DNA.
SQ SEQUENCE 15 AA; 1832 MW; 012D0180A8C7089D CRC64;

Query Match 26.8%; Score 26; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIFPPT 13
DB 2 NVFEXT 7

RESULT 7
Q7M198 STFR PRELIMINARY; PRT; 18 AA.
AC Q7M198;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE 24k serine proteinase (EC 3.4.21.-) (Fragment).
OS Streptomyces fradiae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxId=1906;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92155439; PubMed=1786859; DOI=10.1016/0020-711X(91)90133-8;
RA Sinha U., Wolz S.A., Lad P.J.;
RT "Two new extracellular serine proteases from Streptomyces fradiae";
RL Int. J. Biochem. 23:979-984(1991).
DR PIR, A61577; A61577.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2004 MW; 6D6DA167845934A5 CRC64;

Query Match 26.8%; Score 26; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 4.7e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGKATNIPY 12
DB 2 VQGTBAAGEPW 13

RESULT 8
Q9UR63 EMENI PRELIMINARY; PRT; 15 AA.
AC Q9UR63;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Beta-D-FRUCTOFURANOSIDE FRUCTOHYDROLASE 60 kDa high molecular weight
isoform (EC 3.2.1.26) (Fragment).
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxId=162425;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96409246; PubMed=8814228; DOI=10.1016/0167-4838(96)00073-8;
RA Chen U.S., Saxon J., Hemming F.W., Peberdy J.F.;
RT "Purification and partial characterization of the high and low
RT molecular weight form (S- and F-form) of invertase secreted by
RT Aspergillus nidulans";
RL Biochim. Biophys. Acta 1296:207-218(1996).
DR GO, GO:0004564; F-beta-fructofuranosidase activity; IEA.
SQ SEQUENCE 15 AA; 1588 MW; 2C992B42211366BB CRC64;

Query Match 25.8%; Score 25; DB 2; Length 15;

Best Local Similarity 80.0%; Pred. No. 5.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAP 15
DB 10 PYTEP 14

RESULT 9
Q714T5 9CRYP PRELIMINARY; PRT; 14 AA.
ID Q714T5_9CRYP
AC Q714T5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE tRNA, proteolysis tag (Fragment).
GN Name=serA;
OS Rhodomonas salina.
OC Chloviplast.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
OX NCBI_TaxId=52970;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CCMP1319;
RX PubMed=14681369; DOI=10.1093/nar/9kh102;
RA Guenau de Nova P., Williams K.P.;
RT "The tRNA website: reductive evolution of tRNA in plastids and other
RT endosymbionts";
RL Nucleic Acids Res. 32:D104-D108(2004).
DR EMBL, AF550355; AAQ12671.1; -; Genomic DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 14 AA; 1528 MW; D95F9B3698210B9 CRC64;

Query Match 24.7%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 7.9e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 ATNIPPT 13
DB 1 ANNIVPFS 8

RESULT 10
Q7TPH9 PHOSU PRELIMINARY; PRT; 16 AA.
AC Q7TPH9;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Per2 protein (Fragment).
GN Name=Per2;
OS Phodopus sungorus (Striped hairy-footed hamster) (Djungarian hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OX Muridae; Cricetinae; Phodopus.
OX NCBI_TaxId=10044;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Soua V., Semakhdoski A.G., Loudon A.S.I.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, AY316536; AAP87362.1; -; mRNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 16 AA; 1831 MW; 845C849B44AE531 CRC64;

Query Match 24.7%; Score 24; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 9.2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 PYTAGKQ 18
DB 6 PUTSPKE 13

```

RESULT 11
Q65YZ6_HORSE PRELIMINARY; PRT; 17 AA.
AC Q65YZ6;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Asparagine-linked glycosylation 8 homolog (Fragment).
GN Name=ALG8;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxId=9796;
RN NUCLEOTIDE SEQUENCE.
RA Hasegawa T., Sato F., Tozaki T., Hirota K.;
RT "Fine mapping of equine chromosomes corresponding to HSA11."
RU Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB167785; BAD44704.1; -; Genomic_DNA.
FT NON TER 1 1
FT NON TER 17 17
SQ SEQUENCE 17 AA; 1907 MW; 24AB4757508FF8FC CRC64;

Query Match 24.7%; Score 24; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 9.8e+03;
Matches 5; Conservative 3; Mismatches 0; Indels 2; Gaps 1;

OY 8 NIPP--YTAP 15
DB 6 SLPLPLTAP 15

RESULT 12
Q9Z1B1_CLODI PRELIMINARY; PRT; 10 AA.
AC Q9Z1B1;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE Toxin B (Fragment).
GN Name=ToxB;
OS Clostridium difficile.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxId=1496;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=8864;
RA Dodson A.P., Borriello S.P.;
RU Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035716; AAD02038.1; -; Genomic_DNA.
FT NON TER 1 1
FT NON TER 10 AA; 1120 MW; 913DA042C736D0C1 CRC64;

Query Match 23.7%; Score 23; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 PYTA 14
DB 1 PYTA 4

RESULT 13
Q7M2G3_VICFA PRELIMINARY; PRT; 12 AA.
AC Q7M2G3;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE NADH2 dehydrogenase (EC 1.6.99.3) 26k chain (Fragment).
OS Vicia faba (Broad Bean).
OX NCBI_TaxId=4097;
RN NUCLEOTIDE SEQUENCE.

```

```

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Vicia.
OX NCBI_TaxId=3906;
RN NUCLEOTIDE SEQUENCE.
RA MEDLINE=94151437; PubMed=8108509; DOI=10.1104/pp.102.2.435;
RA Letenne S., Boutry M.;
RT "Purification and preliminary characterization of mitochondrial
RT complex I (NADH:ubiquinone reductase) from broad bean (Vicia faba
RT L.)".
RL Plant Physiol. 102:435-443(1993).
DR PIR; PQ0786; PQ0786.
DR GO; GO:0003954; F:NADH dehydrogenase activity; IEA.
FT NON TER 1 1
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1171 MW; 29C1BC39CE476047 CRC64;

Query Match 23.7%; Score 23; DB 2; Length 12;
Best Local Similarity 53.8%; Pred. No. 1e+04;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

OY 6 ATNI-FPYTAPK 17
DB 1 ATGVPIPY-APGE 12

RESULT 14
P78359_HUMAN PRELIMINARY; PRT; 14 AA.
AC P78359;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NF-kappa-B transcription factor p65 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxId=9606;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Umbilical vein;
RA Remacle J.E., Brys R., Pye S., Nelles L., Huylebroeck D.;
RU Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88316; AAB48487.1; -; mRNA.
FT NON TER 14 14
FT NON TER 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

Query Match 23.7%; Score 23; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 9 IFPYTAP 15
DB 8 IFPQSQP 14

RESULT 15
P82435_TOBAC PRELIMINARY; PRT; 14 AA.
AC P82435;
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE 29 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxId=4097;
RN NUCLEOTIDE SEQUENCE.

```

RC STRAIN=CV. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Siabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
DR GO:0005618; C:cell wall; IEA.
KW Cell wall.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1645 MW; CA0D490EF7F851B2 CRC64;
Query Match 23.7%; Score 23; DB 2; Length 14;
Best Local Similarity 30.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 4 OKATNIFPYT 13
:|:|:|:
Db 4 RKTVDVFTFT 13

Search completed: December 12, 2005, 21:23:54
Job time : 61.6667 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:37:19 ; Search time 97.6034 Seconds
(without alignment)
81.030 Million cell updates/sec

Title: US-10-758-165A-10
Perfect score: 97
Sequence: 1 VDGQKATNIPFYTAPEKQ 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	18	ADRI0610	Cat IGE e
2	97	100.0	431	ADG73237	Cat immun
3	97	100.0	496	ABP96580	Cat IGE h
4	97	100.0	496	ABU09338	Feline Ig
5	97	100.0	496	ABU09336	Feline Ig
6	97	100.0	496	ADG73251	Cat parti
7	97	100.0	496	ADG73225	Cat parti
8	87	88.7	18	ADRI0609	Dog IGE e
9	87	88.7	312	AAI79995	Dog immun
10	87	89.7	417	AAW23067	Canine Ig
11	87	89.7	426	AAAR9753	Canine Ig
12	87	89.7	426	ABP96583	Dog IGE h
13	72	79.4	577	ABP96584	Duckhille
14	72	79.4	343	AAAB06204	Platyphus
15	60	61.9	337	ADP90022	Opossum-r
16	60	61.9	337	ADN00643	ORO prote
17	60	61.9	338	ADN00643	Opossum-h
18	60	61.9	338	ADN00646	OSO prote
19	60	61.9	341	AAAB06206	Opossum-h
20	60	61.9	341	AAAB03644	Opossum I
21	60	61.9	341	AAAB06208	Immunogen
22	60	61.9	342	AAAB06205	Immunogen
23	60	61.9	345	AAAB06207	Immunogen
24	60	61.9	347	ADP90033	Opossum-h

25	60	61.9	347	8	ADN00654	Adn00654 OSO-H pro
26	60	61.9	353	8	ADN00661	Adn00661 H-OCO-H p
27	60	61.9	427	6	ABP96591	Abp96591 Bruchtail
28	60	61.9	446	6	ABP96587	Abp96587 Opossum I
29	60	61.9	555	8	ADP90027	Adp90027 Opossum-r
30	60	61.9	555	8	ADN00648	Adn00648 OROKO pro
31	60	61.9	557	8	ADP90031	Adp90031 Opossum-h
32	60	61.9	557	8	ADP90035	Adp90035 Opossum-h
33	60	61.9	557	8	ADN00656	Adn00656 OSO pro
34	60	61.9	557	8	ADN00652	Adn00652 modOSO
35	60	61.9	566	8	ADP90029	Adp90029 Opossum-h
36	60	61.9	566	8	ADP90037	Adp90037 Opossum-h
37	60	61.9	566	8	ADN00658	Adn00658 OSO-H p
38	60	61.9	566	8	ADN00650	Adn00650 modOSO
39	55	56.7	18	8	ADRI0612	Adri0612 Sheep IGE
40	55	56.7	342	3	AAAB06202	Abab06202 Immunogen
41	55	56.7	342	3	AAAB06201	Abab06201 Immunogen
42	55	56.7	567	6	ABP96588	Abp96588 Pig IGE h
43	44	45.4	87	3	AAAY83167	AAy83167 PAGE1 p01
44	44	45.4	99	7	ADG42685	Adg42685 Human PAG
45	44	45.4	99	7	ADJ55754	Adj55754 Peptide h

ALIGNMENTS

RESULT 1
ADRI0610
ID ADRI0610 standard; peptide: 18 AA.

AC ADRI0610;
XX
XX
DT 21-OCT-2004 (first entry)
XX
DE Cat IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.
XX
KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW cat.
XX
OS Fells catue.
XX
PN WO2004065936-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.
XX
XX (UWNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hammerberg B;
XX
XX WPI; 2004-593545/57.
XX
PT Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
PS Example 6; Page 9; 14pp; English.
XX
CC The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGEs, e.g. dog IGE.
CC (I) is useful for testing an allergen reactivity of an IGE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IGE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IGE. The present sequence is the
CC cat IGE 3.76 recognition site.

XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGGKATNIPFYTPAGKQ 18
1 VDGGKATNIPFYTPAGKQ 18

RESULT 2
ADG73237
ID ADG73237 standard; protein; 431 AA.

XX
AC ADG73237;

XX
DT 11-MAR-2004 (first entry)

XX
DE Cat immunoglobulin E (IGE) constant region.

XX
KW antiallergic; IGE-modulator; vaccine; feline; IGF; immunoglobulin E;

XX
KW immune response; IGE-mediated response; allergy; cat; constant region.

XX
OS Felis catus.

XX
PN US2003216565-A1.

XX
PD 20-NOV-2003.

XX
PE 07-APR-2003; 2003US-00409772.

XX
PR 07-JAN-1999; 99US-0115033P.

XX
PR 07-JAN-2000; 2000US-00479614.

XX
PA (MCCA/) MCCALL C.

XX
PA (WEBE/) WEBER E.

XX
PI Mccall C, Weber E;

XX
DR WPI: 2004-010802/01.

XX
DR N-PSDB; ADG73236.

XX
PT New isolated nucleic acid molecule encoding a portion of a feline IGE
PT heavy chain protein, useful for treating and/or eliciting feline immune
PT responses for IGE-mediated responses, such as allergies.

XX
PS Claim 12; SEQ ID NO 14; 44pp; English.

XX
CC The invention describes an isolated nucleic acid molecule (1) encoding a
CC portion of a feline IGE heavy chain protein. The methods and compositions
CC of the present invention are useful for eliciting feline immune responses
CC for and/or treating IGE-mediated responses, such as allergies. This is
CC the amino acid sequence of a cat immunoglobulin E (IGE) constant region.

XX
SQ Sequence 431 AA;

Query Match 100.0%; Score 97; DB 8; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGGKATNIPFYTPAGKQ 18
1 VDGGKATNIPFYTPAGKQ 18

RESULT 3

ABP96580
ID ABP96580 standard; protein; 496 AA.

XX
AC ABP96580;

XX
DT 28-MAY-2003 (first entry)

XX
DE Cat IGE heavy chain amino acid sequence SEQ ID NO:25.

XX
KW Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
KW immune response; major histocompatibility complex; MHC; immunogenic;
KW antiallergic; antisthmatic; immunosuppressive; vasotropic; cytostatic;
KW dermatological; antiinflammatory; IGE-mediated condition; food allergy;
KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
KW urticaria hives.

XX
OS Felis catus.

XX
PN WO2003015716-A2.

XX
PD 27-FEB-2003.

XX
PE 08-AUG-2002; 2002WO-US026986.

XX
PR 13-AUG-2001; 2001US-0312120P.

XX
PA (IGET-) IGE THERAPEUTICS INC.

XX
PI Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX
DR WPI: 2003-268242/26.

XX
PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
PT against IGE, by identifying peptide eliciting CTL response to IGE
PT peptides naturally presented by major histocompatibility complex class I
PT protein.

XX
PS Example 7; Page 145-147; 187pp; English.

XX
CC The present invention describes a method (M1) for identifying peptides
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
CC E (IGE), comprising providing a test peptide (T) suspected of being able
CC to bind to major histocompatibility complex (MHC) class I molecule, and
CC evaluating (T) for ability to elicit in a mammal a CTL response to
CC naturally processed and presented IGE peptides, where a peptide that
CC induces such a response is identified. Also described are compositions:
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
CC (C2) comprising at least one isolated polynucleotide encoding (I); and
CC (C3) comprising antigen-presenting cells that recognise at least one (I).
CC Where C1-3 are able to bind to at least one MHC class I molecule and to
CC elicit in a mammal a CTL response to naturally processed and presented
CC IGE peptides, C1-3 have antiallergic, antisthmatic, immunosuppressive,
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
CC and can be used as inducers of a CTL response against IGE, and in
CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as
CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
CC useful for treating atopic hypersensitivity conditions (such as allergic
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
CC hives). The present sequence represents an IGE heavy chain amino acid
CC sequence, which is given in an example from the present invention

XX
SQ Sequence 496 AA;

Query Match 100.0%; Score 97; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGGKATNIPFYTPAGKQ 18
1 VDGGKATNIPFYTPAGKQ 18

Db 216 VDGOKATNIFPYTAPGKQ 233

RESULT 4
ABU09338
ID ABU09338 standard; protein; 496 AA.
AC ABU09338;
XX
XX 27-JUN-2003 (first entry)
XX
XX Feline IGE epsilon heavy chain #2.
DE
XX Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;
KW IGE-mediated immune response; allergy; neoplasia; vaccine technology;
KW antibody technology; antiallergic; antiparasitic; cytostatic.
OS Felis catus.
XX
XX US2003013183-A1.
XX
XX 16-JAN-2003.
XX
XX 07-JAN-2000; 2000US-00479614.
XX
XX 07-JAN-1999; 99US-0115033P.
XX
XX (MCCA/) MCCALL C.
XX (WEBER/) WEBER E.
XX
XX Mccall C, Weber E;
XX
XX MPI: 2003-391997/37.
XX N-PSDB; ABX95715.
XX
XX New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or
PT light chain protein, useful for treating feline IGE-mediated responses
PT e.g. allergies, parasitic infections or neoplasia.
XX
XX
XX Claim 1; Page 37-39; 45pp; English.
XX
XX The present invention relates to the isolation of feline immunoglobulin E
CC (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the
CC polynucleotide sequences encoding them. The sequences of the invention
CC are useful for treating feline IGE-mediated immune responses (e.g.
CC allergies, parasitic infections or neoplasia), in vaccine technology,
CC small molecule/antibody technology, molecular biology, and various
CC immunological techniques related to feline IGE and its functions. The
CC present sequence represents feline IGE epsilon heavy chain #2
XX
XX
SQ Sequence 496 AA;
Query Match 100.0%; Score 97; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDGOKATNIFPYTAPGKQ 18
Db 216 VDGOKATNIFPYTAPGKQ 233

RESULT 5
ABU09336
ID ABU09336 standard; protein; 496 AA.
XX
XX ABU09336;
XX
XX 27-JUN-2003 (first entry)
XX
XX Feline IGE epsilon heavy chain #1.
XX
XX Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;
KW IGE-mediated immune response; allergy; neoplasia; vaccine technology;

KW antibody technology; antiallergic; antiparasitic; cytostatic.
OS Felis catus.
XX
XX
XX Key Location/Qualifiers
FH Region 66..496
FT /note= "This sequence is given as SEQ ID No:14 and is
FT specifically claimed in Claim 12"
FT Region 284..309
FT /note= "This sequence is given as SEQ ID No:11 and is
FT specifically claimed in Claim 9"
FT Region 288..305
FT /note= "This sequence is given as SEQ ID No:8 and is
FT specifically claimed in Claim 10"
FT Region 291..302
FT /note= "This sequence is given as SEQ ID No:5 and is
FT specifically claimed in Claim 11"
XX
XX
XX US2003013183-A1.
XX
XX
XX 16-JAN-2003.
XX
XX 07-JAN-2000; 2000US-00479614.
XX
XX 07-JAN-1999; 99US-0115033P.
XX
XX (MCCA/) MCCALL C.
XX (WEBER/) WEBER E.
XX
XX Mccall C, Weber E;
XX
XX MPI: 2003-391997/37.
XX N-PSDB; ABX95713.
XX
XX New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or
PT light chain protein, useful for treating feline IGE-mediated responses
PT e.g. allergies, parasitic infections or neoplasia.
XX
XX
XX Claim 1; Page 24-25; 45pp; English.
XX
XX The present invention relates to the isolation of feline immunoglobulin E
CC (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the
CC polynucleotide sequences encoding them. The sequences of the invention
CC are useful for treating feline IGE-mediated immune responses (e.g.
CC allergies, parasitic infections or neoplasia), in vaccine technology,
CC small molecule/antibody technology, molecular biology, and various
CC immunological techniques related to feline IGE and its functions. The
CC present sequence represents feline IGE epsilon heavy chain #1
XX
XX
SQ Sequence 496 AA;
Query Match 100.0%; Score 97; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDGOKATNIFPYTAPGKQ 18
Db 216 VDGOKATNIFPYTAPGKQ 233

RESULT 6
ADG73251
ID ADG73251 standard; protein; 496 AA.
XX
XX ADG73251;
XX
XX 11-MAR-2004 (first entry)
XX
XX Cat partial immunoglobulin E (IGE) heavy chain #2.
XX
XX antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;
KW immune response; IGE-mediated response; allergy; cat; heavy chain.
KW

OS	Felis catus.
XX	
FN	US2003216565-A1.
XX	
PD	20-NOV-2003.
XX	
PE	07-APR-2003; 2003US-00409772.
XX	
PR	07-JAN-1999; 99US-0115033P.
XX	
PA	(MCCA/) MCCALL C.
XX	
PI	(WEBE/) WEBER E.
XX	
DR	Mccall C, Weber E;
XX	
DR	WPI; 2004-010802/01.
XX	
DR	N-PsDB; ADG73250.
XX	
PT	New isolated nucleic acid molecule encoding a portion of a feline IGE heavy chain protein, useful for treating and/or eliciting feline immune responses for IGE-mediated responses, such as allergies.
XX	
PS	Claim 8; SEQ ID NO 29; 44pp: English.
XX	
CC	The invention describes an isolated nucleic acid molecule (I) encoding a portion of a feline IGE heavy chain protein. The methods and compositions of the present invention are useful for eliciting feline immune responses for and/or treating IGE-mediated responses, such as allergies. This is the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy chain.
CC	
XX	
SQ	Sequence 496 AA;
XX	
Query Match	100.0%; Score 97; DB 8; Length 496;
Best Local Similarity	100.0%; Pred. NO. 1.7e-07;
Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 VDGOKATNIFPYTAPGKQ 18 216 VDGOKATNIFPYTAPGKQ 233
Db	
RESULT 7	
ID	ADG73225
XX	ADG73225 standard; protein; 496 AA.
AC	ADG73225;
XX	
DT	11-MAR-2004 (first entry)
XX	
DE	Cat partial immunoglobulin E (IGE) heavy chain #1.
KW	antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E; immune response; IGE-mediated response; allergy; cat; heavy chain.
XX	
OS	Felis catus.
XX	
PN	US2003216565-A1.
XX	
PD	20-NOV-2003.
XX	
PF	07-APR-2003; 2003US-00409772.
XX	
PR	07-JAN-1999; 99US-0115033P.
XX	
PA	(MCCA/) MCCALL C.
XX	
PI	(WEBE/) WEBER E.
XX	
DR	Mccall C, Weber E;
XX	
DR	WPI; 2004-010802/01.

DR	N-PSDB; ADG73224.
XX	
PT	New isolated nucleic acid molecule encoding a portion of a feline IGE
PT	heavy chain protein, useful for treating and/or eliciting feline immune
PT	responses for IGE-mediated responses, such as allergies.
XX	
PS	Claim 8; SEQ ID NO 2; 44pp; English.
XX	
CC	The invention describes an isolated nucleic acid molecule (I) encoding a
CC	portion of a feline IGE heavy chain protein. The methods and compositions
CC	of the present invention are useful for eliciting feline immune responses
CC	for and/or treating IGE-mediated responses, such as allergies. This is
CC	the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy
CC	chain.
XX	
SQ	Sequence 496 AA;
XX	
Query Match	100.0%; Score 97; DB 8; Length 496;
Best Local Similarity	100.0%; Pred. No. 1.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Oy	1 VDGQKATNIFPYTAGKQ 18
Db	216 VDGKATNIFPYTAGKQ 233
RESULT 8	
ID	ADRI0609
XX	ADRI0609 standard; peptide; 18 AA.
AC	ADRI0609;
XX	
DT	21-OCT-2004 (first entry)
XX	
DE	Dog IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.
XX	
KW	Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asma;
XX	anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
XX	
OS	Canis familiaris.
XX	
PM	WO2004065936-A2.
XX	
PD	05-AUG-2004.
XX	
PE	15-JAN-2004; 2004WO-US003566.
XX	
PR	16-JAN-2003; 2003US-0440472P.
XX	
PA	(UYNC-) UNIV NORTH CAROLINA STATE.
XX	
PI	Hammerberg B;
XX	
DR	WPI; 2004-593545/57.
XX	
PT	Novel antibody that specifically binds to mammalian IGE epitope, useful
PT	for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT	or treating asthma or anaphylactic shock.
XX	
PS	Example 6; Page 9; 14pp; English.
XX	
CC	The present invention relates to a novel monoclonal antibody (I) that
CC	specifically binds to a mammalian IGE epitope, where the epitope is
CC	between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC	(I) is useful for testing an allergen reactivity of an IGE sample. The
CC	allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC	and corn allergens. The sample is a biological sample collected from a
CC	dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC	treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC	antibodies recognise epitopes on canine IGE corresponding to amino acid
CC	residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC	canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
CC	cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC	

CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE.

XX
 SQ Sequence 18 AA;

Query Match 89.7%; Score 87; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAG 16
 |||||
 Db 1 VDGOKATNIFPYTAG 16

RESULT 9
 AAY79995
 ID AAY79995 standard; protein; 312 AA.

XX AAY79995;
 XX
 DT 15-MAY-2000 (first entry)

XX Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

XX Immunoglobulin E; IGE; epsilon heavy chain; antigenic; antigen;
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Canis sp.

XX MO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013959.

XX 20-JUN-1998; 98US-00100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy.

PS Example 1; Page 66-68; 155pp; English.

CC The present invention describes immunoglobulin E (IgE)-CH3 domain
 CC antigenic peptide (I). (I) have anti-allergic, anti-anaphylactic and
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
 CC a target effector site on the epsilon-heavy chain of IGE, and so
 CC preventing triggering and activation of mast cells and basophils and
 CC downregulation of IGE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IGE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe (non-
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid
 CC sequences used in the exemplification of the present invention

XX Sequence 312 AA;

Query Match 89.7%; Score 87; DB 3; Length 312;
 Best Local Similarity 100.0%; Pred. No. 5.1e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VDGOKATNIFPYTAG 16
 |||||
 Db . 48 VDGOKATNIFPYTAG 63

RESULT 10
 AAW23067
 ID AAW23067 standard; protein; 417 AA.

XX AAW23067;

XX 30-JUN-2005 (revised)

XX 16-JUN-2005 (revised)

XX 19-FEB-1998 (first entry)

XX Canine IGE heavy chain constant region (exon 1-4 product).
 KW IGE; immunoglobulin; antibody; heavy chain constant region; allergy;
 KW hypersensitivity; therapy; dog; antisense; immunomodulation.

XX Canis familiaris.

XX Key Location/Qualifiers

XX FT Misc-difference 55 /note= "encoded by ACC"

XX FT Misc-difference 56 /note= "encoded by TAC"

XX FT Misc-difference 67 /note= "encoded by GCC"

XX FT Misc-difference 83 /note= "encoded by NNT"

XX FT Misc-difference 174 /note= "encoded by GGN"

XX FT Misc-difference 175 /note= "encoded by NNG"

XX FT Misc-difference 176 /note= "encoded by TGN"

XX FT Misc-difference 203 /note= "encoded by TCC"

XX FT Misc-difference 204 /note= "encoded by GAC"

XX MO9730156-A2.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US002322.

XX 14-FEB-1996; 96US-00601197.

XX (IDEX-) IDEX LAB INC.

XX Mermer B, Harrie RA, Steffing AE;

XX WPI; 1997-425031/39.

XX N-PSDB; AAT79278.

XX Isolated canine IGE heavy chain constant region DNA - useful to develop
 PT products for treatment of canine allergies and for immunomodulation in
 PT dogs.

XX Disclosure; Page 35-39; 59pp; English.

XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IGE
 CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,
 CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant
 CC peptides encoded by exons 1-6 can be produced in eukaryotic or
 CC prokaryotic cells. Such peptides, and antibodies raised against them, are
 CC used in methods to treat the manifestation of allergy in dogs, e.g. to
 CC treat Type I immediate hypersensitivity, and for immunomodulation

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CC Revised record issued on 30-JUN-2005 : Typo in comments
XX
SQ Sequence 417 AA;

Query Match
Best Local Similarity 89.7%; Score 87; DB 2; Length 417;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 VDGQKATNIPFYTAG 16
141 VDGQKATNIPFYTAG 156

Db
141 VDGQKATNIPFYTAG 156

RESULT 11
AAR97753
ID AAR97753 standard; protein; 426 AA.
XX
AC AAR97753;
XX
DT 28-AUG-1996 (first entry)
XX
DE Canine IGE.
XX
KW IGE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
XX
OS Canis familiaris.
XX
PN MO9614867-A1.
XX
PD 23-MAY-1996.
XX
PF 03-NOV-1995; 95WO-US013795.
XX
PR 09-NOV-1994; 94US-00336583.
PR 09-NOV-1994; 94US-00336891.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Hollis GF, Patel MD;
XX
DR WPI; 1996-277321/28.
DR N-PSDB; AAT29824.
XX
PT New DNA encoding canine IGE and IGA - useful in vaccines, anti-sense
PT therapy, assays, drug screening, etc.
XX
PS Claim 11; Page 29-30; 49pp; English.
XX
CC The canine IGE amino acid sequence (AAR97753) was deduced from an
CC isolated gene (AAT29824) obtd. from a canine liver DNA library. The
CC cloning of the IGE gene allows prodn. of large quantities of recombinant
CC IGE using bacterial, yeast, mammalian, insect or viral systems. The IGE
CC can be used in drug development (e.g. small molecule screening, assay
CC development and anti-IGE antibody generation). Fragments of IGE can be
CC used in vaccines or to prevent IGE-mediated hypersensitivity. The new
CC sequence information permits targeted modulation of IGE-mediated immune
CC responses
XX
SQ Sequence 426 AA;

Query Match
Best Local Similarity 89.7%; Score 87; DB 2; Length 426;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 VDGQKATNIPFYTAG 16
146 VDGQKATNIPFYTAG 161

Db
146 VDGQKATNIPFYTAG 161

RESULT 12
ABP96583
ID ABP96583 standard; protein; 426 AA.
XX

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AC ABP96583;
XX
DT 28-MAY-2003 (first entry)
XX
DE Dog IGE heavy chain amino acid sequence SEQ ID NO:28.
XX
KW Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
KW immune response; major histocompatibility complex; MHC; immunogenic;
KW antiallergic; antisthmatic; immunosuppressive; vasotropic; cytostatic;
KW dermatological; antiinflammatory; IGE-mediated condition; food allergy;
KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
KW urticaria hives.
XX
XX
OS Canis familiaris.
XX
PN MO2003015716-A2.
XX
PD 27-FEB-2003.
XX
PF 08-AUG-2002; 2002WO-US026986.
XX
PR 13-AUG-2001; 2001US-0312120P.
XX
PA (IGET-) IGE THERAPEUTICS INC.
XX
PI Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX
DR WPI; 2003-268242/26.
XX
PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
PT against IGE, by identifying peptide eliciting CTL response to IGE
PT peptides naturally presented by major histocompatibility complex class I
PT protein.
XX
XX
PS Example 7, Page 152-154; 187pp; English.
XX
CC The present invention describes a method (M1) for identifying peptides
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
CC E (IGE), comprising providing a test peptide (T) suspected of being able
CC to bind to major histocompatibility complex (MHC) class I molecule, and
CC evaluating (T) for ability to elicit in a mammal a CTL response to
CC naturally processed and presented IGE peptides, where a peptide that
CC induces such a response is identified. Also described are compositions:
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
CC (C2) comprising at least one isolated polynucleotide encoding (I); and
CC (C3) comprising antigen-presenting cells that recognise at least one (I).
CC Where C1-3 are able to bind to at least one MHC class I molecule and to
CC elicit in a mammal a CTL response to naturally processed and presented
CC IGE peptides, C1-3 have antiallergic, antisthmatic, immunosuppressive,
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
CC and can be used as inducers of a CTL response against IGE, and in
CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as
CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
CC useful for treating atopic hypersensitivity conditions (such as allergic
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
CC hives). The present sequence represents an IGE heavy chain amino acid
CC sequence, which is given in an example from the present invention
XX
SQ Sequence 426 AA;

Query Match
Best Local Similarity 89.7%; Score 87; DB 6; Length 426;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 VDGQKATNIPFYTAG 16
146 VDGQKATNIPFYTAG 161

Db
146 VDGQKATNIPFYTAG 161

```

```

RESULT 13
ID ABP96584
XX ABP96584 standard; protein; 577 AA.
AC ABP96584;
XX
XX 28-MAY-2003 (first entry)
XX
DE Duckbilled platypus IGE heavy chain amino acid sequence SEQ ID NO:29.
XX
XX Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
XX immune response; major histocompatibility complex; MHC; immunogenic;
XX antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
XX dermatological; antiinflammatory; IGE-mediated condition; food allergy;
XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
XX urticaria hives.
XX Ornithorhynchus anatinus.
XX
XX MO2003015716-A2.
XX
XX 27-FEB-2003.
XX
XX 08-AUG-2002; 2002WO-US026986.
XX
XX 13-AUG-2001; 2001US-0312120P.
XX
XX (IGET-) IGE THERAPEUTICS INC.
XX
XX Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX WPI; 2003-268242/26.
XX
XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
XX against IGE, by identifying peptide eliciting CTL response to IGE
XX peptides naturally presented by major histocompatibility complex class I
XX protein.
XX
XX Example 7; Page 154-157; 187pp; English.
XX
XX The present invention describes a method (M1) for identifying peptides
XX that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
XX E (IGE), comprising providing a test peptide (T) suspected of being able
XX to bind to major histocompatibility complex (MHC) class I molecule, and
XX evaluating (T) for ability to elicit in a mammal a CTL response to
XX naturally processed and presented IGE peptides, where a peptide that
XX induces such a response is identified. Also described are compositions:
XX (C1) comprising at least one immunogenic peptide (I) identified by (M1);
XX (C2) comprising at least one isolated polynucleotide encoding (I); and
XX (C3) comprising antigen-presenting cells that recognise at least one (I).
XX Where C1-3 are able to bind to at least one MHC class I molecule and to
XX elicit in a mammal a CTL response to naturally processed and presented
XX IGE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,
XX vasotropic, dermatological, antiinflammatory and cytostatic activities,
XX and can be used as inducers of a CTL response against IGE, and in
XX vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
XX mammal. C1-3 are useful for modulating an IGE-mediated condition such as
XX IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
XX hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
XX useful for treating atopic hypersensitivity conditions (such as allergic
XX rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
XX atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
XX hives). The present sequence represents an IGE heavy chain amino acid
XX sequence, which is given in an example from the present invention
XX
XX Sequence 577 AA:
XX
XX Query Match 79.4%; Score 77; DB 6; Length 577;
XX Best Local Similarity 77.8%; Pred. No. 0.00047;
XX Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX 1 VDGOKATNIFPYTAPGKQ 18
XX

```

```

Db 235 VDGOKAENLFPYTAPPKR 312
||||| :||||| :
RESULT 14
ID AAB06204
XX AAB06204 standard; protein; 343 AA.
XX
XX AAB06204;
XX
XX 22-NOV-2000 (first entry)
XX
XX Platypus IGE heavy chain constant regions 2, 3 and 4.
XX
XX Platypus; immunoglobulin E; IGE; vaccination; infection; allergy; asthma;
XX eczema; immunogenic peptide.
XX Ornithorhynchus anatinus.
XX
XX Key location/Qualifiers
XX MISC-difference 1..343
XX FT /label= OTHER
XX FT /note= "Xaa=unknown"
XX
XX WO200025722-A2.
XX
XX 11-MAY-2000.
XX
XX 21-OCT-1999; 99WO-SE001896.
XX
XX 02-NOV-1998; 98US-010652P.
XX
XX 22-SEP-1999; 99US-00401636.
XX
XX (RESI-) RESISTENTIA PHARM AB.
XX
XX Hellman LT;
XX WPI; 2000-365342/31.
XX
XX Immunogenic polypeptides useful for preventing the harmful effects of
XX immunoglobulin E in mammals.
XX
XX Disclosure; Fig 2; 50pp; English.
XX
XX The present sequence is an immunogenic peptide consisting of the heavy
XX chain constant regions 2, 3 and 4 of the platypus IGE. It was used to
XX construct a number of immunogenic peptides which consisted of regions of
XX IGE from different mammals, which appear to cause a stronger polyclonal
XX anti-self IGE response than peptides consisting of the same regions from
XX one mammal. Immunogenic peptides, particularly those consisting of
XX different heavy chain constant regions, can be used for vaccination in
XX humans, against bacterial and viral infections and allergies, such as
XX asthma, fur, pollen and food allergies and eczema
XX
XX Sequence 343 AA:
XX
XX Query Match 74.2%; Score 72; DB 3; Length 343;
XX Best Local Similarity 72.2%; Pred. No. 0.0019;
XX Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX 1 VDGOKATNIFPYTAPGKQ 18
XX 61 VDGOKAENLFPYTAPPKR 78
XX
XX RESULT 15
XX ADF90022
XX ID ADF90022 standard; protein; 337 AA.
XX
XX ADF90022;
XX
XX 26-FEB-2004 (first entry)
XX

```

DE Opossum-rat chimeric IGE polypeptide.

XX IGE; immunoglobulin; antibody; opossum; rat; vaccine; antiallergic;
 KW antiaesthetic; dermatological.

XX Chimeric.

OS Didelphis virginiana.

OS Rattus sp.

PN WO200309696-A2.

XX 27-NOV-2003.

XX 15-MAY-2003; 2003WO-IB002503.

XX 21-MAY-2002; 2002US-0382552P.

XX (RESI-) RESISTENTIA PHARM AB.

XX Lundgren M, Fuentes A, Magnusson A;

XX WPI; 2004-042496/04.

DR N-PSDB; ADF90020, ADF90021.

PT New host cell comprising a nucleic acid vector comprising a
 PT cytomagalovirus promoter, an Ig leader sequence, an insert sequence or
 PT Sv40 late polyadenylation sequence, useful in producing a chimeric IGE
 PT polypeptide.

XX PS Claim 3; SEQ ID NO 3; 23pp; English.

CC The present sequence is the protein sequence of an opossum CH2-rat CH3-
 CC opossum CH4 (ORO) chimeric IGE polypeptide. A vector comprising a nucleic
 CC acid encoding ORO can be used for recombinant production of this chimeric
 CC IGE in host, e.g. CHO, cells. The invention provides methods and
 CC materials related to expressing chimeric IGE proteins. Nucleic acid
 CC vectors, host cells, and methods for producing chimeric IGE polypeptides
 CC are provided. When administered to a mammal, the chimeric polypeptides
 CC can reduce the IGE antibody effects of IGE-related diseases such as
 CC asthma, allergies and eczema.

XX SQ Sequence 337 AA;

Query Match 61.9%; Score 60; DB 8; Length 337;

Best Local Similarity 61.1%; Pred. No. 0.19;

Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 VDGGKATNIPPTABGKQ 18

Db 56 VDGGGAENLFPYTTPKR 73

Search completed: December 12, 2005, 20:30:30
 Job time : 98.6034 secs

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OW protein - protein search, using sw model

Run on: December 12, 2005, 19:23:41 ; Search time 24.5172 Seconds
(without alignments)
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Title: US-10-758-165A-10
Perfect score: 97
Sequence: 1 VDGQKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	431	2	US-09-479-614-14
2	97	100.0	496	2	US-09-479-614-2
3	97	100.0	496	2	US-09-479-614-29
4	87	89.7	108	2	US-09-281-760E-35
5	87	89.7	312	2	US-09-701-623C-2
6	87	89.7	426	1	US-08-336-583-2
7	87	89.7	426	4	PCT-US95-13795-2
8	77	79.4	343	2	US-09-401-636-7
9	60	61.9	341	2	US-09-401-636-3
10	60	61.9	341	2	US-09-401-636-4
11	60	61.9	341	2	US-09-401-636-6
12	60	61.9	341	2	US-09-401-636-9
13	60	61.9	342	2	US-09-401-636-11
14	60	61.9	342	2	US-09-401-636-5
15	60	61.9	342	2	US-09-401-636-8
16	60	61.9	345	2	US-09-401-636-10
17	42	43.3	449	2	US-09-252-991A-28547
18	42	43.3	985	2	US-09-993-777-6
19	42	43.3	985	2	US-09-993-777-66
20	42	43.3	985	4	PCT-US96-03916-6
21	42	43.3	985	4	PCT-US96-03916-66
22	41	42.3	135	2	US-09-252-991A-30004
23	41	42.3	232	2	US-09-489-039A-8106
24	40	41.2	497	2	US-10-077-699C-5
25	40	41.2	63	2	US-09-612-402B-29
26	40	41.2	63	2	US-09-542-520-29
27	40	41.2	242	2	US-09-286-690-8

28	40	41.2	391	2	US-09-721-870-38	Sequence 38, Appl
29	40	41.2	503	2	US-09-147-009-11	Sequence 11, Appl
30	40	41.2	505	2	US-09-612-402B-17	Sequence 17, Appl
31	40	41.2	505	2	US-09-542-520-17	Sequence 17, Appl
32	40	41.2	659	2	US-09-248-796A-24809	Sequence 24809, A
33	40	41.2	670	2	US-10-197-220-169	Sequence 169, Appl
34	40	41.2	829	2	US-10-055-364-46	Sequence 1589, Ap
35	40	41.2	854	2	US-09-350-841A-1589	Sequence 1589, Ap
36	40	41.2	856	2	US-08-486-099-103	Sequence 103, App
37	40	41.2	856	2	US-08-484-223B-103	Sequence 103, App
38	40	41.2	856	2	US-08-919-597-103	Sequence 103, App
39	40	41.2	856	2	US-08-475-668A-103	Sequence 103, App
40	40	41.2	856	2	US-08-485-551A-103	Sequence 103, App
41	40	41.2	856	2	US-08-471-913A-103	Sequence 103, App
42	40	41.2	856	2	US-08-485-264A-103	Sequence 103, App
43	40	41.2	856	2	US-08-474-349A-103	Sequence 103, App
44	40	41.2	856	2	US-08-470-896-103	Sequence 103, App
45	40	41.2	856	2	US-08-485-546A-103	Sequence 103, App

ALIGNMENTS

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RESULT 1
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match      100.0%; Score 97; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 8.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIFPYTAPGKQ 18
      |||||
Db      151 VDGQKATNIFPYTAPGKQ 168

RESULT 2
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2
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Query Match 100.0%; Score 97; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 9.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGKATNIPFYTPGKQ 18
|||
Db 216 VDGKATNIPFYTPGKQ 233

RESULT 3

US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match 100.0%; Score 97; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 9.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGKATNIPFYTPGKQ 18
|||
Db 216 VDGKATNIPFYTPGKQ 233

RESULT 4

US-09-281-760E-35
; Sequence 35, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Mermet, Brion
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Canis familiaris

FEATURE:
; NAME/KEY: misc feature
; LOCATION: (81)..(81)
; OTHER INFORMATION: The 'Xaa' at location 81 stands for Lys, Arg, Thr, Met, Glu, Gly,
; OTHER INFORMATION: Ala, Val, Gln, Pro, Leu, a stop codon, Trp, or Ser.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82)..(82)
; OTHER INFORMATION: The 'Xaa' at location 82 stands for a stop codon, Trp, or Cys.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (136)..(136)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (413)..(414)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (451)..(451)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (460)..(462)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (500)..(500)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (530)..(530)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (568)..(568)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (847)..(849)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (853)..(853)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (1382)..(1382)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (1832)..(1832)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (1832)..(1832)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (1832)..(1832)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (1832)..(1832)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (1832)..(1832)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (1832)..(1832)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (1832)..(1832)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (136)..(136)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

NAME/KEY: misc feature

LOCATION: (136)..(136)

OTHER INFORMATION: "n" stands for any nucleic acid

FEATURE:

US-09-701-623C-2

Sequence 2, Application US/09701623C

Patent No. 6811782

GENERAL INFORMATION:

APPLICANT: Wang Ph.D., Chang Yi

TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

FILE REFERENCE: 11514153US1

CURRENT APPLICATION NUMBER: US/09/701,623C

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: PCT/US99/13959

PRIOR FILING DATE: 1999-06-21

PRIOR APPLICATION NUMBER: 09/100,287

PRIOR FILING DATE: 1998-06-20

NUMBER OF SEQ ID NOS: 91

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 312

TYPE: PRT

ORGANISM: Dog

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; FEATURE:
; OTHER INFORMATION: CH2Chn of dog IgE
; PUBLICATION INFORMATION:
; AUTHORS: Patel.
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
; US-09-701-623C-2

Query Match      89.7%; Score 87; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIFPYTAPG 16
      |||||
Db      48 VDGQKATNIFPYTAPG 63

RESULT 6
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5639415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-583-2

Query Match      89.7%; Score 87; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIFPYTAPG 16
      |||||
Db      146 VDGQKATNIFPYTAPG 161

RESULT 7
PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
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; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-13795-2

Query Match      89.7%; Score 87; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIFPYTAPG 16
      |||||
Db      146 VDGQKATNIFPYTAPG 161

RESULT 8
US-09-401-636-7
; Sequence 7, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-7

Query Match      79.4%; Score 77; DB 2; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00012;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VDGQKATNIFPYTAPGKQ 18
      |||||
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Db 61 VDGGKATNIPFYTPAPRK 78

RESULT 9
US-09-401-636-3
; Sequence 3, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-3

Query Match 61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.072;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 VDGGKATNIPFYTPAPRK 18
||||:|:|||||:
Db 62 VDGGKATNIPFYTPAPRK 79

RESULT 10
US-09-401-636-4
; Sequence 4, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-4

Query Match 61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.072;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 VDGGKATNIPFYTPAPRK 18
||||:|:|||||:
Db 62 VDGGKATNIPFYTPAPRK 79

RESULT 11
US-09-401-636-6
; Sequence 6, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-6

; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-6

Query Match 61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.072;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 VDGGKATNIPFYTPAPRK 18
||||:|:|||||:
Db 62 VDGGKATNIPFYTPAPRK 79

RESULT 12
US-09-401-636-9
; Sequence 9, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9

Query Match 61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.072;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 VDGGKATNIPFYTPAPRK 18
||||:|:|||||:
Db 62 VDGGKATNIPFYTPAPRK 79

RESULT 13
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

Query Match 61.9%; Score 60; DB 2; Length 341;
Best Local Similarity 61.1%; Pred. No. 0.072;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTPGKQ 18
|||:|:|:|:|:
DB 62 VDGQEAENLFPYTRPKR 79

RESULT 14
US-09-401-636-5
Sequence 5, Application US/09401636
Patent No. 6913749

GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 342
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-5

Query Match 61.9%; Score 60; DB 2; Length 342;
Best Local Similarity 61.1%; Pred. No. 0.072;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTPGKQ 18
|||:|:|:|:|:
DB 62 VDGQEAENLFPYTRPKR 79

RESULT 15
US-09-401-636-8
Sequence 8, Application US/09401636
Patent No. 6913749
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 342
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-8

Query Match 61.9%; Score 60; DB 2; Length 342;
Best Local Similarity 61.1%; Pred. No. 0.072;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTPGKQ 18
|||:|:|:~|:|:~|:~|:
DB 62 VDGQEAENLFPYTRPKR 79

Search completed: December 12, 2005, 19:37:06
Job time : 25.5172 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:33:42 ; Search time 80.3793 Seconds
(without alignments)
93.568 Million cell updates/sec

Title: US-10-758-165A-10

Sequence: 1 VDGQKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA Main:

1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US10a_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US10b_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	5	US-10-758-165-10
2	97	100.0	431	3	US-09-479-614-14
3	97	100.0	431	4	US-10-409-772-14
4	97	100.0	496	3	US-09-479-614-2
5	97	100.0	496	3	US-09-479-614-29
6	97	100.0	496	4	US-10-214-524-25
7	97	100.0	496	4	US-10-409-772-2
8	97	100.0	496	4	US-10-409-772-29
9	87	89.7	18	5	US-10-758-165-9
10	87	89.7	426	4	US-10-214-524-28
11	77	79.4	343	3	US-09-401-636-7
12	77	79.4	343	4	US-10-176-664-7
13	77	79.4	343	4	US-10-673-594-7
14	77	79.4	577	4	US-10-214-524-29
15	60	61.9	337	4	US-10-438-794-3
16	60	61.9	337	4	US-10-453-915-3
17	60	61.9	338	4	US-10-438-794-6
18	60	61.9	338	4	US-10-453-915-6
19	60	61.9	341	3	US-09-401-636-3
20	60	61.9	341	3	US-09-401-636-6
21	60	61.9	341	3	US-09-401-636-9
22	60	61.9	341	3	US-09-401-636-9
23	60	61.9	341	3	US-09-401-636-11
24	60	61.9	341	4	US-10-176-664-3
25	60	61.9	341	4	US-10-176-664-4
26	60	61.9	341	4	US-10-176-664-6
27	60	61.9	341	4	US-10-176-664-9

28	60	61.9	341	4	US-10-176-664-11	Sequence 11, Appl
29	60	61.9	341	4	US-10-673-594-3	Sequence 3, Appl
30	60	61.9	341	4	US-10-673-594-4	Sequence 4, Appl
31	60	61.9	341	4	US-10-673-594-6	Sequence 6, Appl
32	60	61.9	341	4	US-10-673-594-9	Sequence 9, Appl
33	60	61.9	341	4	US-10-673-594-11	Sequence 11, Appl
34	60	61.9	342	3	US-09-401-636-5	Sequence 5, Appl
35	60	61.9	342	3	US-09-401-636-8	Sequence 8, Appl
36	60	61.9	342	4	US-10-176-664-5	Sequence 5, Appl
37	60	61.9	342	4	US-10-176-664-8	Sequence 8, Appl
38	60	61.9	342	4	US-10-673-594-5	Sequence 5, Appl
39	60	61.9	342	4	US-10-673-594-8	Sequence 8, Appl
40	60	61.9	345	3	US-09-401-636-10	Sequence 10, Appl
41	60	61.9	345	4	US-10-176-664-10	Sequence 10, Appl
42	60	61.9	345	4	US-10-673-594-10	Sequence 10, Appl
43	60	61.9	347	4	US-10-438-794-14	Sequence 14, Appl
44	60	61.9	347	4	US-10-453-915-14	Sequence 14, Appl
45	60	61.9	353	4	US-10-453-915-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-758-165-10
; Sequence 10, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-10

Query Match 100.0%; Score 97; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAPGKQ 18
DB 1 VDGQKATNIFPYTAPGKQ 18

RESULT 2
US-09-479-614-14
; Sequence 14, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match 100.0%; Score 97; DB 3; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGOKATNIPFYTA PGKQ 18
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Db 151 VDGOKATNIPFYTA PGKQ 168

RESULT 3
US-10-409-772-14
; Sequence 14, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-14

Query Match 100.0%; Score 97; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGOKATNIPFYTA PGKQ 18
|||
Db 151 VDGOKATNIPFYTA PGKQ 168

RESULT 4
US-09-479-614-2
; Sequence 2, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric
; APPLICANT: McCall, Catherine
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match 100.0%; Score 97; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGOKATNIPFYTA PGKQ 18
|||
Db 216 VDGOKATNIPFYTA PGKQ 233

RESULT 5
US-09-479-614-29
; Sequence 29, Application US/09479614
; Publication No. US20030013183A1

; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match 100.0%; Score 97; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGOKATNIPFYTA PGKQ 18
|||
Db 216 VDGOKATNIPFYTA PGKQ 233

RESULT 6
US-10-214-524-25
; Sequence 25, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGB-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Cat (Felis catus)
US-10-214-524-25

Query Match 100.0%; Score 97; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGOKATNIPFYTA PGKQ 18
|||
Db 216 VDGOKATNIPFYTA PGKQ 233

RESULT 7
US-10-409-772-2
; Sequence 2, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric
; APPLICANT: McCall, Catherine
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2
LENGTH: 496
TYPE: PRT
ORGANISM: Felis catus
US-10-409-772-2

Query Match 100.0%; Score 97; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPGKQ 18
|||||
Db 216 VDGOKATNIFPYTAPGKQ 233

RESULT 8
US-10-409-772-29
Sequence 29, Application US/10409772
Publication No. US20030216565A1
GENERAL INFORMATION:
APPLICANT: McCall, Catherine
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/10/409,772
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US/09/479,614
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 496
TYPE: PRT
ORGANISM: Felis catus
US-10-409-772-29

Query Match 100.0%; Score 97; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPGKQ 18
|||||
Db 216 VDGOKATNIFPYTAPGKQ 233

RESULT 9
US-10-758-165-9
Sequence 9, Application US/10758165
Publication No. US20050196816A1
GENERAL INFORMATION:
APPLICANT: Hammerberg, Bruce
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
FILE REFERENCE: 5051-661
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: US 60/440,472
PRIOR FILING DATE: 2003-01-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9
LENGTH: 18
TYPE: PRT
ORGANISM: Canis familiaris
US-10-758-165-9

Query Match 89.7%; Score 87; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPG 16
|||||
Db 1 VDGOKATNIFPYTAPG 16

RESULT 10
US-10-214-524-28
Sequence 28, Application US/10214524
Publication No. US20030073142A1
GENERAL INFORMATION:
APPLICANT: Chen, Swei-Shen Alex
APPLICANT: Yang, Yong-Min
APPLICANT: Barankiewicz, Theresa J.
APPLICANT: Chen, Zhong
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
FILE REFERENCE: IGE-00101.P.1.1
CURRENT APPLICATION NUMBER: US/10/214,524
CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: 60/312,120
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
LENGTH: 426
TYPE: PRT
ORGANISM: Dog (Canis familiaris)
US-10-214-524-28

Query Match 89.7%; Score 87; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPG 16
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Db 146 VDGOKATNIFPYTAPG 161

RESULT 11
US-09-401-636-7
Sequence 7, Application US/09401636
Patent No. US20010038843A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 343
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-7

Query Match 79.4%; Score 77; DB 3; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00031;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPGKQ 18
|||||
Db 61 VDGOKATNIFPYTAPGKQ 78

RESULT 12
US-10-176-664-7
Sequence 7, Application US/10176664
Publication No. US20030031663A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/10/176,664

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; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-7

Query Match          79.4%; Score 77; DB 4; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00031;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VDGQKATNIPPYTAPGKQ 18
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        61 VDGQKAENLFPYTAPPKR 78

RESULT 13
US-10-673-594-7
; Sequence 7, Application US/10673594
; Publication No. US20040076625A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-7

Query Match          79.4%; Score 77; DB 4; Length 343;
Best Local Similarity 77.8%; Pred. No. 0.00031;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VDGQKATNIPPYTAPGKQ 18
        |||||:|||||:|
        61 VDGQKAENLFPYTAPPKR 78

RESULT 14
US-10-214-524-29
; Sequence 29, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Duckbilled platypus (Ornithorhynchus anatinus)
US-10-214-524-29

Query Match          79.4%; Score 77; DB 4; Length 577;
Best Local Similarity 77.8%; Pred. No. 0.00054;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 VDGQKATNIPPYTAPGKQ 18
        |||||:|||||:|
        295 VDGQKAENLFPYTAPPKR 312

RESULT 15
US-10-438-794-3
; Sequence 3, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSSON, Ann-Christin
; TITLE OF INVENTION: Chimeric IGE Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated ORO
US-10-438-794-3

Query Match          61.9%; Score 60; DB 4; Length 337;
Best Local Similarity 61.1%; Pred. No. 0.0.2;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 VDGQKATNIPPYTAPGKQ 18
        |||||:|||||:|
        56 VDGQKAENLFPYTAPPKR 73

Search completed: December 12, 2005, 20:19:25
Job time : 80.3793 secs
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:34:33 : Search time 2.94828 Seconds
(without alignments)
34.094 Million cell updates/sec

Title: US-10-758-165a-10

Perfect score: 97

Sequence: 1 VDGGKATNIFPYTAPGKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_New:*
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3: /cgn2_6/pcdata/1/pubpaa/us07_NEW_PUB.pep:*
4: /cgn2_6/pcdata/1/pubpaa/us08_NEW_PUB.pep:*
5: /cgn2_6/pcdata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /cgn2_6/pcdata/1/pubpaa/us10_NEW_PUB.pep:*
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8: /cgn2_6/pcdata/1/pubpaa/us60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	89.7	312	6	US-10-723-207-2
2	44	45.4	102	6	US-10-821-234-1457
3	43	44.3	254	6	US-10-485-517-188
4	41	42.3	497	6	US-10-763-712A-24
5	41	42.3	430	6	US-10-763-712A-91
6	40	41.2	497	6	US-10-467-657-2346
7	39	40.2	121	6	US-10-793-626-2524
8	38	39.2	241	6	US-10-485-517-189
9	37	38.1	345	6	US-10-793-626-3168
10	36	37.1	532	7	US-11-184-380-6
11	36	37.1	588	7	US-11-184-380-5
12	36	37.1	724	7	US-11-184-380-4
13	36	37.1	805	7	US-10-518-599-4
14	35.5	36.6	1045	7	US-11-113-424-54
15	35.5	36.6	1094	6	US-10-821-234-1097
16	35.5	36.6	2376	7	US-11-096-051-4
17	35.5	36.6	2715	7	US-11-096-051-2
18	35.5	36.6	2715	7	US-11-113-424-51
19	35.5	36.6	2721	7	US-11-096-051-10
20	35.5	36.6	2725	7	US-11-096-051-8
21	35	36.1	288	6	US-10-467-657-1682
22	35	36.1	433	6	US-10-131-826A-6
23	35	36.1	605	6	US-10-821-234-1207
24	35	36.1	636	6	US-10-763-712A-29
25	35	36.1	636	6	US-10-763-712A-93

26	35	36.1	805	6	US-10-518-599-24	Sequence 24, Appl
27	35	36.1	826	6	US-10-793-626-1066	Sequence 1066, Ap
28	35	36.1	853	6	US-10-821-234-1110	Sequence 1110, Ap
29	35	36.1	1006	6	US-10-467-657-8400	Sequence 8400, Ap
30	35	36.1	2335	6	US-10-821-234-1610	Sequence 1610, Ap
31	34	35.1	72	6	US-10-986-501-118	Sequence 118, Ap
32	34	35.1	232	6	US-10-510-386-116	Sequence 116, App
33	34	35.1	233	6	US-10-467-657-5470	Sequence 5470, Ap
34	34	35.1	409	6	US-10-793-626-2002	Sequence 2002, Ap
35	34	35.1	409	6	US-10-793-626-2306	Sequence 2306, Ap
36	34	35.1	410	6	US-10-858-730-233	Sequence 233, App
37	34	35.1	424	6	US-10-485-517-405	Sequence 405, App
38	34	35.1	485	6	US-10-467-657-4512	Sequence 4512, Ap
39	34	35.1	1892	7	US-11-075-185-6	Sequence 5, Appl
40	34	35.1	3655	7	US-11-075-185-5	Sequence 5, Appl
41	33.5	34.5	2011	7	US-11-080-991-56	Sequence 56, Appl
42	33	34.0	139	6	US-10-467-657-5292	Sequence 5292, Ap
43	33	34.0	154	6	US-10-467-657-2034	Sequence 2034, Ap
44	33	34.0	481	6	US-10-467-657-4396	Sequence 4396, Ap
45	33	34.0	530	6	US-10-131-826A-130	Sequence 130, App

ALIGNMENTS

RESULT 1
US-10-723-207-2
Sequence 2, Application US/10723207
Publication No. US20050250934A1
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Walfield, Alan M.
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
FILE REFERENCE: 1151-4153US2
CURRENT FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: US/10/723,207
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/701,623
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US99/13959
PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 09/100,287
PRIOR FILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 312
TYPE: PRT
ORGANISM: Dog
FEATURE:
OTHER INFORMATION: CH2CHN of dog Ige
PUBLICATION INFORMATION:
AUTHORS: Patel,
JOURNAL: Immunogenetics
VOLUME: 41
PAGES: 282-286
DATE: 1995
US-10-723-207-2
Query Match 89.7%; Score 87; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDGGKATNIFPYTAPG 16
DB 48 VDGGKATNIFPYTAPG 63
RESULT 2
US-10-821-234-1457
Sequence 1457, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:

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; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pf SEQ_genes Version 1.0
; SEQ ID NO 1457
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1457

Query Match      45.4% Score 44; DB 6; Length 102;
Best Local Similarity 43.8%; Pred. No. 0.32;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      2 DGKATNIFPYTAPGK 17
DB      14 DQGAADVAVFVAPGE 29

RESULT 3
US-10-485-517-188
; Sequence 188, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biolexnexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; PRIOR FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-188

Query Match      44.3% Score 43; DB 6; Length 254;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 KATNIFPYT 13
DB      58 KOTNIFPYT 66

RESULT 4
US-10-763-712A-24
; Sequence 24, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
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; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-10-763-712A-24

Query Match      42.3% Score 41; DB 6; Length 497;
Best Local Similarity 50.0%; Pred. No. 5.9;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      1 VDQKATNIFPYTAPGKO 18
DB      324 MDGKETNITWVPAPGSK 341

RESULT 5
US-10-763-712A-91
; Sequence 91, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 497
; TYPE: PRT
; ORGANISM: C. reinhardtii
US-10-763-712A-91

Query Match      42.3% Score 41; DB 6; Length 497;
Best Local Similarity 50.0%; Pred. No. 5.9;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      1 VDQKATNIFPYTAPGKO 18
DB      324 MDGKETNITWVPAPGSK 341

RESULT 6
US-10-467-657-2346
; Sequence 2346, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
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;; PRIOR FILING DATE: 2001-02-12
;; NUMBER OF SEQ ID NOS: 9218
;; SOFTWARE: SeqMan9, version 1.04
;; SEQ ID NO: 2346
;; LENGTH: 430
;; TYPE: PRT
;; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2346

Query Match 41.2%; Score 40; DB 6; Length 430;
Best Local Similarity 46.7%; Pred. No. 7.4;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VDGKATNIFPYTAP 15
Db 127 LDGDITKLAPDRP 141

RESULT 7
US-10-793-626-2524
;; Sequence 2524, Application US/10793626
;; Publication No. US20050255478A1
;; GENERAL INFORMATION:
;; APPLICANT: KIMMERLY, WILLIAM JOHN
;; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;; FILE REFERENCE: PU3480US
;; CURRENT APPLICATION NUMBER: US/10/793,626
;; CURRENT FILING DATE: 2004-03-04
;; PRIOR APPLICATION NUMBER: 60/164,258
;; PRIOR FILING DATE: 1999-11-09
;; NUMBER OF SEQ ID NOS: 4472
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 2524
;; LENGTH: 121
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2524

Query Match 40.2%; Score 39; DB 6; Length 121;
Best Local Similarity 57.1%; Pred. No. 2.8;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GOKATNIFPYTAPG 16
Db 44 GKATNIERYTSQG 57

RESULT 8
US-10-485-517-189
;; Sequence 189, Application US/10485517
;; Publication No. US20050256299A1
;; GENERAL INFORMATION:
;; APPLICANT: University of Sheffield
;; APPLICANT: Biosynex Incorporated
;; APPLICANT: Foster, Simon
;; TITLE OF INVENTION: Antigenic Polypeptides
;; FILE REFERENCE: P100629MO
;; CURRENT APPLICATION NUMBER: US/10/485,517
;; CURRENT FILING DATE: 2004-02-02
;; PRIOR APPLICATION NUMBER: GB 0118825.9
;; PRIOR FILING DATE: 2001-08-02
;; PRIOR APPLICATION NUMBER: GB 0200349.9
;; PRIOR FILING DATE: 2002-01-09
;; NUMBER OF SEQ ID NOS: 424
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 189
;; LENGTH: 241
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus

US-10-485-517-189

Query Match 39.2%; Score 38; DB 6; Length 241;
Best Local Similarity 87.5%; Pred. No. 8.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 KATNIFPY 12
Db 46 KOTNIFPY 53

RESULT 9
US-10-793-626-3168
;; Sequence 3168, Application US/10793626
;; Publication No. US20050255478A1
;; GENERAL INFORMATION:
;; APPLICANT: KIMMERLY, WILLIAM JOHN
;; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;; FILE REFERENCE: PU3480US
;; CURRENT APPLICATION NUMBER: US/10/793,626
;; CURRENT FILING DATE: 2004-03-04
;; PRIOR APPLICATION NUMBER: 60/164,258
;; PRIOR FILING DATE: 1999-11-09
;; NUMBER OF SEQ ID NOS: 4472
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 3168
;; LENGTH: 345
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3168

Query Match 38.1%; Score 37; DB 6; Length 345;
Best Local Similarity 63.6%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDGKATNIFP 11
Db 223 LDGKATNIFP 233

RESULT 10
US-11-184-380-6
;; Sequence 6, Application US/11184380
;; Publication No. US20050255089A1
;; GENERAL INFORMATION:
;; APPLICANT: Chlorini, John
;; APPLICANT: Kotin, Robert M.
;; TITLE OF INVENTION: RAYS NUCLEIC ACIDS
;; FILE REFERENCE: 14014.0323U3
;; CURRENT APPLICATION NUMBER: US/11/184,380
;; CURRENT FILING DATE: 2005-07-19
;; PRIOR APPLICATION NUMBER: PCT/US99/11958
;; PRIOR FILING DATE: 1999-05-28
;; PRIOR APPLICATION NUMBER: 60/087,029
;; PRIOR FILING DATE: 1998-05-28
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 6
;; LENGTH: 532
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence; Note =
US-11-184-380-6

Query Match 37.1%; Score 36; DB 7; Length 532;
Best Local Similarity 46.7%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Oy 1 VDGKATNIFPYTAP 15
Db 63 VDGSNANAYFGYSTP 77

RESULT 11
US-11-184-380-5
; Sequence 5, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Kiorini, John
; APPLICANT: Kiorini, Robert M.
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.0323U3
; CURRENT APPLICATION NUMBER: US/11/184,380
; PRIOR FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
US-11-184-380-5
OTHER INFORMATION: synthetic construct

Query Match 37.1%; Score 36; DB 7; Length 588;
Best Local Similarity 46.7%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Oy 1 VDGKATNIFPYTAP 15
Db 119 VDGSNANAYFGYSTP 133

RESULT 12
US-11-184-380-4
; Sequence 4, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Kiorini, John
; APPLICANT: Kiorini, Robert M.
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.0323U3
; CURRENT APPLICATION NUMBER: US/11/184,380
; PRIOR FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
US-11-184-380-4
OTHER INFORMATION: synthetic construct

Query Match 37.1%; Score 36; DB 7; Length 724;
Best Local Similarity 46.7%; Pred. No. 63;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Oy 1 VDGKATNIFPYTAP 15
Db 255 VDGSNANAYFGYSTP 269

RESULT 13
US-10-518-599-4
; Sequence 4, Application US/10518599
; Publication No. US20050251873A1
; GENERAL INFORMATION:
; APPLICANT: PENNINGER, JOSEPH M.
; APPLICANT: CRACKOWER, MICHAEL A.
; TITLE OF INVENTION: ACE2 ACTIVATION FOR TREATMENT OF HEART, LUNG AND
; FILE REFERENCE: SONN.064US
; CURRENT APPLICATION NUMBER: US/10/518,599
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/CA03/00882
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: US 60/389,709
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-518-599-4

Query Match 37.1%; Score 36; DB 6; Length 805;
Best Local Similarity 43.8%; Pred. No. 70;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 3 GOKATNIFPYTAPGKQ 18
Db 272 GREWTNLYPLTVPPAQ 287

RESULT 14
US-11-113-424-54
; Sequence 54, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; PRIOR FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 1045
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-54

Query Match 36.6%; Score 35.5; DB 7; Length 1045;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;

Matches 8; Conservative 3; Mismatches 4; Indels 3; Gaps 1;
Oy 2 DG---QKATNPPYTPG 16
|||:|||||:
Db 540 DGFRLRGRTETFEYSKG 557

RESULT 15
US-10-821-234-1097
; Sequence 1097, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1097
; LENGTH: 1094
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1097

Query Match 36.6%; Score 35.5; DB 6; Length 1094;
Best Local Similarity 44.4%; Pred. No. 1.2e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

Oy 2 DG---QKATNPPYTPG 16
|||:|||||:
Db 589 DGFRLRGRTETFEYSKG 606

Search completed: December 12, 2005, 20:19:49
Job time : 2.94828 secs

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OW protein - protein search, using sw model

Run on: December 12, 2005, 20:10:49 ; Search time 15.2069 Seconds
(without alignments)
113.889 Million cell updates/sec

Title: US-10-758-165A-10

Perfect score: 97

Sequence: 1 VDGQKATNIPPYTAPGKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.5	270	2	T16880
2	43	44.3	633	2	S62057
3	43	44.3	658	2	AH0110
4	42	43.3	381	2	AD2436
5	42	43.3	643	1	S15623
6	42	43.3	683	2	B71325
7	42	43.3	1032	2	S74487
8	42	43.3	1686	2	A87692
9	41	42.3	544	2	T17798
10	41	42.3	544	2	D88449
11	41	42.3	623	2	T22177
12	41	42.3	713	2	J60230
13	41	42.3	2298	2	T49648
14	40.5	41.8	363	2	C82607
15	40.5	41.8	1371	2	D82606
16	40	41.2	101	2	G69203
17	40	41.2	109	2	F89886
18	40	41.2	179	2	D90167
19	40	41.2	227	2	C75582
20	40	41.2	240	2	C89967
21	40	41.2	242	1	LXBS
22	40	41.2	258	2	AF0306
23	40	41.2	327	2	S40753
24	40	41.2	374	2	G81926
25	40	41.2	391	2	T33714
26	40	41.2	419	2	C81179
27	40	41.2	454	2	AH2821
28	40	41.2	470	2	H97599
29	40	41.2	506	2	T07942

30	40	41.2	645	2	T16078	hypothetical prote
31	40	41.2	812	2	T07745	phosphatidylinosit
32	40	41.2	814	2	T07761	coat protein gamma
33	40	41.2	831	2	T05265	glycoprotein B - h
34	40	41.2	857	1	Q0BE1L	hypothetical prote
35	40	41.2	915	2	T12526	probable outer mem
36	40	41.2	1013	2	G71460	isoenzyme1-trna syn
37	40	41.2	1064	2	T40751	hypothetical prote
38	40	41.2	1203	2	T28895	fatty-acid synthas
39	40	41.2	1069	2	H70656	fatty acid synthas
40	40	41.2	3076	2	A87058	transcription elon
41	39	40.2	157	2	A69637	hypothetical prote
42	39	40.2	213	2	C64041	hypothetical prote
43	39	40.2	308	2	H95965	hypothetical prote
44	39	40.2	308	2	F95416	hypothetical prote
45	39	40.2	374	2	G86267	T604.7 protein - A

ALIGNMENTS

RESULT 1
T16880
hypothetical protein T14G12.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-Oct-2004
C:Accession: T16880
R:Wilcox, L.
Submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid T14G12.
A:Reference number: Z18596
A:Accession: T16880
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-270 <MIL>
A:Cross-References: UNIPROT:Q22510, UNIPARC:UPI0000075025, EMBL:U41268, NID:G1086843, PI
C:Genetics:
A:Gene: CBSP:T14G12.4
A:Introns: 37/1; 72/3; 164/1
F:93-185/Domain: fork head DNA-binding domain homology <FHD>

Query Match 49.5%; Score 48; DB 2; Length 270;
Best Local Similarity 57.1%; Pred. No. 1.8;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 GQKATNIPPYTAPG 16
DB 205 GAANAALPPYFSPG 218

RESULT 2
S62057
proline-rich protein LAS17 - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein Q4724; protein YOR181w
C:Species: *Saccharomyces cerevisiae*
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: S62057; S67073
R:Hon-e, A.
Submitted to the EMBL Data Library, December 1995
A:Description: Yeast mutants sensitive to local anesthetics.
A:Reference number: S62057
A:Accession: S62057
A:Molecule type: DNA
A:Residues: 1-633 <TOH>
A:Cross-References: UNIPROT:Q12446, UNIPARC:UPI000003CA29, EMBL:D78487, NID:G1101756, PI
R:Hughes, B.; Pohl, T.M.
Submitted to the Protein Sequence Database, July 1996
A:Reference number: S66685
A:Accession: S67073
A:Molecule type: DNA
A:Residues: 1-633 <HUG>
A:Cross-References: UNIPARC:UPI000003CA29, EMBL:Z75089, NID:G1420436, PID:e252060, PID:G1
A:Experimental source: strain S288C

C:Genetics:
A:Gene: SGD:LAS17
A:Cross-references: SGD:S0005707; MIPS:YOR181w
A:Map position: 15R

Query Match 44.3%; Score 43; DB 2; Length 633;
Best Local Similarity 53.3%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 QKATNPFYTPARKQ 18
Db 283 QKATNPFYTPARKQ 297

RESULT 3
AH0110
Probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)

C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH0110
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Taranga, A.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0110
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-658 <KUR>
A:Cross-references: UNIPROT:Q8ZHU0, UNIPARC:UPI00000CD765; GB:AL590842; PIDN:CAC89747.1;
C:Genetics:

A:Gene: YPO0902
Query Match 44.3%; Score 43; DB 2; Length 658;
Best Local Similarity 61.5%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VDGGKATNIPFYTP 13
Db 99 LMGKATNLAIPAT 111

RESULT 4

AD2436
ATP-binding protein of polyamine ABC transporter all5044 [imported] - Nostoc sp. (strain
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 31-Dec-2004
C:Accession: AD2436
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD2436
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-381 <KUR>
A:Cross-references: UNIPROT:Q8WY92, UNIPARC:UPI00000CEB3F; GB:BA000019; PIDN:BA076743.1;
A:Experimental source: strain PCC 7120
C:Genetics:

A:Gene: all5044

Query Match 43.3%; Score 42; DB 2; Length 381;
Best Local Similarity 53.3%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VDGGKATNIPFYTP 15
Db 80 IGGPMTNIPFYTP 94

RESULT 5
S15623
E1 protein - human papillomavirus type 57

C:Species: human papillomavirus type 57
A:Note: host Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: S15623
R:Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A:Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and 5

A:Reference number: S15614; MUID:91188699; PMID:1964523
A:Accession: S15623
A:Molecule type: DNA
A:Residues: 1-643 <HIR>
A:Cross-references: UNIPROT:P22153; UNIPARC:UPI000013813; EMBL:X55965; NID:G60882; PIDN
C:Superfamily: papillomavirus E1 protein
C:Keywords: early protein

Query Match 43.3%; Score 42; DB 1; Length 643;
Best Local Similarity 53.8%; Pred. No. 51;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 5 KATNIPFYTPARK 17
Db 581 KATNIPFYTPARK 593

RESULT 6

B71325
conserved hypothetical protein TP0421 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: B71325
R:Fraser, C.M.; Norris, S.V.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetzelback, T.; McDer
they, L.; Weidman, U.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: B71325
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-683 <COL>
A:Cross-references: UNIPROT:O83436; UNIPARC:UPI00000COA71; GB:AE001220; GB:AE000520; NID
A:Experimental source: strain Nichols
C:Genetics:

A:Gene: TP0421

Query Match 43.3%; Score 42; DB 2; Length 683;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKATNIPFYTPAG 16
Db 278 GQKATNIPFYTPAG 291

RESULT 7

S74487
hypothetical protein s111060 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.

A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S74487
R:Kaneko, T.; Sato, S.; Korani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okunura, S.; Shimp, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S74487
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

C:Superfamily: NADPH-ferrithemoprotein reductase; flavodoxin homology; NADPH-ferrithemoprd
 C:Keywords: Flavoprotein; oxidoreductase
 F:107-712/Domain: NADPH-ferrithemoprotein reductase homology <FEH>
 F:109-257/Domain: flavodoxin homology <FLX>

Query Match 42.3%; Score 41; DB 2; Length 713;
 Best Local Similarity 57.1%; Pred. No. 85;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDQGKATNIPFYTA 14
 Db 265 LDGDDATRATPYTA 278

RESULT 13

T49648
 hypochlorite protein B8B20.20 (imported) - Neurospora crassa

C:Species: Neurospora crassa
 C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C/Accession: T49648

R:Schulte, U.; Algen, V.; Hehnel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25022

A:Accession: T49648
 A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2298 <SCH>

A:Cross-references: UNIPROT:Q96U00; UNIPARC:UPI00001784BA; EMBL:AL355933; GSPDB:GN00116;
 C:Genetics:

A:Gene: NCSP:B8B20.20

A:Map position: 6

A:introns: 426/3

Query Match 42.3%; Score 41; DB 2; Length 2298;
 Best Local Similarity 42.9%; Pred. No. 3.1e+02;
 Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 4 QKATNIPFYTAGK 17
 Db 1694 ERVTQVLPYFQPK 1707

RESULT 14

C82607
 DNA primase XF2025 (imported) - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C/Accession: C82607

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: C82607

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-363 <SIM>

A:Cross-references: UNIPROT:Q9PBW0; UNIPARC:UPI00000C28BE; GB:AE004021; GB:AE003849; NIT

R:Simpson, A.D.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carver, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, B

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsubako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Contents: annotation
 C:Genetics:
 A:Gene: XF2025

Query Match 41.8%; Score 40.5; DB 2; Length 363;
 Best Local Similarity 55.6%; Pred. No. 49;
 Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

Qy 1 VDQGKATNIPFYTAGK 18
 Db 264 VDG--TAFPIFAPGEO 298

RESULT 15

D82606
 DNA primase XF2061 (imported) - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C/Accession: D82606

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82606

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1371 <SIM>

A:Cross-references: UNIPROT:Q9PBW0; UNIPARC:UPI00000C290E; GB:AE004022; GB:AE003849; NID

R:Simpson, A.D.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carver, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, B

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsubako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Contents: annotation

C:Genetics:

A:Gene: XF2061

Query Match 41.8%; Score 40.5; DB 2; Length 1371;
 Best Local Similarity 55.6%; Pred. No. 2.2e+02;
 Matches 10; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

Qy 1 VDQGKATNIPFYTAGK 18
 Db 1292 VDG--TAFPIFAPGEO 1306

Search completed: December 12, 2005, 20:42:51
 Job time : 16.2069 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:41 ; Search time 97.7586 Seconds
(without alignments)
129.907 Million cell updates/sec

Title: US-10-758-165a-10
Perfect score: 97
Sequence: 1 VDQKATNIFPYAPGKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_crembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	52.6	382	2	Q7PSV1_FUSNV
2	51	52.6	382	2	Q8R6B3_FUSNN
3	48	49.5	168	2	Q95QAG_CABEL
4	48	49.5	270	2	Q22510_CABEL
5	47	48.5	1054	2	Q608X6_METCA
6	47	48.5	1538	2	Q94H26_ORYSA
7	46	47.4	408	2	Q565U8_9BACT
8	45	46.4	279	2	Q619H6_CABBR
9	45	46.4	445	1	ALN_STRCO
10	45	46.4	811	2	Q4IFN3_GIBZE
11	44	45.4	102	1	GAGC1_HUMAN
12	44	45.4	102	2	Q61B11_HUMAN
13	44	45.4	340	2	Q9AYAO_ORYSA
14	44	45.4	525	2	Q6A1L1_DESPA
15	44	45.4	589	2	Q53Q04_ORYSA
16	44	45.4	760	2	Q6UDM4_ORYSA
17	44	45.4	875	2	Q7FAL9_ORYSA
18	44	45.4	884	2	Q53JX1_ORYSA
19	44	45.4	1037	2	Q55IS1_CRYNE
20	44	45.4	1037	2	Q5KX8_CRYNE
21	44	45.4	1336	2	Q7PAL2_ORYSA
22	44	45.4	1685	2	Q7XSP1_ORYSA
23	43	44.8	1338	2	Q5FK37_LACAC
24	43	44.3	52	2	Q7WYM4_BACSH
25	43	44.3	104	2	Q5TSY2_ANOGA
26	43	44.3	120	2	Q52EG8_MAGGR
27	43	44.3	166	2	Q6GCH5_STAAS
28	43	44.3	166	2	Q8NTE3_STAW
29	43	44.3	240	2	Q9KH50_STAW
30	43	44.3	240	2	Q6G8C2_STAAS
31	43	44.3	240	2	Q8NVX6_STAW

32	43	44.3	240	2	Q5HEW1_STAAC	Q5HEW1 staphylococ
33	43	44.3	343	1	QUBA_BORBU	Q51053 borrelia bu
34	43	44.3	346	2	Q662Z1_BORGA	Q662Z1 borrelia ga
35	43	44.3	400	2	Q8G6D4_CORST	Q8G6D4 corynebacte
36	43	44.3	633	1	LAS17_YEAST	Q12446 saccharomyc
37	43	44.3	641	2	Q8CKM1_YERPE	Q8CKM1 yersinia pe
38	43	44.3	658	2	Q8ZHU0_YERPE	Q8ZHU0 yersinia pe
39	43	44.3	1175	2	Q7XG40_ORYSA	Q7XG40 oryza sativ
40	43	44.3	1175	2	Q94124_ORYSA	Q94124 oryza sativ
41	43	44.3	1207	2	Q4P6A9_USYMA	Q4P6A9 usyllago ma
42	43	44.3	1271	2	Q7XW55_ORYSA	Q7XW55 oryza sativ
43	43	44.3	1335	2	Q9LA54_9CAUD	Q9LA54 bacterioph
44	43	44.3	1335	2	Q9LA58_9CAUD	Q9LA58 prophage P-
45	42.5	43.8	480	2	Q82A46_STAW	Q82A46 streptomyce

ALIGNMENTS

RESULT 1					
ID	Q7PSV1_FUSNV	PRELIMINARY;	PRT;	382 AA.	
AC	Q7PSV1;				
DT	01-MAR-2004 (TREMBLrel. 26, Created)				
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	(R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.-).				
GN	Name=FNVI343;				
OS	Fusobacterium nucleatum subsp. vincentii ATCC 49256.				
OC	Bacteria; Fusobacteriales; Fusobacteriaceae;				
OC	Fusobacterium.				
OX	NCBI_Taxid=209882;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=ATCC 49256;				
RA	Karpatsch V., Ivanova N., Anderson I., Reznik G., Bhattacharya A.,				
RA	Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,				
RA	Haselkorn R., Overbeek R., Kyriides N.;				
RU	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.				
CC	-!- CAUTION: The sequence shown here is derived from an				
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is				
CC	preliminary data.				
DR	EMBL; AABF0100055; EAA24105.1; -; Genomic_DNA.				
DR	GO; GO:0016829; F-lyase activity; IEA.				
DR	InterPro; IPR010327; HGD-D.				
DR	Pfam; PF06050; HGD-D; 1.				
KW	lyase.				
SQ	SEQUENCE 382 AA; 43893 MW; 441C73816E1C761E CRC64;				
Query Match					
	Best local similarity	52.6%;	Score 51;	DB 2;	Length 382;
	Matches 9;	Conservative	2;	Mismatches 3;	Indels 0;
QY	2	VDQKATNIPYAP 15			
DB	28	EGKAVGIRPYAP 41			
RESULT 2					
ID	Q8R6B3_FUSNN	PRELIMINARY;	PRT;	382 AA.	
AC	Q8R6B3;				
DT	01-JUN-2002 (TREMBLrel. 21, Created)				
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	(R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.-).				
OS	OrderedococcusNemes-FN0208;				
OS	Fusobacterium nucleatum (subsp. nucleatum).				
OC	Bacteria; Fusobacteriales; Fusobacteriaceae;				
OC	Fusobacterium.				
OX	NCBI_Taxid=76856;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				

```

RC STRAIN=ATCC 25586;
RX MEDLINE=21866394; PubMed=11889109;
RX DOI=10.1128/JB.184.7.2005-2018.2002;
RA Kaparatel V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goldsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fomstein M., Kyriplides N.C., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586."
RL J. Bacteriol. 184:2005-2018 (2002).
DR EMBL: AE009951; AAL9414.1; -, Genomic_DNA.
DR InterPro: IPR010327; HGD-D.
DR Pfam: PF06050; HGD-D; 1.
KW Complete proteome; Lyase.
SQ SEQUENCE 382 AA; 43923 MW; 93038D4296AE34CD CRC64;

Query Match 52.6%; Score 51; DB 2; Length 382;
Best Local Similarity 64.3%; Pred. No. 6.9;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGKATNIPYTPAP 15
Db 28 BGKXAVGIFPYAP 41

RESULT 3
0950A9 CAEEL PRELIMINARY; PRT; 168 AA.
AC 0950A9;
RT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Forkhead transcription factor family protein 2, isoform b.
GN Name=Fkh-2; ORFNames=TI4G12.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018 (1998).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL: U41268; AAL02521.1; -, Genomic_DNA.
DR HSSP: Q99958; 1D5V.
DR SMR: Q950A9; 2-68.
DR WormBase: WBGene0001434; Fkh-2.
DR WormPep: T14G12.4b; CE29342.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR InterPro: IPR011991; TF_Fork_head.
DR InterPro: IPR011991; Wing_hlx_DNA_bd.
DR Pfam: PF00250; Fork_head; 1.
DR PRINTS: PD00053; FORKHEAD.
DR PRODOM: PD000425; TF_Fork_head; 1.
DR SMART: SM00339; FH; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS50039; FORK_HEAD_3; 1.
KW Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 168 AA; 19239 MW; 8E01AC4E6968572 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 168;
Best Local Similarity 57.1%; Pred. No. 9.2;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy 3 GQKATNIPYTPAG 16
Db 103 GAAANLFPYFSPG 116

RESULT 4
022510 CAEEL PRELIMINARY; PRT; 270 AA.
ID 022510;
AC 022510;
RT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Forkhead transcription factor family protein 2, isoform a.
GN Name=Fkh-2; ORFNames=TI4G12.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018 (1998).
CC -1- INTERACTION:
CC 021648; R02F2.5; NDEXP=1; InAct=EBI-327741, EBI-314179;
CC 09XW88; Y75B8A.1; NDEXP=1; InAct=EBI-327741, EBI-316766;
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL: U41268; AAB82436.1; -, Genomic_DNA.
DR PIR: T16880; T16880.
DR HSSP: Q99958; 1D5V.
DR SMR: Q22510; 93-170.
DR InAct: Q22510; -.
DR WormBase: WBGene0001434; Fkh-2.
DR WormPep: T14G12.4a; CE04965.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR InterPro: IPR011991; TF_Fork_head.
DR InterPro: IPR011991; Wing_hlx_DNA_bd.
DR Pfam: PF00250; Fork_head; 1.
DR PRINTS: PD00053; FORKHEAD.
DR PRODOM: PD000425; TF_Fork_head; 1.
DR SMART: SM00339; FH; 1.
DR PROSITE: PS00657; FORK_HEAD_1; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS50039; FORK_HEAD_3; 1.
KW Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 270 AA; 30491 MW; 7C49116E5EC76175 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 270;
Best Local Similarity 57.1%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKATNIPYTPAG 16
Db 205 GAAANLFPYFSPG 218

RESULT 5
0608X6 METCA PRELIMINARY; PRT; 1054 AA.
ID 0608X6;
AC 0608X6;
RT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hydrophobe/amphiphile Efflux-1 (HAEl) family protein.

```

```

GN OrderedLocustNames=MCA1360;
OS Methylococcus capsulatus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
OC Methylococcaceae; Methylococcus.
RN NCB1_TaxId=414;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Bach / NCIMB 11132;
RX PubMed=1538840; DOI=10.1371/journal.pbio.0020303;
RA Ward N.L., Larsen O., Sakwa J., Brueseth L., Khouri H.M., Durkin A.S.,
RA Dimitrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E.,
RA Methe B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E.,
RA Rayle J., Tettelin H., Ren Q., Read T.D., Deboy R.T., Seshadri R.,
RA Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,
RA Girdung S.H., Holt I.E., Eidhammer I., Jonassen I., Vanaken S.,
RA Uterback T.R., Feldblyum T.V., Fraser C.M., Lilienhaug J.R.,
RA Eiesen J.A.;
RT "Genomic insights into methanotrophy: the complete genome sequence of
RT Methylococcus capsulatus (Bach).";
RL Plos Biol. 2:1616-1628(2004).
DR EMBL; AE017282; AAU92574.1; -; Genomic_DNA.
DR TIGR; MCA1360; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001036; Acrflavin_res.
DR InterPro; IPR004764; HAEI.
DR Pfam; PF00873; ACR_tran; 1.
DR PRINTS; PR00702; ACRIFLAVINP.
DR TIGRFAMs; TIGR00915; 2A0602; 1.
DR Complete proteome.
SQ SEQUENCE 1054 AA; 115004 MW; BB032CB91B3BD1A8 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 1054;
Best Local Similarity 56.2%; Pred. No. 97;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPG 16
DB 294 VNGHKSIOIVYTLPG 309

RESULT 6
Q94H26 ORYSA
ID Q94H26_ORYSA PRELIMINARY; PRT; 1538 AA.
AC Q94H26;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative gag-pol polyprotein.
GN Name=OSUN80077G22.13;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhacridae; Oryzaceae; Oryza.
OX NCB1_TaxId=4530;
RN NCB1_TaxId=4530;
RN NUCLEOTIDE SEQUENCE.
RP Buell R.;
RX Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC084831; AA52152.1; -; Genomic_DNA.
DR Gramene; Q94H26; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.

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DR GO; GO:0003674; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0006310; F:DNA recombination; IEA.
DR GO; GO:0006278; F:DNA-dependent DNA replication; IEA.
DR InterPro; IPR001562; Retrotrans_gag.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; Rve.
DR Pfam; PF03732; Retrotrans_gag; 1.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF00665; rve; 1.
DR PROSITE; PS50879; RNase_H; 1.
DR PolyProtein.
SQ SEQUENCE 1538 AA; 174627 MW; 5E7A521B398BC776 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 1538;
Best Local Similarity 61.5%; Pred. No. 1,5e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYT 13
DB 740 VDGRAAVNLMPT 752

RESULT 7
Q565U8 9BACT PRELIMINARY; PRT; 408 AA.
ID Q565U8_9BACT PRELIMINARY;
AC Q565U8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE 3-oxoacyl-CoA thiolase.
GN ORFNames=fc62;
OS Uncultured bacterium.
OC Bacteria; environmental samples.
OX NCB1_TaxId=77133;
RN NCB1_TaxId=77133;
RN NUCLEOTIDE SEQUENCE.
RP Kube M., Beck A., Meyerlietks A., Amann R., Reinhardt R., Rabus R.;
RT "A catalytic gene cluster for anaerobic benzoate degradation in
RT methanotrophic microbial Black Sea mats.";
RL Syst. Appl. Microbiol. 28:287-294(2005).
DR EMBL; CR31837; CAI78864.1; -; Genomic_DNA.
SQ SEQUENCE 408 AA; 43368 MW; F9BEC546FA32193 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 408;
Best Local Similarity 38.9%; Pred. No. 52;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPGKQ 18
DB 45 IDASIGANVYQFTAPGAQ 62

RESULT 8
Q619H6 CAEBR PRELIMINARY; PRT; 279 AA.
ID Q619H6_CAEBR PRELIMINARY;
AC Q619H6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG14280.
GN Name=CBG14280;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Felodermidae; Caenorhabditis.
OX NCB1_TaxId=6238;
RN NCB1_TaxId=6238;
RN NUCLEOTIDE SEQUENCE.
RP The C. briggsae Sequencing Consortium;
RX Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CL -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; CAACO1000068; CAB88479.1; -; Genomic_DNA.
DR SMR; Q619H6; 101-178.
DR GO; GO:0005634; C:nucleus; IEA.

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DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR001766; TP Fork head.
DR InterPro: IPR011991; Wing_hlx_DNA_bd.
DR Pfam: PF00250; Fork_head_1.
DR PRINTS: PR00053; FORKHEAD.
DR ProDom: PD000425; TF_Fork_head_1.
DR SMART: SM00339; FH_1.
DR PROSITE: PS00657; FORK_HEAD_1; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS00039; FORK_HEAD_3; 1.
DR DNA-binding, Hypothetical protein; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 279 AA; 31322 MW; 0C926B95AD122D9B CRC64;

Query Match 46.4%; Score 45; DB 2; Length 279;
Best Local Similarity 57.1%; Pred. No. 52;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 GQKATNIFPYTAPG 16
Db 213 GAAANLFPYFPG 226

RESULT 9
ALN_STRCO STANDARD; PRT; 445 AA.
AC O9RKU5;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable allantoinase (EC 3.5.2.5).
GN OrderedLocustNames=SCOC247; ORFNames=SCAH10.12, STAH10.12;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bertley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Sanders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- CATALYTIC ACTIVITY: (S)-allantoin + H(2)O = allantate.
CC -1- COFACTOR: Zinc (By similarity).
CC -1- PATHWAY: Degradation of allantoin (purine catabolism); first step.
CC -1- SIMILARITY: Belongs to the DHOase family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AL939126; CAB60166.1; -, Genomic_DNA.
CC HSSP: P81006; IGRK.
CC InterPro: IPR006680; Amidohydro_1.
CC InterPro: IPR005847; DHOase.
CC Pfam: PF01979; Amidohydro_1; 1.
CC ProDom: PD000518; DHOase; 1.
KW Complete proteome; Hydrolase; Hypothetical protein; Metal-binding;
KW Purine metabolism; Zinc.
FT METAL 63 Zinc (Potential).

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FT METAL 65 Zinc (Potential).
SQ SEQUENCE 445 AA; 47492 MW; 75955C5F98632570 CRC64;

Query Match 46.4%; Score 45; DB 1; Length 445;
Best Local Similarity 53.3%; Pred. No. 85;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDQKATNIFPYTAP 15
Db 26 VTGEKITAVLPYDAP 40

RESULT 10
Q4IFN3_GIBZE PRELIMINARY; PRT; 811 AA.
ID Q4IFN3;
AC Q4IFN3;
DT 13-SEP-2005 (TREMURel. 31, Last sequence update)
DT 13-SEP-2005 (TREMURel. 31, Last sequence update)
DT 13-SEP-2005 (TREMURel. 31, Last annotation update)
DE Hypothetical protein.
DE ORFNames=FG03975.1;
GN Gibberella zeae PH-1.
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nussbaum C., Abouelleil A., Allen N., Anderson S.,
RA Archchi H.M., Barna N., Baetien V., Bloom T., Boguslavsky L.,
RA Boukhalter B., Butler J., Calvo S.B., Camarata J., Chang Y.,
RA Choepel Y., Collamore A., Cook A., Cooke P., Corman B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gierke S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamel M., Kamet A., Karatae A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Maucelli E., McCarthy M., Meldrum J., Menues L.,
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunhkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Rette R., Rife C., Rogov P.,
RA Roman J., Schauer S., Schepback T., Seaman S., Severy N., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence."
RT Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC DR EMBL: AAC01000168; EAA73443.1; -, Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 811 AA; 84248 MW; C2C5A4A02E10DA79 CRC64;

Query Match 46.4%; Score 45; DB 2; Length 811;
Best Local Similarity 58.8%; Pred. No. 1.66+02;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 DGQKATNIFPYTAPGK 18
Db 676 DDDKETAATGCTAPGK 692

RESULT 11
GAGC1_HUMAN STANDARD; PRT; 102 AA.
ID GAGC1_HUMAN
AC G08025;
DT 16-OCT-2001 (Rel. 40, Created)

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DR Gramene; Q9AYA0; -.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
 DR Polyprotein.
 SQ SEQUENCE 340 AA; 37731 MW; 88DE72BBA5A44C9C CRC64;

Query Match 45.4%; Score 44; DB 2; Length 340;
 Best Local Similarity 61.5%; Pred. No. 94;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 VDGOKATNIPYPT 13
 DB 128 VDGGAAYVNLMPYT 140

RESULT 14

06ALL1 DESPS
 ID 06ALL1 DESPS PRELIMINARY; PRT; 525 AA.
 AC 06ALL1;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Related to Mtr restriction system protein.
 GN OrderedLocustNames=DP2035;
 OS Desulfotalea psychrophila.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
 OC Desulfobulbaceae; Desulfotalea.
 OX NCBI_TaxID=84980;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=LSV54 / DSM 12343;
 RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
 RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
 RA Klenk H.-P.;
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
 from permanently cold Arctic sediments.";
 RL Environ. Microbiol. 6:887-902(2004).
 DR EMBL; CRS52870; CAG36764.1; -; Genomic_DNA.
 DR InterPro: IPR007560; Mtr_cat.
 DR Pfam; PF04471; Mtr_cat; I.
 KM Complete proteome.
 SQ SEQUENCE 525 AA; 58444 MW; 22D0BB93FD105099 CRC64;

Query Match 45.4%; Score 44; DB 2; Length 525;
 Best Local Similarity 70.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 TNIFPYTAPG 16
 DB 106 TNLFPIYIKPG 115

RESULT 15

Q53Q04 ORYSA PRELIMINARY; PRT; 589 AA.
 AC 053Q04;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Retrotransposon protein, putative, unclassified.
 GN ORFNames=LOC_Os11g19590;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriatloideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Maiti R., Lin H.,
 RA Zhu W., Hamilton J., Jones K., Talton L., Feldblyum T., Tsirlin T.,

RA Bera J., Kim M., Jin S., Fadrosh D., Vuong H., Overton II L.,
 RA Reardon M., Weaver B., Johni S., Lewis M., Uteirack T., Van Aken S.,
 RA Wortman J., Haas B., Koo H., Zismann V., Hsieh J., Iobst S.,
 RA de Vazelles A., White O., Salzberg S., Fraser C.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RA Buell R.; (APR-2005) to the EMBL/GenBank/DBJ databases.
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC120306; AAX94889.1; -; Genomic DNA.
 SQ SEQUENCE 589 AA; 67737 MW; 21931C5BDD43DB7 CRC64;

Query Match 45.4%; Score 44; DB 2; Length 589;
 Best Local Similarity 61.5%; Pred. No. 1.7e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 VDGOKATNIPYPT 13
 DB 333 VDGGAAYVNLMPYT 345

Search completed: December 12, 2005, 20:41:11
 Job time : 98.7586 secs

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: December 12, 2005, 21:20:50 ; Search time 109.333 Seconds
(without alignments)
72.337 Million cell updates/sec

Title: US-10-758-165A-11
Perfect score: 96
Sequence: 1 IDGQKVDQEPQHGIVKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 827869

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*
9: Geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	8	ADRI0611 Horse IGB
2	78	81.2	15	7	ADc64569 Horse Imm
3	36	37.5	14	5	ABP46438 Human Bly
4	36	37.5	14	7	ADG97265 scfV VHCD
5	35	36.5	18	8	ADRI0610 Cat IGE e
6	34	35.4	15	2	AAR50232 Sequence
7	34	35.4	15	6	ABP94693 HLA prote
8	34	35.4	15	6	ABP95588 HLA prote
9	34	35.4	15	6	ABP95194 HLA prote
10	34	35.4	17	8	ADM96833 Tissue fa
11	34	35.4	18	8	ADRI0609 Dog IGE e
12	33	34.4	10	8	ADL98126 Candida k
13	33	34.4	15	6	ABP94247 HLA prote
14	33	34.4	15	6	ABP95554 HLA prote
15	33	34.4	15	6	ABP94098 HLA prote
16	33	34.4	15	6	ABP95117 HLA prote
17	33	34.4	15	6	ABP94539 HLA prote
18	33	34.4	15	6	ABP94780 HLA prote
19	33	34.4	15	6	ABP95372 HLA prote
20	33	34.4	15	6	ABR32079 Human can
21	33	34.4	15	6	ABR32127 Human can
22	33	34.4	15	8	ADV31901 Human 109
23	33	34.4	15	8	ADV31853 Human 109
24	33	33.3	10	2	AAW15125 Aeperg111

25	32	33.3	14	4	AAG98200 Human SNP
26	32	33.3	14	5	ABP46692 Human Bly
27	32	33.3	14	5	ABP46435 Human Bly
28	32	33.3	14	7	ADG97262 scfV VHCD
29	32	33.3	14	7	ADG97519 scfV VHCD
30	32	33.3	15	6	ABP95187 HLA prote
31	32	33.3	15	6	ABP94687 HLA prote
32	32	33.3	15	6	ABP94184 HLA prote
33	32	33.3	15	6	ABP94689 HLA prote
34	32	33.3	15	6	ABP95591 HLA prote
35	32	33.3	15	6	ABP95184 HLA prote
36	32	33.3	15	6	ABP95593 HLA prote
37	32	33.3	15	6	ABP94179 HLA prote
38	31	32.3	14	5	ABP46135 Human Bly
39	31	32.3	14	5	ABP46140 Human Bly
40	31	32.3	14	7	ADG96967 scfV VHCD
41	31	32.3	14	7	ADG96962 scfV VHCD
42	31	32.3	15	6	ABP94547 HLA prote
43	31	32.3	15	6	ABP94779 HLA prote
44	31	32.3	15	6	ABP95264 HLA prote
45	31	32.3	15	6	ABP95553 HLA prote

ALIGNMENTS

RESULT 1
ID ADR10611 standard, peptide, 18 AA.
XX
XX ADR10611;
XX
XX 21-OCT-2004 (first entry)
XX
XX 21-OCT-2004 (first entry)
XX
XX Horse IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 11.
XX
XX Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX horse.
XX
XX Equus caballus.
XX
XX WO2004065936-A2.
XX
XX PD 05-AUG-2004.
XX
XX PF 15-JAN-2004; 2004WO-US003566.
XX
XX PR 16-JAN-2003; 2003US-0440472P.
XX
XX (UNNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hammerberg B;
XX
XX WPI; 2004-593545/57.
XX
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGB, e.g. dog IGE.
CC (I) is useful for testing an allergen reactivity of an IGE sample.
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IGE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IGE. The present sequence is the
CC horse IGE 3.76 recognition site.

XX Sequence 18 AA;

Query Match 100.0%; Score 96; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDGQKVDGPPQHGVLKQ 18
Db 1 IDGQKVDGPPQHGVLKQ 18

RESULT 2

AD64569 standard; peptide; 15 AA.

XX AD64569;

XX 18-DEC-2003 (first entry)

XX Horse immunoglobulin E, IGE, heavy chain immunogenic peptide PS.

XX Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.

XX Equus caballus.

XX US2003087314-A1.

XX 08-MAY-2003.

XX 08-NOV-2001; 2001US-00052788.

XX 08-NOV-2001; 2001US-00052788.

XX (REGC) UNIV CALIFORNIA.

XX Gershwin LJ, Pettigrew HD, Kalina WV;

XX WPI; 2003-765437/72.

XX Immunogenic composition comprising an isolated equine immunoglobulin E
XX polypeptide that induces production of antibodies which specifically bind
XX to equine immunoglobulin E.

XX Example 1; Page 8; 14pp; English.

XX The invention relates to an immunogenic composition comprising an
XX isolated polypeptide having an amino acid sequence that is at least 80%
XX identical to 6 (S1-S6), is amino acid peptide sequences derived from
XX equine immunoglobulin E (the composition induces production of an
XX antibody that specifically binds to equine immunoglobulin (Ig)E), the six
XX polypeptides are not explicitly identified in the specification. Also
XX included are a composition comprising an antibody that specifically binds
XX to a polypeptide at least 80% identical to (S1)-(S6), an antibody that
XX specifically binds to equine IGE made by the process of immunising an
XX animal with a polypeptide at least 80% identical to (S1)-(S6), making an
XX antibody that specifically binds to equine IGE (involving immunising an
XX animal with a composition further comprising an isolated polypeptide (the
XX amino acid sequence of the polypeptide is at least 80% identical to (S1)-
XX (S6)), and collecting antiserum from the animal) and a kit for detection
XX of equine IGE in a biological sample comprising the antibody and means
XX for detecting specific binding of the antibody to equine IGE. The
XX antibody is useful for detecting equine IGE protein in a biological
XX sample (serum) which involves contacting the sample with the antibody,
XX thus forming an antigen/antibody complex, and detecting the presence or
XX absence of the antigen/antibody complex. The antibody and antigen are
XX immobilised on a solid surface. The antibody is labelled such that the
XX complex can be detected. The complex is detected using a second labelled

CC antibody. The peptides are useful for generating antibodies specific for
CC IGE which can serve as a diagnostic test for allergy. The present
CC sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic
CC peptide from the middle portion of the C2 region.

XX Sequence 15 AA;

Query Match 81.2%; Score 78; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDGQKVDGPPQHG 14
Db 2 IDGQKVDGPPQHG 15

RESULT 3

ABP4638 standard; peptide; 14 AA.

XX ABP4638;

XX 19-AUG-2002 (first entry)

XX Human Blys binding scfv VH CDR3 SEQ ID 2449.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

XX 17-OCT-2000; 2000US-0240816P.

XX 16-MAR-2001; 2001US-0276248P.

XX 21-MAR-2001; 2001US-0277379P.

XX 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.

XX Claim 2; Page 2992; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antineumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and

CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 14 AA;
Query Match 37.5%; Score 36; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 10 FPQHGL 15
Db 7 FPQHGL 12
RESULT 4
ADG97265
ID ADG97265 standard; peptide; 14 AA.
XX
AC ADG97265;
XX
DT 11-MAR-2004 (first entry)
XX
DE scFv VHCDR3 peptide that immunospecifically binds Blys SegID 2449.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
XX B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX WPI; 2003-505530/47.
DR
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 2449; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC peptide sequence is a single chain antibody variable heavy CDR3 peptide

CC that immunospecifically binds Blys of the invention.
XX
SQ Sequence 14 AA;
Query Match 37.5%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 10 FPQHGL 15
Db 7 FPQHGL 12
RESULT 5
ADR10610
ID ADR10610 standard; peptide; 18 AA.
XX
AC ADR10610;
XX
DT 21-OCT-2004 (first entry)
XX
DE Cat Ige epitope recognised by monoclonal antibody 3.76, SEQ ID 10.
XX
KW Antiasthmatic; Antiallergic; Immunosuppressive; Ige; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW cat.
XX
OS Fells catus.
XX
PN WO2004065936-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.
XX
PA (UNNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hammerberg B;
XX WPI; 2004-593545/57.
DR
XX
PT Novel antibody that specifically binds to mammalian Ige epitope, useful
PT for testing an allergen reactivity of Ige sample, detecting mammalian Ige
PT or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
CC The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian Ige epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian Ige, e.g. dog Ige.
CC (I) is useful for testing an allergen reactivity of an Ige sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian Ige and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine Ige corresponding to amino acid
CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
CC canine Ige epsilon-chain. Recognition of epsilon-chains from Ige from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of Ige from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of Ige. The present sequence is the
CC cat Ige 3.76 recognition site.
XX
SQ Sequence 18 AA;
Query Match 36.5%; Score 35; DB 8; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.9e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
OY 1 IDGQKVDQFPQHGLVKKQ 18

Db 1 VDGQKATNIFPYTAPGKQ 18

|||||

RESULT 6
AAR50232
ID AAR50232 standard; protein; 15 AA.

XX AAR50232;

DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 09-OCT-1994 (first entry)

XX Sequence of NH2 terminal fragment of Group A streptococcal surface protein M3.

XX B subunit; labile toxin; M protein; fusion protein; antigen;
XX Group A streptococci; rheumatic fever; pharyngitis; ss.

XX Streptococcus sp.

XX MO9406465-A1.

XX 31-MAR-1994.

XX 15-SEP-1993; 93WO-US008704.

XX 16-SEP-1992; 92US-00945860.

XX (UYTE-) UNIV TENNESSEE RES CORP.

XX Dale JB;

XX WPI; 1994-118162/14.

XX New recombinant hybrid streptococcal M protein antigen(s) - which elicit
PT opsonic antibodies without eliciting cross-reactive antibodies to
PT mammalian heart tissue.

XX Disclosure; Page 11; 45pp; English.

XX The surface M protein of Group A streptococci is the major virulence
CC factor and protective antigen of these organisms. However, there are a
CC tremendous number of M protein serotypes. The invention provides
CC recombinant M protein antigens comprising a gene encoding a carrier
CC protein and an NH2 or COOH terminal M protein fragment carrying one or
CC more epitopes. AAR50232 is a suitable NH2-terminal fragment of M3 protein
CC for constructing antigens which elicit opsonic antibodies in an immunised
CC animal when linked or fused to an appropriate carrier. (Updated on 25-
CC MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS
CC field.)

XX Sequence 15 AA;

Query Match 35.4%; Score 34; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 DQKRVDEQFPQH 13
| : : : : :
| : : : : :
1 DARSVNGEFPFRH 12

RESULT 7
ABP94693
ID ABP94693 standard; peptide; 15 AA.

XX ABP94693;

DT 28-MAR-2003 (first entry)

XX HLA protein 121P2A3 peptide #11048.

XX Human, 121P2A3; cytosolic; immunostimulant; vaccine; SSH;
KW humoral immune response; cellular immune response;
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

XX WO200283068-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002MO-US011359.

XX 10-APR-2001; 2001US-0282739P.

XX 25-APR-2001; 2001US-0286630P.

XX 22-JUN-2001; 2001US-0300373P.

XX (AGEN-) AGENSYS INC.

XX Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC,
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A,
XX WPI; 2003-092956/08.

XX New composition comprising a substance that modulates the status of
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT responses or in assessing the status of 121P2A3 gene products in normal
PT versus cancerous tissues.

XX Claim 13; Page 270; 362pp; English.

XX The invention relates to a novel composition comprising a substance that
CC modulates the status of a protein, 121P2A3. The composition of the
CC invention has cytostatic and immunostimulant activity, and is useful as a
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC eliciting humoral or cellular immune response. The polynucleotides are
CC useful for characterizing cytogenetic abnormalities of this chromosomal
CC locus, as tools that can be used to delineate cytogenetic abnormalities
CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene products
CC in normal versus cancerous tissues. The proteins are useful for
CC generating and characterizing domain-specific antibodies, for identifying
CC agents or cellular factors that bind to 121P2A3 or a particular structure
CC domain, and in various therapeutic and diagnostic contexts, including
CC cancer vaccines. The antibodies or T cells reactive with the product are
CC useful in passive or active immunisation, and in imaging methodologies
CC for the management of cancer. The sequences shown in ABP95595
CC represent peptides from the 121P2A3 variants of the invention

XX Sequence 15 AA;

Query Match 35.4%; Score 34; DB 6; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 DQKRVDEQFPQHGIV 16
| : : : : :
| : : : : :
1 ENKELDRQHVQHQL 15

RESULT 8
ABP95588
ID ABP95588 standard; peptide; 15 AA.

XX ABP95588;

DT 28-MAR-2003 (first entry)

XX HLA protein 121P2A3 peptide #11943.

XX Human, 121P2A3; cytosolic; immunostimulant; vaccine; SSH;
KW humoral immune response; cellular immune response;
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

```
XX OS Homo sapiens.
XX PN WO000283068-A2.
XX
XX 24-OCT-2002.
XX
XX PF 09-APR-2002; 2002MO-US011359.
XX
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PR 22-JUN-2001; 2001US-0300373P.
XX
XX PA (AGEN-) AGENSYS INC.
XX
XX PI Chailita-Bid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX DR WPI; 2003-092956/08.
XX
XX PT New composition comprising a substance that modulates the status of
XX PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX PT responses or in assessing the status of 121P2A3 gene products in normal
XX PT versus cancerous tissues.
XX
XX PS Claim 13; Page 287; 362pp; English.
XX
XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a protein, 121P2A3. The composition of the
XX CC invention has cytostatic and immunostimulant activity, and is useful as a
XX CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
XX CC eliciting humoral or cellular immune response. The polynucleotides are
XX CC useful for characterizing cytogenetic abnormalities of this chromosomal
XX CC locus, as tools that can be used to delineate cytogenetic abnormalities
XX CC in the chromosomal region that encodes 121P2A3 that may contribute to
XX CC malignant phenotype, and in assessing the status of 121P2A3 gene products
XX CC in normal versus cancerous tissues. The proteins are useful for
XX CC generating and characterizing domain-specific antibodies, for identifying
XX CC agents or cellular factors that bind to 121P2A3 or a particular structure
XX CC domain, and in various therapeutic and diagnostic contexts, including
XX CC cancer vaccines. The antibodies or T cells reactive with the product are
XX CC useful in passive or active immunisation, and in imaging methodologies
XX CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
XX CC represent peptides from the 121P2A3 variants of the invention
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 35.4%; Score 34; DB 6; Length 15;
XX Best Local Similarity 40.0%; Pred. No. 2.3e+02;
XX Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 2 DGQKVDQFPQHGIV 16
XX : : | : | : | : | :
XX Db 1 ENKKLDKQHVQHQL 15
XX
XX RESULT 9
XX ABP95194
XX ID ABP95194 standard; peptide; 15 AA.
XX
XX AC ABP95194;
XX
XX DT 28-MAR-2003 (first entry)
XX
XX DE HLA protein 121P2A3 peptide #11549.
XX
XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX KW humoral immune response; cellular immune response;
XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
XX OS Homo sapiens.
XX
XX PN WO000283068-A2.
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XX XX 24-OCT-2002.
XX PD
XX XX 09-APR-2002; 2002MO-US011359.
XX PF
XX XX 10-APR-2001; 2001US-0282739P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PR 22-JUN-2001; 2001US-0300373P.
XX
XX PA (AGEN-) AGENSYS INC.
XX
XX PI Chailita-Bid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX DR WPI; 2003-092956/08.
XX
XX PT New composition comprising a substance that modulates the status of
XX PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX PT responses or in assessing the status of 121P2A3 gene products in normal
XX PT versus cancerous tissues.
XX
XX PS Claim 13; Page 279; 362pp; English.
XX
XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a protein, 121P2A3. The composition of the
XX CC invention has cytostatic and immunostimulant activity, and is useful as a
XX CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
XX CC eliciting humoral or cellular immune response. The polynucleotides are
XX CC useful for characterizing cytogenetic abnormalities of this chromosomal
XX CC locus, as tools that can be used to delineate cytogenetic abnormalities
XX CC in the chromosomal region that encodes 121P2A3 that may contribute to
XX CC malignant phenotype, and in assessing the status of 121P2A3 gene products
XX CC in normal versus cancerous tissues. The proteins are useful for
XX CC generating and characterizing domain-specific antibodies, for identifying
XX CC agents or cellular factors that bind to 121P2A3 or a particular structure
XX CC domain, and in various therapeutic and diagnostic contexts, including
XX CC cancer vaccines. The antibodies or T cells reactive with the product are
XX CC useful in passive or active immunisation, and in imaging methodologies
XX CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
XX CC represent peptides from the 121P2A3 variants of the invention
XX
XX SQ Sequence 15 AA;
XX
XX Query Match 35.4%; Score 34; DB 6; Length 15;
XX Best Local Similarity 40.0%; Pred. No. 2.3e+02;
XX Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 2 DGQKVDQFPQHGIV 16
XX : : | : | : | : | :
XX Db 1 ENKKLDKQHVQHQL 15
XX
XX RESULT 10
XX ADM96833
XX ID ADM96833 standard; peptide; 17 AA.
XX
XX AC ADM96833;
XX
XX DT 29-JUL-2004 (first entry)
XX
XX DE Tissue factor VIIa (TFVIIa) peptide antagonist #249.
XX
XX KW tissue factor VIIa; chronic thromboembolic disease;
XX KW fibrin formation; vascular disorders; deep venous thrombosis;
XX KW arterial thrombosis; stroke; atherosclerosis; septicaemia.
XX
XX OS Synthetic.
XX
XX PN US200408767-A1.
XX
XX PD 06-MAY-2004.
XX
XX PF 30-JAN-2003; 2003US-00356257.
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XX 06-FEB-2002; 2002US-0355420P.
PR (GETH ) GENENTECH INC.
XX
XX Lazarus RA, Maun HR;
XX WPI; 2004-356247/33.
DR
XX New peptide, useful for preventing or treating chronic thromboembolic
PT diseases or disorders associated with fibrin formation including vascular
PT disorders, such as deep venous thrombosis, arterial thrombosis, and
PT stroke.
XX
XX Example 2; SEQ ID NO 255; 102pp; English.
XX
CC The invention relates to peptide antagonists of tissue Factor VIIa
CC (FVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
CC with the peptide in the presence of tissue factor and under conditions
CC that allow binding of the compound to FVIIa to occur. The peptides are
CC useful for preventing or treating chronic thromboembolic diseases or
CC disorders associated with fibrin formation including vascular disorders,
CC such as deep venous thrombosis, arterial thrombosis, stroke,
CC atherosclerosis, or septicemia. The present sequence represents a tFVIIa
CC peptide antagonist of the invention.
XX
SQ Sequence 17 AA;
XX
Query Match 35.4%; Score 34; DB 8; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 3 GQKVDQEPQ 12
Db 1 GEGVEEFPE 10
XX
RESULT 11
ADRI0609
ID ADRI0609 standard; peptide; 18 AA.
XX
AC ADRI0609;
XX
DT 21-OCT-2004 (first entry)
XX
DE Dog IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.
XX
XX Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
XX
XX Canis familiaris.
OS
XX WO2004065936-A2.
PN
XX 05-AUG-2004.
PD
XX 15-JAN-2004; 2004WO-US003566.
PF
XX 16-JAN-2003; 2003US-0440472P.
PR
XX (UYNC-) UNIV NORTH CAROLINA STATE.
PA
XX Hammerberg B;
XX
XX WPI; 2004-593545/57.
DR
XX
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
CC The present invention relates to a novel monoclonal antibody (1) that
```

```
CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC (1) is useful for testing an allergen reactivity of an IGE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (1) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IGE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IGE.
XX
SQ Sequence 18 AA;
XX
Query Match 35.4%; Score 34; DB 8; Length 18;
Best Local Similarity 54.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 IDGKVDQEP 11
Db 1 VDGGKATNTP 11
XX
RESULT 12
ADL98126
ID ADL98126 standard; peptide; 10 AA.
XX
AC ADL98126;
XX
DT 17-JUN-2004 (first entry)
XX
DE Candida kefyr enone reductase peptide SEQ ID NO:9.
XX
XX enone reductase; enzyme; levodione; ketoisophorone; carotenoid;
KW Candida kefyr; Kluyveromyces marxianus.
XX
XX Kluyveromyces marxianus.
OS
XX WO2004027065-A2.
PN
XX 01-APR-2004.
PD
XX 19-SEP-2003; 2003WO-EP010473.
PF
XX 23-SEP-2002; 2002EP-00021098.
PR
XX (STM ) DSM IP ASSETS BV.
PA
XX Karaoka M, Shimizu S;
XX
XX WPI; 2004-295422/27.
DR
XX
XX New enone reductase, useful in improving the production process of
PT levodione, which is important in the synthesis of optically active
PT carotenoids.
XX
XX Example 1; SEQ ID NO 9; 31pp; English.
XX
CC The present invention describes an isolated DNA (1) comprising a
CC nucleotide sequence coding for an enzyme having enone reductase activity.
CC Also described: (1) a vector or a plasmid comprising (1); (2) a host cell
CC transformed or transfected by (1) or the vector or the plasmid of (1);
CC (3) a polypeptide encoded by (1); and (4) a process for the production of
CC levodione which comprises contacting ketoisophorone with the polypeptide
CC of (3) or with the host cell of (2) or a cell-free extract under
CC conditions for the production of levodione, e.g. at pH 4.0-9.0 and at a
CC temperature of 10-60 degrees Celsius for 5 minutes to 72 hours or at pH
CC 5.0-8.0 and at a temperature of 20-60 degrees Celsius for 15 minutes to
CC 48 hours. The DNA (1) and the encoded polypeptide can be used in
CC improving the production process of levodione, which is important in the
```

CC synthesis of optically active carotenoids. The present sequence
CC represents a Candida kefyr (Kluyveromyces marxianus) enone reductase
CC peptide, which is used in the exemplification of the present invention.
XX
SQ Sequence 10 AA;

Query Match 34.4%; Score 33; DB 8; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 POGGLVK 17
| | | | |
Db 4 POGGITK 10

RESULT 13

ABP94247
ID ABP94247 standard; peptide; 15 AA.

XX AC ABP94247;

XX DT 28-MAR-2003 (first entry)

XX DE HLA protein 121P2A3 peptide #10602.

XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

XX KW humoral immune response; cellular immune response;
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283068-A2.

XX PD 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US011359.

XX PR 10-APR-2001; 2001US-0282739P.

XX PR 25-APR-2001; 2001US-0286630P.

XX PR 22-JUN-2001; 2001US-0300373P.

XX PA (AGEN-) AGENSYS INC.

XX PI Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX DR WPI; 2003-092956/08.

XX PT New composition comprising a substance that modulates the status of
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT responses or in assessing the status of 121P2A3 gene products in normal
PT versus cancerous tissues.

XX PS Claim 13; Page 261; 362pp; English.

XX The invention relates to a novel composition comprising a substance that
CC modulates the status of a protein, 121P2A3. The composition of the
CC invention has cyostatic and immunostimulant activity, and is useful as a
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC eliciting humoral or cellular immune response. The polynucleotides are
CC useful for characterising cytogenetic abnormalities of this chromosomal
CC locus, as tools that can be used to delineate cytogenetic abnormalities
CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene products
CC in normal versus cancerous tissues. The proteins are useful for
CC generating and characterising domain-specific antibodies, for identifying
CC agents or cellular factors that bind to 121P2A3 or a particular structure
CC domain, and in various therapeutic and diagnostic contexts, including
CC cancer vaccines. The antibodies or T cells reactive with the product are
CC useful in passive or active immunisation, and in imaging methodologies
CC for the management of cancer. The sequences shown in ABP93646 - ABP95595
XX represent peptides from the 121P2A3 variants of the invention

SQ Sequence 15 AA;

Query Match 34.4%; Score 33; DB 6; Length 15;
Best Local Similarity 42.9%; Pred. No. 3.3e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 DQKVDQEPQHGL 15
: | : | | | |
Db 2 ENEKUDRQHVOHQ 15

RESULT 14

ABP95554
ID ABP95554 standard; peptide; 15 AA.

XX AC ABP95554;

XX DT 28-MAR-2003 (first entry)

XX DE HLA protein 121P2A3 peptide #11909.

XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

XX KW humoral immune response; cellular immune response;
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX OS Homo sapiens.

XX PN WO200283068-A2.

XX PD 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US011359.

XX PR 10-APR-2001; 2001US-0282739P.

XX PR 25-APR-2001; 2001US-0286630P.

XX PR 22-JUN-2001; 2001US-0300373P.

XX PA (AGEN-) AGENSYS INC.

XX PI Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX DR WPI; 2003-092956/08.

XX PT New composition comprising a substance that modulates the status of
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT responses or in assessing the status of 121P2A3 gene products in normal
PT versus cancerous tissues.

XX PS Claim 13; Page 286; 362pp; English.

XX The invention relates to a novel composition comprising a substance that
CC modulates the status of a protein, 121P2A3. The composition of the
CC invention has cyostatic and immunostimulant activity, and is useful as a
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC eliciting humoral or cellular immune response. The polynucleotides are
CC useful for characterising cytogenetic abnormalities of this chromosomal
CC locus, as tools that can be used to delineate cytogenetic abnormalities
CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene products
CC in normal versus cancerous tissues. The proteins are useful for
CC generating and characterising domain-specific antibodies, for identifying
CC agents or cellular factors that bind to 121P2A3 or a particular structure
CC domain, and in various therapeutic and diagnostic contexts, including
CC cancer vaccines. The antibodies or T cells reactive with the product are
CC useful in passive or active immunisation, and in imaging methodologies
CC for the management of cancer. The sequences shown in ABP93646 - ABP95595
XX represent peptides from the 121P2A3 variants of the invention

SQ Sequence 15 AA;

Query Match 34.4%; Score 33; DB 6; Length 15;
Best Local Similarity 42.9%; Pred. No. 3.3e+02;

	Matches	6;	Conservative	3;	Mismatches	5;	Indels	0;	Gaps	0;
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		: :								
Db	2	ENEKIDRQHQQL	15							

Db 2 ENEKLDROHVQHQL 15

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Search completed: December 12, 2005, 21:52:05
Job time : 111.333 secs
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RESULT 15
ABP94098
ID      ABP94098  standard; peptide; 15 AA.
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AC ABP94098;

DT 28-MAR-2003 (first entry)

HLA protein 121P2A3 peptide #10453.

KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

OS Homo sapiens.

PN WO200283068-A2.

PD 24-OCT-2002

PF 09-APR-2002; 2002WO-US011359.

PR 10-APR-2001; 2001US-0282739P.

PR 22-JUN-2001; 2001US-0300373P.

PA (AGEN-) AGENSYS INC.

PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;

[illegible]

XX
DE

PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune

PT versus cancerous tissues.

PS Claim 13; Page 258; 362pp; English
xx

CC The invention relates to a novel composition comprising a substance that modulates the structure of a protein.

CC invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 131D23 protein and polypeptides are useful for

eliciting humoral or cellular immune response. The polynucleotide is useful for characterizing abnormalities of this response.

CC locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 131p32 that may contribute to

CC malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for

generating and characterising domain-specific antibodies, for identifying

CC domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reacting with the product are

useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The authors thank Dr. J. A. J. van der Vliet for the management of cancer. The authors thank Dr. J. A. J. van der Vliet for the management of cancer.

CC represent peptides from the 121P2A3 variants of the invention.

sequence 15 AA;

Query Match	Score	DB	Length
Best Local Similarity	43.9%	Prod	330,031
Query Match	34.4%	Score 33;	Length 15,

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Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
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2 DGQKVNDEQFPQHGL 15

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 21:05:57 ; Search time 27 Seconds
(without alignments)
55.117 Million cell updates/sec

Title: US-10-758-165A-11
Perfect score: 96
Sequence: 1 IDGQKVDQEPFHGLVKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 208455

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*

- 1: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/ECTUS COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RE COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	34	35.4	15	2	US-08-914-479A-11
2	32	33.3	10	1	US-08-151-574-3
3	32	33.3	10	1	US-08-419-448-3
4	32	33.3	10	2	US-09-233-510-3
5	30	31.2	11	1	US-08-486-839-8
6	30	31.2	11	2	US-09-151-011-8
7	30	31.2	11	2	US-09-343-623-8
8	30	31.2	11	2	US-09-977-827-8
9	29	30.2	10	1	US-08-166-195A-23
10	29	30.2	10	1	US-08-436-772-23
11	29	30.2	10	1	US-08-436-883B-23
12	29	30.2	11	1	US-08-486-839-12
13	29	30.2	11	1	US-09-151-011-12
14	29	30.2	11	2	US-09-343-623-12
15	29	30.2	11	2	US-09-977-827-13
16	29	30.2	15	1	US-08-006-341-2
17	29	30.2	15	1	US-09-511-625B-64
18	28	29.2	15	2	US-07-895-503A-10
19	28	29.2	15	1	US-08-390-510-10
20	28	29.2	15	1	US-08-390-790-10
21	28	29.2	15	1	US-08-390-509-10
22	28	29.2	15	2	US-09-149-860A-10
23	28	29.2	17	2	US-08-836-561-41
24	28	29.2	17	2	US-09-434-122-41
25	27	28.1	10	2	US-08-371-680-10
26	27	28.1	11	1	US-08-486-839-14
27	27	28.1	11	1	US-09-151-011-14

28	27	28.1	11	2	US-09-343-623-14	Sequence 14, Appl
29	27	28.1	11	2	US-09-977-827-15	Sequence 15, Appl
30	27	28.1	15	2	US-08-475-955-75	Sequence 75, Appl
31	27	28.1	15	2	US-07-867-819D-75	Sequence 75, Appl
32	27	28.1	16	2	US-09-701-588C-107	Sequence 107, Appl
33	26	27.1	11	1	US-08-486-839-13	Sequence 13, Appl
34	26	27.1	11	2	US-09-151-011-13	Sequence 13, Appl
35	26	27.1	11	2	US-09-343-623-13	Sequence 13, Appl
36	26	27.1	11	2	US-09-685-010-49	Sequence 49, Appl
37	26	27.1	11	2	US-09-977-827-14	Sequence 14, Appl
38	26	27.1	11	2	US-09-978-309A-49	Sequence 49, Appl
39	26	27.1	11	2	US-09-978-309A-84	Sequence 84, Appl
40	26	27.1	12	1	US-08-151-574-9	Sequence 9, Appl
41	26	27.1	12	1	US-08-196-940-3	Sequence 3, Appl
42	26	27.1	12	1	US-08-419-448-9	Sequence 9, Appl
43	26	27.1	12	2	US-09-233-510-9	Sequence 9, Appl
44	26	27.1	12	2	US-09-685-010-12	Sequence 12, Appl
45	26	27.1	12	2	US-09-685-010-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-914-479A-11
Sequence 11, Application US/08914479A
Patent No. 6419932
GENERAL INFORMATION:
APPLICANT: Dale, James B.
TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
FILE REFERENCE: 481112.404C2
CURRENT APPLICATION NUMBER: US/08/914,479A
PRIOR APPLICATION NUMBER: 08/409,270
PRIOR FILING DATE: 1995-03-23
PRIOR APPLICATION NUMBER: 07/945,860
PRIOR FILING DATE: 1992-09-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 15
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: N-2-terminal fragment of M protein for
OTHER INFORMATION: constructing antigens, which elicit opsonic
US-08-914-479A-11
OTHER INFORMATION: antibodies in an immunized animal

Query Match
Best Local Similarity 35.4%; Score 34; DB 2; Length 15;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGQKVDQEPFH 13
Db 1 DARSVNGEPFH 12

RESULT 2
US-08-151-574-3
Sequence 3, Application US/08151574
Patent No. 5436156
GENERAL INFORMATION:
APPLICANT: Robert F. M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Seilen
TITLE OF INVENTION: Cloning and Expression of Microbial
NUMBER OF SEQUENCES: 52

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Morrison & Foerster
;; STREET: 545 Middlefield Road, Suite 200
;; CITY: Menlo Park
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94025-3471
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/151,574
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/688,578
;; FILING DATE: 24-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Murashige, Kate H.
;; REGISTRATION NUMBER: 29,959
;; REFERENCE/DOCKET NUMBER: 24615-20026.00
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-327-7250
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHEICAL: NO
;; FRAGMENT TYPE: N-terminal
;;
US-08-151-574-3

Query Match 33.3%; Score 32; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 VDEQFPQHG 14
|||:|
Db 2 VDERFPYTG 10

RESULT 3
US-08-419-448-3
; Sequence 3, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/419,448
;; FILING DATE: 10-APR-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Murashige, Kate H.
;; REGISTRATION NUMBER: 29,959
;; REFERENCE/DOCKET NUMBER: 24615-20026.10
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-887-1500
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHEICAL: NO
;; FRAGMENT TYPE: N-terminal
;;
US-08-419-448-3

Query Match 33.3%; Score 32; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 VDEQFPQHG 14
|||:|
Db 2 VDERFPYTG 10

RESULT 4
US-09-233-510-3
; Sequence 3, Application US/09233510
; Patent No. 6350602
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,510
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
US-09-233-510-3

Query Match 33.3%; Score 32; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 VDEQVDFPFG 14
|||:|:|
DB 2 VDEREPYTG 10

RESULT 5
US-08-486-839-8
Sequence 8, Application US/08486839
Patent No. 5928928
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: A human chitinase, its recombinant
production, its use for decomposing chitin, its use
in therapy or prophylaxis against infection diseases.
TITLE OF INVENTION: 16
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: United States of America
ZIP: 11758

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,839
FILING DATE: 07 - June - 1995
ATTORNEY/AGENT INFORMATION:
NAME: Baron, Ronald J.
REGISTRATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 294-26
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-08-486-839-8

Query Match 31.2%; Score 30; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 85;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DQGVDFPFG 11
|||:|:|
DB 2 DQVDFPFG 11

RESULT 6
US-09-151-011-8
Sequence 8, Application US/09151011
Patent No. 6057142
GENERAL INFORMATION:
APPLICANT:

TITLE OF INVENTION: A Human Chitinase, Its Recombinant
production, its use for decomposing chitin, its use in
therapy or prophylaxis against infection diseases.
TITLE OF INVENTION: 16
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron, LLP
STREET: 6900 Jericho Turnpike
CITY: Syosset
STATE: New York
COUNTRY: United States of America
ZIP: 11791

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,011
FILING DATE: 10 - September - 1998
ATTORNEY/AGENT INFORMATION:
NAME: Morris, Robert C.
REGISTRATION NUMBER: 42,910
REFERENCE/DOCKET NUMBER: 294-32 DIV
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-09-151-011-8

Query Match 31.2%; Score 30; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 85;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DQGVDFPFG 11
|||:|:|
DB 2 DQVDFPFG 11

RESULT 7
US-09-343-623-8
Sequence 8, Application US/09343623
Patent No. 6303118
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A human chitinase, its recombinant
production, its use for decomposing chitin, its use
in therapy or prophylaxis against infection diseases.
TITLE OF INVENTION: 16
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: United States of America
ZIP: 11758

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/343,623
FILING DATE:
PRIOR APPLICATION DATA:

US-09-151-011-8
Sequence 8, Application US/09151011
Patent No. 6057142
GENERAL INFORMATION:
APPLICANT:

APPLICATION NUMBER: US/08/486,839
FILING DATE: 07-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baron, Ronald J.
REGISTRATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 294-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
US-09-343-623-8

Query Match 31.2%; Score 30; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 85;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFP 11
|||:|:
Db 2 DGVIDWEPF 11

RESULT 8
US-09-977-827-8
Sequence 8, Application US/09977827
Patent No. 6896884
GENERAL INFORMATION:
APPLICANT: Aeris, Johannes Maria F.G.
TITLE OF INVENTION: A human chitinase, its recombinant production, its use for decont
TITLE OF INVENTION: chitin, its use in therapy or prophylaxis against infectious dis
FILE REFERENCE: Docket 294-32 DIVII/CON
CURRENT APPLICATION NUMBER: US/09/977,827
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 11
TYPE: PRT
ORGANISM: Autographa californica
US-09-977-827-8

Query Match 31.2%; Score 30; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 85;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFP 11
|||:|:
Db 2 DGVIDWEPF 11

RESULT 9
US-08-166-195A-23
Sequence 23, Application US/08166195A
Patent No. 5480799
GENERAL INFORMATION:
APPLICANT: O'Rand, Michael G.
APPLICANT: Widgren, Esther E.
APPLICANT: Richardson, Richard T.
APPLICANT: Lea, Isabel
TITLE OF INVENTION: Sperm Antigen Corresponding to a
TITLE OF INVENTION: Sperm Zona Binding Protein Autoantigenic Epitope
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Box 34009
CITY: Charlotte
STATE: No. 5480799th Carolina

COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/166,195A
FILING DATE: 10 DEC 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470/73
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-166-195A-23

Query Match 30.2%; Score 29; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1,1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQKVDQFP 10
|||:|:
Db 1 GAKVDRF 8

RESULT 10
US-08-436-772-23
Sequence 23, Application US/08436772
Patent No. 5814456
GENERAL INFORMATION:
APPLICANT: O'Rand, Michael G.
APPLICANT: Widgren, Esther E.
APPLICANT: Richardson, Richard T.
APPLICANT: Lea, Isabel
TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Box 34009
CITY: Charlotte
STATE: No. 5814456th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,772
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-73B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-436-772-23

Query Match 30.2% Score 29; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 GOKVDEOF 10
| | | | |
DB 1 GAKVDRF 8

RESULT 11
US-08-436-883B-23
Sequence 23, Application US/08436883B
Patent No. 5820861
GENERAL INFORMATION:
APPLICANT: O'Rand, Michael G.
APPLICANT: Widgren, Esther E.
APPLICANT: Richardson, Richard T.
APPLICANT: Lea, Isabel
TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: P. O. Box 34009
CITY: Charlotte
STATE: No. 5820861th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,883B
FILING DATE: 08-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-73C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-436-883B-23

Query Match 30.2% Score 29; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 GOKVDEOF 10
| | | | |
DB 1 GAKVDRF 8

RESULT 12
US-08-486-839-12
Sequence 12, Application US/08486839
Patent No. 5928928

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A human chitinase, its recombinant
TITLE OF INVENTION: production, its use for decomposing chitin, its use
TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: United States of America
ZIP: 11758

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,839
FILING DATE: 07-June-1995

ATTORNEY/AGENT INFORMATION:
NAME: Baron, Ronald J.
REGISTRATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 294-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
US-08-486-839-12

Query Match 30.2% Score 29; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 DGQKVDGOF 11
| | | | |
DB 2 DGLNLDWQTP 11

RESULT 13
US-09-151-011-12
Sequence 12, Application US/09151011
Patent No. 6057142
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A Human Chitinase, Its Recombinant
TITLE OF INVENTION: Production, Its Use For Decomposing Chitin, Its Use In
TITLE OF INVENTION: Therapy or Prophylaxis Against Infection Diseases.
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron, LLP
STREET: 6900 Jericho Turnpike
CITY: Syosset
STATE: New York
COUNTRY: United States of America
ZIP: 11791

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,011

FILING DATE: 10 - September - 1998
ATTORNEY/AGENT INFORMATION:
NAME: Morris, Robert C.
REGISTRATION NUMBER: 42,910
REFERENCE/DOCKET NUMBER: 294-32 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-151-011-12

Query Match 30.2%; Score 29; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGQKVDQFP 11
Db 2 DGLNLDWQYP 11

RESULT 14
US-09-343-623-12
Sequence 12, Application US/09343623
Patent No. 6303118
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A human chitinase, its recombinant
production, its use for decomposing chitin, its use
TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: United States of America
ZIP: 11758
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/343,623
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,839
FILING DATE: 07-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baron, Ronald J.
REGISTRATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 294-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-343-623-12

Query Match 30.2%; Score 29; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGQKVDQFP 11
Db 2 DGLNLDWQYP 11

RESULT 15
US-09-977-827-13
Sequence 13, Application US/09977827
Patent No. 6896884
GENERAL INFORMATION:
APPLICANT: Aerts, Johannes Maria F.G.
TITLE OF INVENTION: A human chitinase, its recombinant production, its use for decomposing
chitin, its use in therapy or prophylaxis against infectious diseases
FILE REFERENCE: Docket 294-32 DIVII/CON
CURRENT APPLICATION NUMBER: US/09/977,827
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 11
TYPE: PRT
ORGANISM: Mus musculus
US-09-977-827-13

Query Match 30.2%; Score 29; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGQKVDQFP 11
Db 2 DGLNLDWQYP 11

Search completed: December 12, 2005, 21:20:09
Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:20:19 ; Search time 95 Seconds
(without alignments)
79.168 Million cell updates/sec

Title: US-10-758-165A-11

Perfect score: 96

Sequence: 1 IDGQKVDQFPQHGVLVKQ 18

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 356231

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
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4: /cgn2_6/ptodata/1/pubppaa/US10a_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	5	US-10-758-165-11
2	78	81.2	15	4	US-10-052-788-5
3	36	37.5	14	3	US-09-880-748-2449
4	36	37.5	14	4	US-10-293-418-2449
5	35	36.5	18	5	US-10-758-165-10
6	34	35.4	15	4	US-10-141-627-11
7	34	35.4	17	4	US-10-356-257-255
8	34	35.4	18	5	US-10-758-165-9
9	32	33.3	10	4	US-10-079-709-3
10	32	33.3	14	3	US-09-880-748-2446
11	32	33.3	14	3	US-09-880-748-2703
12	32	33.3	14	4	US-10-293-418-2446
13	32	33.3	14	4	US-10-293-418-2703
14	32	33.3	14	5	US-10-865-748-842
15	31	32.3	14	3	US-09-880-748-2146
16	31	32.3	14	4	US-09-880-748-2151
17	31	32.3	14	4	US-10-293-418-2146
18	31	32.3	14	4	US-10-293-418-2151
19	31	32.3	15	4	US-10-059-261-108
20	31	32.3	15	4	US-10-059-261-216
21	31	32.3	15	5	US-10-627-649-108
22	31	32.3	15	5	US-10-627-649-216
23	31	32.3	18	5	US-10-758-165-15
24	30	31.2	10	4	US-10-353-929-166
25	30	31.2	11	3	US-09-977-827-8
26	30	31.2	17	3	US-09-864-761-46580
27	29.5	30.7	17	4	US-10-356-257-314

28	29	30.2	11	3	US-09-977-827-13	Sequence 13, Appl
29	29	30.2	14	5	US-10-476-362-26	Sequence 26, Appl
30	29	30.2	15	4	US-10-282-960-23	Sequence 23, Appl
31	29	30.2	17	5	US-10-996-316-125	Sequence 125, Appl
32	28	29.2	11	4	US-10-432-234A-13	Sequence 13, Appl
33	28	29.2	11	4	US-10-362-527-52	Sequence 52, Appl
34	28	29.2	11	6	US-11-005-794-107	Sequence 107, Appl
35	28	29.2	13	4	US-10-415-165-21	Sequence 21, Appl
36	28	29.2	14	3	US-09-880-748-2366	Sequence 2366, Ap
37	28	29.2	14	3	US-09-880-748-2452	Sequence 2452, Ap
38	28	29.2	14	3	US-09-880-748-2545	Sequence 2545, Ap
39	28	29.2	14	3	US-10-293-418-2366	Sequence 2366, Ap
40	28	29.2	14	4	US-10-293-418-2452	Sequence 2452, Ap
41	28	29.2	15	4	US-10-293-418-2545	Sequence 2545, Ap
42	28	29.2	15	3	US-09-836-861-10	Sequence 10, Appl
43	28	29.2	15	4	US-10-084-813-1231	Sequence 1231, Ap
44	28	29.2	17	4	US-10-283-349-41	Sequence 41, Appl
45	28	29.2	17	4	US-10-225-567A-1964	Sequence 1964, Ap

ALIGNMENTS

```
RESULT 1
US-10-758-165-11
; Sequence 11, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-11

Query Match      100.0%; Score 96; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 8,6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IDGQKVDQFPQHGVLVKQ 18
DB      1 IDGQKVDQFPQHGVLVKQ 18

RESULT 2
US-10-052-788-5
; Sequence 5, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
; APPLICANT: Gerstwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kalina, Warren V.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Eps10 Immunoglobulin Chain Derived Peptides for
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052,788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
```

OTHER INFORMATION: Description of Artificial Sequence:epitope peptide
OTHER INFORMATION: p5, middle portion of C2 of equine IGF epsilon
OTHER INFORMATION: heavy chain
US-10-052-788-5

Query Match 81.2%; Score 78; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6,7e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IDGQKVDQFPQHG 14
Db 2 IDGQKVDQFPQHG 15

RESULT 3
US-09-880-748-2449
Sequence 2449, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2449
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2449

Query Match 37.5%; Score 36; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 FPOHGL 15
Db 7 FPOHGL 12

RESULT 4
US-10-293-418-2449
Sequence 2449, Application US/10293418
Publication No. US2003022396A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2449
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-2449

Query Match 37.5%; Score 36; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 FPOHGL 15
Db 7 FPOHGL 12

RESULT 5
US-10-758-165-10
Sequence 10, Application US/10758165
Publication No. US20050196816A1
GENERAL INFORMATION:
APPLICANT: Hammerberg, Bruce
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
FILE REFERENCE: 5051-661
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: 60/440,472
PRIOR FILING DATE: 2003-01-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Version 3.2
SEQ ID NO 10
LENGTH: 18
TYPE: PRT
ORGANISM: Felis catus
US-10-758-165-10

Query Match 36.5%; Score 35; DB 5; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 1 IDGQKVDQFPQHGIVKQ 18
Db 1 VDGQKATNIFPYTAPGKQ 18

RESULT 6
US-10-141-627-11
Sequence 11, Application US/10141627
Publication No. US20020176863A1
GENERAL INFORMATION:
APPLICANT: Dale, James B.
TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
FILE REFERENCE: 481112.404C3
CURRENT APPLICATION NUMBER: US/10/141,627
CURRENT FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: NH2-terminal fragment of M protein for
constructing antigens, which elicit opsonic
OTHER INFORMATION: antibodies in an immunized animal
US-10-141-627-11

Query Match 35.4%; Score 34; DB 4; Length 15;

	Best Local Similarity	41.7%	Pred. No. 1,3e+02;	
Matches	5;	Conservative	4;	Mismatches 3; Indels 0; Gaps 0
QY	2 DGQRVDGEQFPOH	13	: : :	
Dd	1 DARSVNGEFPFH	12		

```

1 RESULT 7
2 US-10-356-257-255
3 : Sequence 255, Application US/103556257
4 : Publication No US20040087767A1
5 : GENERAL INFORMATION:
6 : APPLICANT: LAZARUS, ROBERT A.
7 : APPLICANT: MAUN, HENRY R.
8 : TITLE OF INVENTION: Fvlla Antagonists
9 : FILE REFERENCE: P1950R1
10 : CURRENT APPLICATION NUMBER: US/10/356,257
11 : PRIOR FILING DATE: 2003-01-30
12 : PRIOR APPLICATION NUMBER: US 60/355,420
13 : PRIOR FILING DATE: 2002-02-06
14 : NUMBER OF SEQ ID NOS: 355
15 : SEQ ID NO 255
16 : LENGTH: 17
17 : TYPE: prt
18 : ORGANISM: Artificial sequence
19 : FEATURE:
20 : OTHER INFORMATION: sequence is synthesized
21 US-10-356-257-255

```

Query Match	35.4%	Score 34;	DB 4;	Length 17;
Best Local Similarity	50.0%	Pred. NO.	1.5e+02;	
Matches	5;	Conservative	4;	Mismatches 1;
				Indels 0;
				Gaps 0

```

RESULT 8
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammeberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-10-758-165-9

```

Query Match	35.4%	Score 34;	DB 5;	Length 18;
Best Local Similarity	54.5%	Pred. NO. 1.6e+02;		
Matches	6;	Conservative	1;	Mismatches 4;
			Indels	0;
			Gaps	0

```

RESULT 9
US-10-079-709-3
; Sequence 3, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:

```

APPLICANT: Robert F.M. Van Gorcum
 APPLICANT: Willem Van Haringsveldt
 APPLICANT: Petrus A. Van Paridon
 APPLICANT: Annemarie E. Veenstra
 APPLICANT: Rudolf G.M. Juntin
 APPLICANT: Gerardus Seltan
 TITLE OF INVENTION: Cloning and Expression of Microbial
 TITLE OF INVENTION: phytase
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Morrison & Foerster
 STREET: 545 Middlefield Road, Suite 200
 CITY: Menlo Park
 STATE: California
 COUNTRY: USA
 ZIP: 94025-3471
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 SOFTWARE:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/079,709
 FILING DATE: 02-FEB-2002
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/233,510
 FILING DATE: 20-JAN-1999
 APPLICATION NUMBER: 07/688,578
 FILING DATE: 24-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/POCKET NUMBER: 24615-20026.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-327-7250
 TELEFAX: 415-327-2951
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHEICAL: NO
 FRAGMENT TYPE: N-terminal
 IS-10-079-709-3

Query Match	33.3%	Score 32;	DB 4;	Length 10;
Best Local Similarity	66.7%	Pred. No. 1.8e+02;		
Matches	6;	Conservative	1;	Mismatches 2;
			Indels	0;
			Gaps	0

RESULT 10
US-09-880-748--2446
Sequence 2446, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: P5523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16

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; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 2446
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2446
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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      10 PPOHG 14
        |||||
Db       7 PPOHG 11
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RESULT 11
US-09-880-748-2703
; Sequence 2703, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 2703
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2703
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Query Match          33.3%; Score 32; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      10 PPOHG 14
        |||||
Db       7 PPOHG 11
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RESULT 12
US-10-293-418-2446
; Sequence 2446, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
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; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2446
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2446
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Query Match          33.3%; Score 32; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      10 PPOHG 14
        |||||
Db       7 PPOHG 11
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RESULT 13
US-10-293-418-2703
; Sequence 2703, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2703
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2703
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Query Match          33.3%; Score 32; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      10 PPOHG 14
        |||||
Db       7 PPOHG 11
```

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RESULT 14
US-10-865-478-842
; Sequence 842, Application US/10865478
; Publication No. US20040235041A1
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Search completed: December 12, 2005, 21:29:24
Job time : 96 secs

GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A.
APPLICANT: Leach, Martin D.
TITLE OF INVENTION: csingle Nucleotide Polymorphisms for Known Genes
FILE REFERENCE: 15866-534-CIP1
CURRENT FILING DATE: 2004-06-10
PRIOR APPLICATION NUMBER: 60/109,024
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 09/443,199
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 09/442,129
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 09/442,849
PRIOR FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 880
SOFTWARE: Curagen Patent Formatter Version 0.9
SEQ ID NO 842
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (7)...(0)
OTHER INFORMATION: csnp translation
US-10-865-478-842

Query Match 33.3%; Score 32; DB 5; Length 14;
Best Local Similarity 54.5%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGGKVDGQFPQ 12
|||:|
DB 3 DGGVDPPNP 13

RESULT 15
US-09-880-748-2146
Sequence 2146; Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2146
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2146

Query Match 32.3%; Score 31; DB 3; Length 14;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 PPOHGL 15
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DB 7 PPHGL 12

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OM protein - protein search, using SW model

Run on: December 12, 2005, 21:17:33 / Search time 3 Seconds
(without alignments)
33.507 Million cell updates/sec

Title: US-10-758-165A-11
Perfect score: 96
Sequence: 1 IDGQKVDQEPQHGVLKQ 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 9754

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	37.5	14	7	US-11-054-515-2449 Sequence 2449, Ap
2	32	33.3	14	7	US-11-054-515-2446 Sequence 2446, Ap
3	32	33.3	14	7	US-11-054-515-2703 Sequence 2703, Ap
4	31	32.3	14	7	US-11-054-515-2146 Sequence 2146, Ap
5	31	32.3	14	7	US-11-054-515-2151 Sequence 2151, Ap
6	28	29.2	14	7	US-11-054-515-2366 Sequence 2366, Ap
7	28	29.2	14	7	US-11-054-515-2452 Sequence 2452, Ap
8	28	29.2	14	7	US-11-054-515-2545 Sequence 2545, Ap
9	28	29.2	18	6	US-10-518-341-5 Sequence 5, Appl
10	27	28.1	14	7	US-11-054-515-2406 Sequence 2406, Ap
11	26	27.1	14	7	US-11-054-515-2414 Sequence 2414, Ap
12	26	27.1	15	7	US-11-054-515-2429 Sequence 2429, Ap
13	26	27.1	14	7	US-11-106-932-134 Sequence 134, Appl
14	26	27.1	15	7	US-11-106-932-135 Sequence 135, Appl
15	26	27.1	18	6	US-10-503-575-77 Sequence 77, Appl
16	25	26.0	9	6	US-10-969-314-32 Sequence 32, Appl
17	25	26.0	14	6	US-10-503-575-25 Sequence 25, Appl
18	25	26.0	14	6	US-10-503-575-26 Sequence 26, Appl
19	25	26.0	14	6	US-10-503-575-27 Sequence 27, Appl
20	25	26.0	14	6	US-10-503-575-28 Sequence 28, Appl
21	25	26.0	14	6	US-10-503-575-29 Sequence 29, Appl
22	25	26.0	14	6	US-10-503-575-30 Sequence 30, Appl
23	25	26.0	14	6	US-10-503-575-31 Sequence 31, Appl
24	25	26.0	14	6	US-10-503-575-32 Sequence 32, Appl
25	25	26.0	14	7	US-11-054-515-2149 Sequence 2149, Ap

26	25	26.0	14	7	US-11-054-515-2152 Sequence 2152, Ap
27	25	26.0	14	7	US-11-054-515-2404 Sequence 2404, Ap
28	25	26.0	14	7	US-11-054-515-2427 Sequence 2427, Ap
29	25	26.0	14	7	US-11-054-515-2543 Sequence 2543, Ap
30	25	26.0	15	6	US-10-503-575-78 Sequence 78, Appl
31	25	26.0	15	7	US-11-106-932-65 Sequence 65, Appl
32	25	26.0	16	7	US-11-106-932-52 Sequence 52, Appl
33	24	25.0	9	7	US-11-097-864-41 Sequence 41, Appl
34	24	25.0	9	7	US-11-097-864-42 Sequence 42, Appl
35	24	25.0	10	7	US-11-097-864-77 Sequence 77, Appl
36	24	25.0	10	7	US-11-097-864-195 Sequence 195, Appl
37	24	25.0	10	7	US-11-097-912-77 Sequence 77, Appl
38	24	25.0	10	7	US-11-097-912-195 Sequence 195, Appl
39	24	25.0	14	6	US-10-503-575-45 Sequence 45, Appl
40	24	25.0	14	7	US-11-054-515-2393 Sequence 2393, Ap
41	24	25.0	14	7	US-11-054-515-2442 Sequence 2442, Ap
42	24	25.0	14	7	US-11-054-515-2570 Sequence 2570, Ap
43	24	25.0	14	7	US-11-054-515-2687 Sequence 2687, Ap
44	23	24.0	9	7	US-11-010-748A-334 Sequence 334, Appl
45	23	24.0	9	7	US-11-010-748A-346 Sequence 346, Appl

ALIGNMENTS

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RESULT 1
US-11-054-515-2449
; Sequence 2449, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFG3393
; CURRENT FILING DATE: 2005-02-10
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2449
; LENGTH: 14
; TYPE: PRP
; ORGANISM: Homo sapiens
US-11-054-515-2449

Query Match      37.5%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PFGHGL 15
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Db       7 PFGHGL 12

RESULT 2
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US-11-054-515-2446
; Sequence 2446, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
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; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2446
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2446

Query Match          33.3%; Score 32; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 FPOHG 14
Db      7 FPOHG 11

RESULT 3
US-11-054-515-2703
; Sequence 2703, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
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; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2146
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2146

Query Match          32.3%; Score 31; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 5.2;
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;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
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;; SEQ ID NO 2703
;; LENGTH: 14
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-2703

Query Match          33.3%; Score 32; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 FPOHG 14
Db      7 FPOHG 11

RESULT 4
US-11-054-515-2146
; Sequence 2146, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2146
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2146

Query Match          32.3%; Score 31; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 5.2;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      7 FPOHGL 12

RESULT 5
US-11-054-515-2151
; Sequence 2151, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
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; PRIOR FILING DATE: 2001-03-21
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; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
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; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2151
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Query Match          32.3% Score 31; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 5,2;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db       7 FPHHGL 12
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RESULT 6
US-11-054-515-2366
; Sequence 2366, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
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; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
```

```

; SEQ ID NO 2366
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2366
```

```

Query Match          29.2% Score 28; DB 7; Length 14;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      10 PPOHGLV 16
         |||||
Db       7 FPKHPLV 13
```

```

RESULT 7
US-11-054-515-2452
; Sequence 2452, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2452
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2452
```

```

Query Match          29.2% Score 28; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      10 PPOHGL 15
         |||||
Db       7 FPOHPL 12
```

```

RESULT 8
US-11-054-515-2545
; Sequence 2545, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
```

```
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2545
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2545
```

```
Query Match          29.2%; Score 28; DB 7; Length 14;
Best Local Similarity 71.4%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      10  FPOHGLV 16
         ||: |||
Db       7  FPRHPLV 13
```

```
RESULT 9
US-10-518-341-5
; Sequence 5, Application US/10518341
; Publication No. US20050249744A1
; GENERAL INFORMATION:
; APPLICANT: VAN ELS, Cecile Antoinette Carola Maria
; APPLICANT: VAN BLUEK, Gerarda Maria
; APPLICANT: BOOG, Marie-Claire Josefa Pia
; TITLE OF INVENTION: MHC class II haplotype specific immunodominancy of
; TITLE OF INVENTION: peptides derived from RSV fusion (F) or attachment
; FILE REFERENCE: 28902.0014
; CURRENT APPLICATION NUMBER: US/10/518,341
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/NL03/00454
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02077461.8
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-10-518-341-5
```

```
Query Match          29.2%; Score 28; DB 6; Length 18;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Oy      3  GQKVDQFPQ 12
         ||: |||
Db       1  GQNTBFFYQ 10
```

```
RESULT 10
US-11-054-515-2406
```

```
; Sequence 2406, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2406
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2406
```

```
Query Match          28.1%; Score 27; DB 7; Length 14;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      10  FPOHG 14
         ||: |||
Db       7  FPHHG 11
```

```
RESULT 11
US-11-054-515-2414
; Sequence 2414, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
```

;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO: 2414
;; LENGTH: 14
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-2414

Query Match 27.1%; Score 26; DB 7; Length 14;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 10 FPOHGLV 16
|||
Db 7 FPAHPLV 13

RESULT 12
US-11-054-515-2429
;; Sequence 2429, Application US/11054515
;; Publication No. US2005025532A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PFS23P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/580,347
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: 10/293,418
;; PRIOR FILING DATE: 2002-11-14
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO: 2429
;; LENGTH: 14
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-2429

Query Match 27.1%; Score 26; DB 7; Length 14;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 10 FPOHGLV 16
|||
Db 7 FPHSL 13

RESULT 13
US-11-106-932-134
;; Sequence 134, Application US/11106932
;; Publication No. US20050260697A1
;; GENERAL INFORMATION:
;; APPLICANT: WANG, KA-WANG KEVIN
;; APPLICANT: HAYES, RONALD

;; APPLICANT: LIU, MING CHEN
;; APPLICANT: OLI, MONIKA
;; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
;; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
;; FILE REFERENCE: 5853-549-1
;; CURRENT APPLICATION NUMBER: US/11/106,932
;; CURRENT FILING DATE: 2005-04-15
;; NUMBER OF SEQ ID NOS: 147
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO: 134
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-106-932-134

Query Match 27.1%; Score 26; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGOXVD 7
|||
Db 7 DGERVD 12

RESULT 14
US-11-106-932-135
;; Sequence 135, Application US/11106932
;; Publication No. US20050260697A1
;; GENERAL INFORMATION:
;; APPLICANT: WANG, KA-WANG KEVIN
;; APPLICANT: HAYES, RONALD
;; APPLICANT: LIU, MING CHEN
;; APPLICANT: OLI, MONIKA
;; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
;; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
;; FILE REFERENCE: 5853-549-1
;; CURRENT APPLICATION NUMBER: US/11/106,932
;; CURRENT FILING DATE: 2005-04-15
;; NUMBER OF SEQ ID NOS: 147
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO: 135
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-106-932-135

Query Match 27.1%; Score 26; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGOXVD 7
|||
Db 10 DGERVD 15

RESULT 15
US-10-503-575-77
;; Sequence 77, Application US/10503575
;; Publication No. US2005024823A1
;; GENERAL INFORMATION:
;; APPLICANT: Drifhout, Jan Wouter
;; APPLICANT: van Veele, Petrus Antonius
;; APPLICANT: Koning, Frits
;; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
;; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
;; FILE REFERENCE: 2799/72843-PCT-US
;; CURRENT APPLICATION NUMBER: US/10/503,575
;; CURRENT FILING DATE: 2004-08-04
;; PRIOR APPLICATION NUMBER: PCT/NL03/00077
;; PRIOR FILING DATE: 2003-02-04
;; PRIOR APPLICATION NUMBER: EP 02075456.0
;; PRIOR FILING DATE: 2002-02-04
;; NUMBER OF SEQ ID NOS: 340

; SOFTWARE: Patentin version 3.1
; SEQ ID NO 77
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-77

Query Match 27.1%; Score 26; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PPOH 13
|||
Db 1 PPOH 4

Search completed: December 12, 2005, 21:20:43
Job time : 4 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 21:18:48 / Search time 10.6667 Seconds
(without alignments)
162.366 Million cell updates/sec

Title: US-10-758-165A-11
Perfect score: 96
Sequence: 1 IDGQKVDQEPQHGIVKQ 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	26.0	14	2	A56632 - neosulfakinin-II -
2	24	25.0	15	2	PT0090 alpha-glucosidase
3	24	25.0	18	2	A61577 24k serine protein
4	23	24.0	11	1	GMR0L leucosulfakinin -
5	23	24.0	11	2	A60656 perisulfakinin - A
6	23	24.0	16	2	D49655 T-cell-receptor be
7	23	24.0	16	2	C90981 his operon leader
8	23	24.0	16	2	A85827 his operon leader
9	23	24.0	18	2	S70340 napin large chain
10	22	22.9	9	2	B39841 dextranucrase (EC
11	22	22.9	11	2	A33917 dihydroorotase (EC
12	22	22.9	18	2	S29379 sorbitol dehydroge
13	21	21.9	7	2	A34818 vicillin 72k chain
14	21	21.9	14	2	EC7075 guanilate cyclase
15	21	21.9	15	2	A30330 neuropeptide pep -
16	21	21.9	17	2	A49226 major outer membra
17	21	21.9	17	2	A52274 glucathione S-tran
18	21	21.9	17	2	G85956 hypothetical prote
19	21	21.9	18	2	I55453 zinc finger homeod
20	21	21.9	18	2	H75063 hypothetical prote
21	20	20.8	10	2	S33844 alpha-2-macroglobu
22	20	20.8	10	2	I48778 small nuclear ribo
23	20	20.8	12	2	G60589 sperm-activating p
24	20	20.8	10	2	S68402 NAD(+) -glycohydrol
25	20	20.8	12	2	S68271 major urinary prot
26	20	20.8	12	2	PN0170 alcohol dehydrogen
27	20	20.8	13	2	S23640 Ig kappa chain J s
28	20	20.8	13	2	S47357 T-cell antigen rec
29	20	20.8	13	2	S47358 T-cell antigen rec

30	20	20.8	14	2	PC4382 dehydrin 4.5K poly
31	20	20.8	14	2	PQ0152 18k iron-sulfur pr
32	20	20.8	15	2	S51735 T-cell receptor be
33	20	20.8	15	2	B49655 T-cell-receptor be
34	20	20.8	15	2	PH0789 T-cell receptor al
35	20	20.8	15	2	S71306 heat shock protein
36	20	20.8	16	2	E49255 T-cell receptor be
37	20	20.8	16	2	F49039 T-cell receptor be
38	20	20.8	18	2	D49570 plasma membrane ca
39	19.5	20.3	17	2	B36727 cytochrome c554 -
40	19	19.8	11	2	A40693 transgalin - sheep
41	19	19.8	11	2	PC2173 triacylglycerol 11
42	19	19.8	11	2	QJ2307 hypothetical 1.5K
43	19	19.8	14	2	C35141 T-cell receptor de
44	19	19.8	14	2	S27140 hypothetical prote
45	19	19.8	15	2	S14749 3-dehydroquinase -

ALIGNMENTS

```

RESULT 1
A56632
neosulfakinin-II - flesh fly (Sarcophaga bullata)
N:Alternate names: Neb-SK-II
N:Contains: neosulfakinin-I (Neb-SK-I)
C:Species: Sarcophaga bullata
C>Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: A56632
R:Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; De Loof, A.
Comp. Biochem. Physiol. C 103, 135-142, 1992
A>Title: Isolation and primary structure of two sulfakinin-like peptides from the fleshf
F:1-14/Product: neosulfakinin-II #status experimental <NSK2>
F:6-14/Product: neosulfakinin-I #status experimental <NSK1>
F:9/Binding site: sulfate (Tyr) (covalent) #status predicted
F:14/Modified site: amidated carboxyl end (Phe) #status experimental
A:Accession: A56632
A:Molecule type: Protein
A:Residues: 1-14 <PON>
A:Cross-references: UNIPROT:P41493; UNIPARC:UPI000013054D
A:Experimental source: heads
A>Note: sequence extracted from NCBI backbone (NCBIP:120391)
C:Keywords: amidated carboxyl end; neuropeptide; sulfoprotein
F:1-14/Product: neosulfakinin-II #status experimental <NSK2>
F:6-14/Product: neosulfakinin-I #status experimental <NSK1>
F:9/Binding site: sulfate (Tyr) (covalent) #status predicted
F:14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match      26.0%; Score 25; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 6;le+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      7 DEQPPHG 14
Db      3 EQFPDYG 10

RESULT 2
PT0090
alpha-glucosidase (EC 3.2.1.20) - honeybee (fragment)
C:Species: Apis mellifera (honeybee)
C>Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C:Accession: PT0090
R:Kimura, A.; Takata, M.; Fukushi, Y.; Mori, H.; Matsui, H.; Chiba, S.
Biosci. Biotechnol. Biochem. 61, 1091-1098, 1997
A>Title: A catalytic amino acid and primary structure of active site in Aspergillus nige
A:Reference number: PT0090; MUID:97399878; PMID:9255970
A:Molecule type: protein
A:Residues: 1-15 <KIM>
A:Cross-references: UNIPROT:Q7M3M5; UNIPARC:UPI000017BF08
C:Keywords: glycosidase; hydrolase

Query Match      25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 9;9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 IDGQKVD 7
||| :
Db 2 IDGFRID 8

RESULT 3

A61577
24k serine proteinase (EC 3.4.21.-) - Streptomyces fradiae (fragment)
C:Species: Streptomyces fradiae
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C:Accession: A61577
R:Sinha, U.; Molz, S.A.; Lad, P.J.
Inc. J. Biochem. 23, 979-984, 1991
A:Title: Two new extracellular serine proteases from Streptomyces fradiae.
A:Reference number: A61577; PMID:92155439; PMID:1768659
A:Accession: A61577
A:Molecule type: protein
A:Residues: 1-18 <SIN>
C:Cross-references: UNIPROT:Q7M198; UNIPARC:UPI000017AE13
C:Keywords: extracellular protein; hydrolase; serine proteinase

Query Match 25.0%; Score 24; DB 2; Length 18;
Best Local Similarity 27.3%; Pred. No. 1.2e+03;
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 IDGQKVDQFP 11
: : :
Db 2 VGGTRAAQEF 12

RESULT 4

GMROL
leucosulfakinin - Madeira cockroach

N:Alternate names: LSK
C:Species: Leucophaea madeira (Madeira cockroach)
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C:Accession: A01622
R:Nachman, R.; Holman, G.M.; Haddon, W.F.; Ling, N.
Science 234, 71-73, 1986
A:Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and ch
A:Reference number: A01622; PMID:86315858; PMID:3749893
A:Accession: A01622
A:Molecule type: protein
A:Residues: 1-11 <NAC>
A:Cross-references: UNIPROT:P04428; UNIPARC:UPI000012B960
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; hormone; sulfoprotein
F:6/Binding site: sulfate (Tyr) (covalent) #status experimental
F:11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 24.0%; Score 23; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 EQPQHG 14
||| :
Db 1 EQFEDYG 7

RESULT 5

A60656
perisulfakinin - American cockroach
C:Species: Periplaneta americana (American cockroach)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C:Accession: A60656
R:Venetia, J.A.
Neuropeptides 14, 145-149, 1989
A:Title: Isolation and structure of two gastrin/CK-like neuropeptides from the American
A:Reference number: A60656; PMID:90137190; PMID:2615921
A:Accession: A60656
A:Molecule type: protein
A:Residues: 1-11 <VEE>

A:Cross-references: UNIPROT:P36885; UNIPARC:UPI000012B962
C:Comment: This neuropeptide stimulates hindgut contractions.
C:Keywords: amidated carboxyl end; neuropeptide; sulfoprotein
F:6/Binding site: sulfate (Tyr) (covalent) #status experimental
F:11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 24.0%; Score 23; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 EQPQHG 14
||| :
Db 1 EQFDDYG 7

RESULT 6

D49655
T-cell-receptor beta chain variable region, TCR V beta (clone 2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: D49655
R:Grom, A.A.; Thompson, S.D.; Luvyink, L.; Passo, M.; Choi, E.; Glaes, D.N.
Proc. Natl. Acad. Sci. U.S.A. 90, 11104-11108, 1993
A:Title: Dominant T-cell-receptor beta chain variable region V beta 14+ clones in juveni
A:Reference number: A49655; PMID:9406553; PMID:8248215
A:Accession: D49655
A:Status: Preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-16 <GRO>
A:Cross-references: UNIPARC:UPI000017C3CA
A:Experimental source: peripheral blood lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIP:140448)
C:Keywords: T-cell receptor

Query Match 24.0%; Score 23; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 DQGRVDEQF 10
||| :
Db 7 DRAPVNEQF 15

RESULT 7

C90981
his operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain RMD (C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: C90981
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A:Reference number: A99629; PMID:21156231; PMID:11258796
A:Accession: C90981
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <HAY>
A:Cross-references: UNIPROT:Q8X8T5; UNIPARC:UPI000000D08D2; GB:BA000007; PIDN:BA836242.1;
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECa2819

Query Match 24.0%; Score 23; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 QPQGH 13
||| :
Db 5 QPQGH 9

RESULT 8

A05827
his operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: A05827
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimmlanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A05460; MUID:21074935; PMID:11206551
A:Accession: A05827
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <STO>
A:Cross-references: UNIPROT:Q086T5; UNIPARC:UPI00000D08D2; GB:AE005174; NID:G12516199; F
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: h18L

Query Match 24.0%; Score 23; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 9 QPPOH 13
|||
Db 5 QPKOH 9

RESULT 9
S70340
napin large chain L1A - Swedish turnip (fragments)
C:Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 31-Dec-2004
C:Accession: S70340
R:Neumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.
Biochim. Biophys. Acta 1295, 34-43, 1996
A:Title: Purification and sequencing of multiple forms of Brassica napus seed napin larg
A:Reference number: S70340; MUID:96283791; PMID:8679671
A:Accession: S70340
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12,13-18 <NEU>
A:Cross-references: UNIPROT:Q39344; UNIPROT:Q9S9F0; UNIPARC:UPI000017B02E; UNIPARC:UPI00
C:Superfamily: Alpha amylase inhibitor

Query Match 24.0%; Score 23; DB 2; Length 18;
Best Local Similarity 36.4%; Pred. No. 1.8e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 4 QKVDQFPOHG 14
||:|:|
Db 1 QOIQQGQDQG 11

RESULT 10
B39841
dextranucrase (EC 2.4.1.5) - Streptococcus sobrinus (fragment)
C:Species: Streptococcus sobrinus
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C:Accession: B39841
R:Mooser, G.; Hefta, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.
J. Biol. Chem. 266, 8916-8922, 1991
A:Title: Isolation and sequence of an active-site peptide containing a catalytic aspart
A:Reference number: A39841; MUID:91224988; PMID:1827439
A:Accession: B39841
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <MOO>
A:Cross-references: UNIPROT:Q7M0L7; UNIPARC:UPI000017AC69
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 22.9%; Score 22; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 DGOQVD 7
||:|
Db 1 DGVQVD 6

RESULT 11
A33917
dihydrocrotase (EC 3.5.2.3) - Chinese hamster (fragment)
C:Species: Cricetus griseus (Chinese hamster)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 07-Nov-1997
C:Accession: A33917
R:Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.T.;
Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989
A:Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain an
A:Reference number: A33917; MUID:89282776; PMID:2543974
A:Accession: A33917
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-11 <SIM>
A:Cross-references: UNIPARC:UPI0000176037; GB:M23652
C:Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Ba
arabamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phos
C:Keywords: hydrolase

Query Match 22.9%; Score 22; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 DGOQV 6
:|:|
Db 2 EQQV 6

RESULT 12
S29379
sorbitol dehydrogenase - sheep
C:Species: Ovis orientalis aries
C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C:Accession: S29379
R:Reiersen, H.; Sletten, K.; McKinley-McKee, J.S.
Eur. J. Biochem. 211, 861-869, 1993
A:Title: Affinity labelling of sorbitol dehydrogenase from sheep liver with alpha-bromo-
A:Reference number: S29379; MUID:93170323; PMID:8436142
A:Accession: S29379
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <REI>
A:Cross-references: UNIPROT:Q9TR15; UNIPARC:UPI0000087DC1
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 22.9%; Score 22; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 7 DEQFPOHG 14
||:|:|
Db 10 DVHWQHG 17

RESULT 13
A34818
vicilin 72k chain - pigeon pea (fragment)
C:Species: Cajanus cajan (pigeon pea)
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C:Accession: A34818
R:Maival, Y.R.; Maival, M.R.; Rantekar, P.K.
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
A:Title: Unusual denaturation properties of vicilin from Cajanus cajan.
A:Reference number: A34818; MUID:90165956; PMID:2306256
A:Accession: A34818
A:Status: preliminary

A;Molecule type: protein
 A;Residues: 1-7 <MAW>
 A;Cross-references: UNIPARC:UPI000017B040

Query Match 21.9%; Score 21; DB 2; Length 7;
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 GQKVDQ 9
 | : || :
 Db 1 GARVDQ 7

RESULT 14

PC7075

guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C;Accession: PC7075

R;Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kano, M.; Matsui, T.; Watanabe, Y.;

Electrophoresis 21, 1853-1871, 2000

A;Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of b

A;Reference number: PC7072

A;Accession: PC7075

A;Molecule type: protein

A;Residues: 1-14 <TSU>

A;Cross-references: UNIPROT:Q7M058; UNIPARC:UPI000017C675

A;Experimental source: strain C57BL/6Cr Slc, male; brain, striatum

C;Keywords: brain; phosphorus-oxygen lyase

Query Match 21.9%; Score 21; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 3e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 KVDEQPO 12
 || : ||
 Db 3 KVGDAPQ 10

RESULT 15

A30330

neuropeptide pep - 'California sea hare

C;Species: Aplysia californica (California sea hare)

C;Date: 02-Feb-1990 #sequence_revision 02-Feb-1990 #text_change 09-Jul-2004

C;Accession: A30330

R;Lloyd, P.E.; Connolly, C.M.

J. Neurosci. 9, 312-317, 1989

A;Title: Sequence of pedal peptide: a novel neuropeptide from the central nervous system

A;Reference number: A30330; MUID:8910403; PMID:2913209

A;Accession: A30330

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <LLO>

A;Cross-references: UNIPROT:Q7M3P8; UNIPARC:UPI000017BD9A

C;Keywords: neuropeptide

Query Match 21.9%; Score 21; DB 2; Length 15;
 Best Local Similarity 30.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 6 VDEQPOHGL 15
 : | : || :
 Db 2 LDSVYGTTHGM 11

Search completed: December 12, 2005, 21:24:33
 Job time : 11.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:17:48 ; Search time 61.6667 Seconds
(without alignments)
205.938 Million cell updates/sec

Title: US-10-758-165a-11
Perfect score: 96
Sequence: 1 IDGQKVDQFPQHGLVKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 11298

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	31.2	16	Q7RPP5_PLAYO	Q7RPP5 Plasmodium
2	29	30.2	13	Q9UPB7_HUMAN	Q9UPB7 homo sapien
3	28	29.2	14	Q9J1U5_MOUSE	Q9J1U5 mus musculi
4	28	29.2	18	Q8QFT3_CHICK	Q8QFT3 gallus gall
5	25	26.0	14	NSR2_SARBU	P81493 sarcophaga
6	25	26.0	15	COX5A_SCYCA	P83012 scyllorhinu
7	25	26.0	18	O12692_PLAVG	O12692 simian-huma
8	24	25.0	15	OSCLX6_SCHJA	OSCLX6 achistosoma
9	24	25.0	15	Q7M3M5_APIME	Q7M3M5 apis mellif
10	24	25.0	15	Q9R563_ECOLI	Q9R563 escherichia
11	24	25.0	18	Q4YL79_PLABE	Q4YL79 plasmodium
12	24	25.0	18	Q5FBR5_SUNMU	Q5FBR5 suncus mur
13	24	25.0	18	Q7M198_STRFR	Q7M198 streptomyce
14	23	24.0	11	LSK1_LEUMA	P04428 leucophaea
15	23	24.0	11	LSKP_PBRAM	P36885 periplaneta
16	23	24.0	14	P78359_HUMAN	P78359 homo sepien
17	23	24.0	15	CX1B_CONBE	P58624 conus betul
18	23	24.0	16	LPH1_ECO57	Q8X8T5 escherichia
19	23	24.0	18	O13167_XIRGL	O13167 xiphias gla
20	22	23.9	9	Q7M017_9STRE	Q7M017 streptococ
21	22	23.9	10	Q5D4Q4_9RHO	Q5D4Q4 dechloromon
22	22	23.9	11	Q48933_MYCBO	Q48933 mycobacteri
23	22	23.9	11	Q79C20_MYCBO	Q79C20 mycobacteri
24	22	23.9	11	Q79C22_MYCTU	Q79C22 mycobacteri
25	22	23.9	13	Q39380_BRAOL	Q39380 brasilia ol
26	22	23.9	15	ODP3_SQITU	P81420 solanum tub
27	22	23.9	16	Q9TRH0_BOVIN	Q9TRH0 bos taurus
28	22	23.9	18	RL24_PROUV	P20032 proteus vul
29	22	23.9	18	Q580F2_9TRYR	Q580F2 trypanosoma
30	22	23.9	18	Q4XFY5_PLACH	Q4XFY5 plasmodium
31	22	23.9	18	Q9TRIS_SHEEP	Q9TRIS ovis aries

32	22	22.9	18	Q8B133_IATX6	Q8B133 influenza a
33	21	21.9	14	GIGS_SPIOL	P55235 spinacia ol
34	21	21.9	14	Q9UNM9_HUMAN	Q9UNM9 homo sapien
35	21	21.9	14	Q7M058_MOUSE	Q7M058 mus musculi
36	21	21.9	14	Q65CH4_9GEMI	Q65CH4 tomato leaf
37	21	21.9	15	Q7M3P8_APLCA	Q7M3P8 aplysia cal
38	21	21.9	15	Q6LC05_PSEAE	Q6LC05 pseudomonas
39	21	21.9	16	Q9UC18_HUMAN	Q9UC18 homo sapien
40	21	21.9	16	Q94F61_TMBAT	Q94F61 triticum ae
41	21	21.9	16	Q44543_ANAVA	Q44543 anabaena va
42	21	21.9	16	Q9R5E9_HABSO	Q9R5E9 haemophilus
43	21	21.9	17	Q9S8U7_SQITU	Q9S8U7 solanum tub
44	21	21.9	17	Q07270_MYCTU	Q07270 mycobacteri
45	21	21.9	17	Q8X4A4_ECO57	Q8X4A4 escherichia

ALIGNMENTS

RESULT 1					
ID	Q7RPP5_PLAYO	PRELIMINARY;	PRT;	16 AA.	
AC	Q7RPP5;				
DT	01-MAR-2004 (TREMBLrel. 26, Created)				
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)				
DE	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Hypothetical protein.				
GN	Name=PY01411;				
OS	Plasmodium yoelii yoelii.				
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.				
OX	NCBI_TaxID=73239;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=17XNL;				
RX	MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;				
RA	Carlton J.M., Angiuoli S.V., Suh B.B., Kooley T.W., Pextea M.,				
RA	Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Xoo H.L.,				
RA	Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,				
RA	Shallow S.J., van Aken S.E., Riedmuller T.V.,				
RA	Cho J.K., Quackenbush J., Sedegah M., Shoahli A., Cummings L.M.,				
RA	Florens L., Yates J.R., Ili, Raine J.D., Sinden R.E., Harris M.A.,				
RA	Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,				
RA	van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,				
RA	Salberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,				
RA	Carracci D.J.,				
RT	"Genome sequence and comparative analysis of the model rodent malaria				
RT	parasite Plasmodium yoelii yoelii."				
RL	Nature 419:512-519(2002).				
CC	-!- CAUTION: The sequence shown here is derived from an				
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is				
CC	preliminary data.				
DR	EMBL; AB01000372; EAA20742.1; -; Genomic DNA.				
KW	Hypothetical protein.				
SQ	SEQUENCE 16 AA; 1778 MW; 22142D73EC2BE109 CRC64;				
Query Match					
	Best Local Similarity	31.2%;	Score 30;	DB 2;	length 16;
	Matches	5;	Conservative	2;	Mismatches 1;
					Indels 0;
					Gaps 0;
OY	1 IDGQKVD 8				
	: : :				
DB	4 INGSKIDE 11				
RESULT 2					
ID	Q9UPB7_HUMAN	PRELIMINARY;	PRT;	13 AA.	
AC	Q9UPB7;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	Inosine monophosphatase 2 (Fragment).				
GN	Name=IMP2;				

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97463449; PubMed=9322233; DOI=10.1038/sj.mp.4000325;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA DeGera-Wadleigh S.D.;
RT "A novel human myo-inositol monophosphatase gene, IMP-10p, maps to a
RT susceptibility region for bipolar disorder.";
RL Mol. Psychiatry 2:393-397(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20284187;
RA Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., DeGera-Wadleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
RT 2.";
RL Mol. Psychiatry 5:165-171(2000).
DR EMBL; AF025882; AAD22136.1; -; Genomic DNA.
FT NON_TER 1 1
FT SEQUENCE 13 AA; 1589 MW; F3415D841F48D401 CRC64;
SQ
Query Match 30.2%; Score 29; DB 2; Length 13;
Best Local Similarity 36.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 8 DEOPHGLVKQ 18
Db 1 ERFPSHRFIAE 11

RESULT 3
Q9JUT5_MOUSE PRELIMINARY; PRT; 14 AA.
ID Q9JUT5_MOUSE PRELIMINARY;
AC Q9JUT5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 15, Last annotation update)
DE B-Raf protein (Fragment).
GN Name=B-raf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Barnier J.V., Papin C., Eychene A., Lecocq O.;
RT "The mouse B-raf gene encodes multiple protein isoforms with tissue-
RT specific expression.";
RL J. Biochem. 270:23381-23389(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Barnier J.V.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ276308; CAB81556.1; -; mRNA.
FT NON_TER 1 1
FT NON_TER 14 14
FT SEQUENCE 14 AA; 1748 MW; D1E0505C44927F02 CRC64;
SQ
Query Match 29.2%; Score 28; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 7 DEOPHGLVKQ 18
Db 1 DEKPEVELDQ 12

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RESULT 4
Q8QFT3_CHICK PRELIMINARY; PRT; 18 AA.
ID Q8QFT3_CHICK PRELIMINARY;
AC Q8QFT3;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sterol regulatory element binding protein 1 (Fragment).
GN Name=SRBP-1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Asaef S., Pitel F., Morrison M., Alizadeh M., Gondret F., Diot C.,
RA Leclercq B., Vignal A., Douaire M., Lagarrigue S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ441122; CAD29619.1; -; Genomic DNA.
FT NON_TER 1 1
FT NON_TER 18 18
FT SEQUENCE 18 AA; 1947 MW; 3206A67750BFD7EA CRC64;
SQ
Query Match 29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 DEOPHGLVKQ 18
Db 1 DSPLCNKGKVKQ 12

RESULT 5
NSK2_SARBU STANDARD; PRT; 14 AA.
ID NSK2_SARBU STANDARD;
AC P41493;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Neosulfakinin-2 (Neosulfakinin-II) (Neb-SK-II).
OS Sarcophaga bullata (Grey Flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga; Neobellieria.
OX NCBI_TaxID=7385;
RN [1]
RP PROTEIN SEQUENCE.
RA TISSUE=Head;
RX MEDLINE=93083101; PubMed=1360367;
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from
RT the fleshfly, Neobellieria bullata.";
RL Comp. Biochem. Physiol. 103C:135-142(1992).
CC -1- FUNCTION: Myotonic peptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC PIR: A56632; A56632.
CC InterPro: IPR001651; Gastrin.
CC PROSITE: PS00259; GASTRIN; 1.
CC Amidaation: Direct protein sequencing; Neuropeptide; Sulfation.
FT MOD_RES 9 9 Sulfotyrosine (Potential).
FT MOD_RES 14 14 Phenylalanine amide (Potential).
FT SEQUENCE 14 AA; 1796 MW; 8B4B06D5B61C62AA CRC64;
SQ

```

Query Match 26.0%; Score 25; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 6.5e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 DEQFQHG 14
 :|||:
 Db 3 EQQFDDYG 10

RESULT 6

COX5A_SCYCA STANDARD; PRT; 15 AA.
 ID COX5A_SCYCA

AC P83012;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Cytochrome c oxidase polypeptide Va, mitochondrial (EC 1.9.3.1) (Fragment).
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 NCBI_TaxId=7830;
 RX MEDLINE=21534268; PubMed=11676495; DOI=10.1006/dbrc.2001.5826;
 RA Schumanns Stekhoven F.M.A.H., Fluk G., Wendelaar Bonga S.E.;
 RT "N-terminal sequences of small ion channels in rectal glands of shark: a biochemical hallmark for classification and phylogeny?";
 RL Biochem. Biophys. Res. Commun. 288:670-675(2001).
 CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.

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 CC GO: GO:0005739; C:mitochondrion; IDA.
 DR InterPro; IPR003204; Cyt_c_ox5a.
 DR Pfam; PF02284; COX5A; 1.
 KW Metal-binding; Mitochondrion; Oxidoreductase.
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1720 MM; 937518D7590B35C5 CRC64;

Query Match 26.0%; Score 25; DB 1; Length 15;
 Best Local Similarity 57.1%; Pred. No. 7e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 QKVDEQF 10
 :|||:
 Db 5 QETDEEF 11

RESULT 7

O12692_9PLVG PRELIMINARY; PRT; 18 AA.
 ID O12692_9PLVG

AC O12692;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Gag polypeptide (Fragment).
 OS Name=gag;
 OS Simian-human immunodeficiency virus.
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Lentivirus; Primate lentivirus group.
 NCBI_TaxId=7460;

OK NCBI_TaxId=57667;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SHIVku1;
 RX MEDLINE=97312452; PubMed=9168893; DOI=10.1006/viro.1997.8534;
 RA Stephens E.B., Mukherjee S., Sahn M., Zhuge W., Raghavan R.,
 RA Singh D.K., Leung K.K., Atkinson R.B., Li Z., Joag S.V., Liu Z.O.,
 RA Narayan O.;
 RT "A cell-free stock of simian-human immunodeficiency virus that causes AIDS in pig-tailed macaques has a limited number of amino acid substitutions in both SIVmac and HIV-1 regions of the genome and has offered cytopathism.";
 RT Virology 231:313-321(1997).
 DR EMBL; U89249; AAC57878.1; -; Genomic DNA.
 DR GO: GO:0019013; C:viral nucleocapsid; IEA.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000071; Imm_lentv_matrix.
 DR Pfam; PF00540; Gag_p17; 1.
 KW AIDS; Core protein; Polyprotein.
 FT NON TER 18 18
 SQ SEQUENCE 18 AA; 1961 MM; E0647725D22E262EB CRC64;

Query Match 26.0%; Score 25; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 8.5e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDGQKVE 8
 :|||:
 Db 8 LSGKQADE 15

RESULT 8

O5C1X6_SCHJA PRELIMINARY; PRT; 15 AA.
 ID O5C1X6_SCHJA

AC O5C1X6;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeididae;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 NCBI_TaxId=6182;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Han Z.;
 RL Submitted (MAR-2005) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY810460; AAX26349.1; -; mRNA.
 KW Hypothetical protein.
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1910 MM; F849301B576FB1D8 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1e+04;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 QFPGGLVQK 18
 :|||:
 Db 6 QFHKHSIVQK 15

RESULT 9

O7M3M5_APIME PRELIMINARY; PRT; 15 AA.
 ID O7M3M5_APIME

AC O7M3M5;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Alpha-glucosidase (EC 3.2.1.20) (Fragment).
 OS Apis mellifera (Honeybee).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apoecrita; Aculeata; Apoidea;
 OC Apidae; Apis.
 NCBI_TaxId=7460;

```

RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=97399878; PubMed=9255970;
RA Kimura A., Takata M., Fukushi Y., Mori H., Matsui H., Chiba S.;
RT "A catalytic amino acid and primary structure of active site in
RL Aspergillus niger alpha-glucosidase.";
DR Biosci. Biotechnol. Biochem. 61:1091-1098(1997).
PT PIR; PT0090; PT0090.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1686 MW; 85730BA8387CB741 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 IDGOKVD 7
DB 2 IDGFRID 8

RESULT 10
09R563_ECOLI PRELIMINARY; PRT; 15 AA.
ID Q9R563;
AC Q9R563;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAY-2004 (TREMBlrel. 26, Last annotation update)
DE 40 kDa porin homolog (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93328296; PubMed=8392972;
RA D'Arcy M., Soti R., Cockrell F.I.II., De Azavedo J., Louie M.,
RA Brunton J., Sherman P.;
RT "Multiple determinants of verotoxin-producing Escherichia coli O157:H7
RT attachment-effacement.";
RL Infect. Immun. 61:3382-3391(1993).
SQ SEQUENCE 15 AA; 1699 MW; 2767AC9298F8754D CRC64;

Query Match 25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGOKVD 7
DB 7 DGNKLD 12

RESULT 11
Q4YLT9_PLABE PRELIMINARY; PRT; 18 AA.
ID Q4YLT9;
AC Q4YLT9;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
DE ORNames=PB400723.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Brittan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;

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RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA101003787; CA101022.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2206 MW; EBBABA563A3085A7 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;
Best Local Similarity 30.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 9 QPQHGVLVKQ 18
DB 1 KFPKYSMMHQ 10

RESULT 12
05FBR5_SUNMU PRELIMINARY; PRT; 18 AA.
ID 05FBR5;
AC 05FBR5;
DT 10-MAR-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Thiorodoxin (Fragment).
GN Name:TXN;
OS Suncus murinus (House shrew) (Musk shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Insectivora; Soricidae;
OC Crociuidinae; Suncus.
OX NCBI_TaxID=9378;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=TKU, WZ, and BAN; TISSUE=Kidney;
RX PubMed=15897627; DOI=10.1538/expan.54.173;
RA Adjei S., Sato A., Tanaka S., Kobayashi E., Tanaka K., Namikawa T.,
RA Ishikawa A.;
RT "Development and characterization of CATS markers for genetic linkage
RT mapping in the house musk shrew, Suncus murinus.";
RL Exp. Anim. 54:173-180(2005).
DR EMBL; AB167758; BAD89500.1; -; Genomic_DNA.
DR EMBL; AB167757; BAD89499.1; -; Genomic_DNA.
DR EMBL; AB167756; BAD93380.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 2020 MW; D0B5FC66463A90F8 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.3e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQKVD 8
DB 8 GQKVG 13

RESULT 13
Q7M198_STRFR PRELIMINARY; PRT; 18 AA.
ID Q7M198;
AC Q7M198;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE 24k serine proteinase (EC 3.4.21.-) (Fragment).
OS Streptomyces fradiae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1906;
RN [1]
RP PROTEIN SEQUENCE.

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RX MEDLINE=92155439; PubMed=1786859; DOI=10.1016/0020-711X(91)90133-8;
RA Saha U., Molt S.A., Lad P.J.;
RT "Two new extracellular serine proteases from Streptomyces fradiae.";
RL Int. J. Biochem. 23:979-984(1991).
DR PIR; A61577; A61577.
FT NON_TER 1
FT TER 18
SQ SEQUENCE 16 AA; 2004 MW; 6D6DA167845934A5 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;
Best Local Similarity 27.3%; Pred. No. 1.3e+04;
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 IDGKVDQFP 11
   :|:|:|
DB 2 VGGTRAQDFP 12

RESULT 14
LSK1 LEUMA
ID LSK1 LEUMA STANDARD; PRT; 11 AA.
AC P04428;
DT 13-AUG-1987 (Rel. 05; Created)
DT 13-AUG-1987 (Rel. 05; Last sequence update)
DT 10-MAY-2005 (Rel. 47; Last annotation update)
DE Leucosulfakinin-1 (Leucosulfakinin-1) (LSK-1).
OS Leucophaea maderae (Maddira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blatelloidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86315858; PubMed=3749893;
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
RT gastrin and cholecystokinin.";
RL Science 234:71-73(1986).
CC -1- FUNCTION: Changes the frequency and amplitude of contractions of
CC the hindgut. Inhibits muscle contraction of hindgut.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01622; GMROL.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 6
FT MOD_RES 11 6 Sulfotyrosine.
FT MOD_RES 11 11 Phenylalanine amide.
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 24.0%; Score 23; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 EQFPQHG 14
   |||:|
DB 1 EQFEDYG 7

RESULT 15
LSKP PERAM
ID LSKP PERAM STANDARD; PRT; 11 AA.
AC P3685;
DT 01-JUN-1994 (Rel. 29; Created)
DT 01-JUN-1994 (Rel. 29; Last sequence update)
DT 05-JUL-2004 (Rel. 44; Last annotation update)
DE Perisulfakinin (Psa-SK-I).

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OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blatelloidea;
OC Blattidae; Blattellinae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=corpora cardiaca;
RX MEDLINE=901337190; PubMed=2615921; DOI=10.1016/0143-4179(89)90038-3;
RA Veenstra J.A.;
RT "Isolation and structure of two gastrin/CK-like neuropeptides from
RT the American cockroach homologous to the leucosulfakinins.";
RL Neuropeptides 14:145-149(1989).
CC -1- FUNCTION: Stimulates hindgut contractions.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
DR PIR; A60656; A60656.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 6
FT MOD_RES 11 6 Sulfotyrosine.
FT MOD_RES 11 11 Phenylalanine amide.
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAB CRC64;

Query Match 24.0%; Score 23; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 EQFPQHG 14
   |||:|
DB 1 EQFEDYG 7

```

Search completed: December 12, 2005, 21:23:56
Job time : 63.6667 secs

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: December 12, 2005, 19:37:19 ; Search time 97.6034 Seconds
(without alignments)
81.030 Million cell updates/sec

Title: US-10-758-165A-11
Perfect score: 96
Sequence: 1 IDGQKVDQFPQHGLVKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	ADRI0611	ADRI0611 Horse IGE
2	96	100.0	424	5 AAM50103	AAM50103 Equine Ig
3	96	100.0	424	5 AAM50104	AAM50104 Equine Ig
4	78	81.2	15	ADC64569	ADC64569 Horse Imm
5	63	65.6	6	ABP96585	ABP96585 Horse IGE
6	49	51.0	6	ADC00951	ADC00951 Enterohae
7	45	46.9	504	6 ABU27912	ABU27912 Protein e
8	45	46.9	685	4 ABB64268	ABB64268 Drosophil
9	45	46.9	1512	6 ADA33876	ADA33876 Actinecto
10	45	46.9	1536	6 ABR53009	ABR53009 Protein s
11	45	46.9	1536	7 ADK61916	ADK61916 Disease t
12	44	45.8	128	4 ABG05706	ABG05706 Novel hum
13	44	45.8	159	4 ABG05705	ABG05705 Novel hum
14	44	45.8	369	4 AAU65086	AAU65086 Proptonib
15	44	45.8	369	6 ABM61605	ABM61605 Proptonib
16	44	45.8	385	6 ABM65825	ABM65825 Proptonib
17	44	45.8	421	4 ABB53051	ABB53051 Escherich
18	44	45.8	616	6 ABM70417	ABM70417 Phototrab
19	44	45.8	686	6 ADL99373	ADL99373 Nanotruc
20	43	44.8	103	4 AAU58156	AAU58156 Proptonib
21	43	44.8	103	6 ABM54675	ABM54675 Proptonib
22	43	44.8	146	8 ADX77153	ADX77153 Plant ful
23	43	44.8	152	8 ADX72974	ADX72974 Plant ful
24	43	44.8	316	9 ADY26835	ADY26835 S. pulver

25	43	44.8	321	3 AAG35242	AAG35242 Zea mays
26	43	44.8	325	8 ADX66768	ADX66768 Plant ful
27	43	44.8	334	3 AAG33393	AAG33393 Zea mays
28	43	44.8	346	8 ADX69083	ADX69083 Plant ful
29	43	44.8	356	9 ADY26853	ADY26853 S. pulver
30	43	44.8	361	3 AAG44780	AAG44780 Zea mays
31	43	44.8	362	3 AAG33392	AAG33392 Zea mays
32	43	44.8	366	8 ADX66926	ADX66926 Plant ful
33	43	44.8	371	8 ADX79458	ADX79458 Plant ful
34	43	44.8	373	3 AAG35241	AAG35241 Zea mays
35	43	44.8	374	3 AAG44779	AAG44779 Zea mays
36	43	44.8	375	3 AAG33391	AAG33391 Zea mays
37	43	44.8	403	8 ADX71093	ADX71093 Plant ful
38	43	44.8	403	8 ADX94569	ADX94569 Plant ful
39	43	44.8	409	8 ADX77253	ADX77253 Plant ful
40	43	44.8	434	8 ADY11529	ADY11529 Plant ful
41	43	44.8	446	3 AAG44778	AAG44778 Zea mays
42	43	44.8	448	3 AAG35240	AAG35240 Zea mays
43	43	44.8	612	7 ABO76981	ABO76981 Pseudomon
44	43	44.8	654	5 ABB54057	ABB54057 Lactococc
45	43	44.8	1427	9 AEB39681	AEB39681 L. pneumo

ALIGNMENTS

RESULT 1
ADRI0611
ID ADRI0611 standard; peptide: 18 AA.
XX
AC ADRI0611;
XX
DT 21-OCT-2004 (first entry)
XX
DE Horse IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 11.
XX
KW Antiaesthetic; Antiallergic; Immunosuppressive; IGF; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW horse.
XX
OS Equus caballus.
XX
PN WO2004065936-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.
XX
(UNNC-) UNIV NORTH CAROLINA STATE.
XX
Hammerberg B;
XX
WPI: 2004-593545/57.
XX
PT Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
PS Example 6; Page 9; 14pp; English.
XX
CC The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC (I) is useful for testing an allergen reactivity of an IGE sample.
CC Allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE. The present sequence is the
 CC horse IgE 3.76 recognition site.

XX Sequence 18 AA;

Query Match 100.0%; Score 96; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.6e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDGKVDQFPQHGVLVKQ 18
 |||||
 Db 1 IDGKVDQFPQHGVLVKQ 18

RESULT 2

AAM50103
 ID AAM50103 standard; protein; 424 AA.

XX AAM50103;

XX 02-SEP-2002 (first entry)

XX Equine IgE heavy chain constant region C-epsilon allotype A.

XX Cea; equine; horse; heavy chain; constant region; allotype a; IgE;
 KW C-epsilon a; immunoglobulin E; antiallergic; allergy.

XX Equus caballus.

XX Key Location/Qualifiers

FT Domain 1..97

FT Domain /note= "CH1 domain"

FT Domain /note= "CH2 domain"

FT Domain /note= "CH3 domain"

FT Domain /note= "CH4 domain"

XX WO200250280-A2.

XX 27-JUN-2002.

XX 20-DEC-2001; 2001WO-DE004810.

XX 21-DEC-2000; 2000DE-01064415.

XX (TIER-) TIERAERZTLICHE HOCHSCHULE HANNOVER.

XX Leibold W, Wagner B, Radbruch A;

XX WPI; 2002-508803/54.

XX N-PSDB; ABL61246.

XX DNA sequence encoding part of an equine immunoglobulin G, useful for

XX preparing isotype-specific antibodies for diagnosis and treatment of

XX allergy in horses.

XX Claim 1; Page 31-32; 37pp; German.

XX This invention describes a novel DNA (I) encoding the constant region

XX (CH) of the heavy chain of a horse immunoglobulin E (IgE) allotype. The

XX products of the invention are capable of neutralising IgE activity and

XX have antiallergic activity. The polynucleotides of the invention are used

XX to produce recombinant IgE (II), and this is used to raise specific

XX monoclonal antibodies (Mab). Both (II) and Mab are useful for diagnosis,

XX particularly of allergy in horses, and Mab can also be used for treatment

XX of allergies. (I) make possible production of isotype-specific

XX antibodies, important for precise evaluation of the immune response. This

XX sequence represents a fragment of the equine IgE heavy chain constant

CC region C-epsilon allotype a (Cea), used in the method of the invention

CC for IgE-isotype recombinant immunoglobulin production

XX Sequence 424 AA;

Query Match 100.0%; Score 96; DB 5; Length 424;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IDGKVDQFPQHGVLVKQ 18
 |||||
 Db 145 IDGKVDQFPQHGVLVKQ 162

RESULT 3

AAM50104
 ID AAM50104 standard; protein; 424 AA.

XX AAM50104;

XX 02-SEP-2002 (first entry)

XX Equine IgE heavy chain constant region C-epsilon allotype b.

XX Ceb; equine; horse; heavy chain; constant region; allotype b; IgE;
 KW C-epsilon b; immunoglobulin E; antiallergic; allergy.

XX Equus caballus.

XX Key Location/Qualifiers

FT Domain 1..97

FT Domain /note= "CH1 domain"

FT Domain /note= "CH2 domain"

FT Domain /note= "CH3 domain"

FT Domain /note= "CH4 domain"

XX WO200250280-A2.

XX 27-JUN-2002.

XX 20-DEC-2001; 2001WO-DE004810.

XX 21-DEC-2000; 2000DE-01064415.

XX (TIER-) TIERAERZTLICHE HOCHSCHULE HANNOVER.

XX Leibold W, Wagner B, Radbruch A;

XX WPI; 2002-508803/54.

XX N-PSDB; ABL61247.

XX DNA sequence encoding part of an equine immunoglobulin G, useful for

XX preparing isotype-specific antibodies for diagnosis and treatment of

XX allergy in horses.

XX Claim 1; Page 34-36; 37pp; German.

XX This invention describes a novel DNA (I) encoding the constant region

XX (CH) of the heavy chain of a horse immunoglobulin E (IgE) allotype. The

XX products of the invention are capable of neutralising IgE activity and

XX have antiallergic activity. The polynucleotides of the invention are used

XX to produce recombinant IgE (II), and this is used to raise specific

XX monoclonal antibodies (Mab). Both (II) and Mab are useful for diagnosis,

XX particularly of allergy in horses, and Mab can also be used for treatment

XX of allergies. (I) make possible production of isotype-specific

XX antibodies, important for precise evaluation of the immune response. This

XX sequence represents a fragment of the equine IgE heavy chain constant

XX region C-epsilon allotype b (Ceb), used in the method of the invention

XX for IgE-isotype recombinant immunoglobulin production

SO Sequence 424 AA;
 Query Match 100.0%; Score 96; DB 5; Length 424;
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IDGKRVDEQFPQHGVLVKQ 18
 |||||
 145 IDGKRVDEQFPQHGVLVKQ 162

Db

RESULT 4
 ADC64569
 ID ADC64569 standard; peptide; 15 AA.
 XX
 AC ADC64569;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Horse immunoglobulin E, IgE, heavy chain immunogenic peptide P5.
 XX
 KW Horse; immunoglobulin E, IgE; heavy chain; immunogen; allergy.
 XX
 OS Equus caballus.
 XX
 PN US2003087314-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 08-NOV-2001; 2001US-00052788.
 XX
 PR 08-NOV-2001; 2001US-00052788.
 PA (REGC) UNIV CALIFORNIA.
 P1 Gerbwin LJ, Pettigrew HD, Kalina WV;
 XX
 DR WPI; 2003-765437/72.
 XX
 PT Immunogenic composition comprising an isolated equine immunoglobulin E
 PT polypeptide that induces production of antibodies which specifically bind
 PT to equine immunoglobulin E.
 XX
 PS Example 1; Page 8; 14pp; English.

XX The invention relates to an immunogenic composition comprising an
 CC isolated polypeptide having an amino acid sequence that is at least 80%
 CC identical to 6 (SI-S6), 15 amino acid peptide sequences derived from
 CC equine immunoglobulin E (the composition induces production of an
 CC antibody that specifically binds to equine immunoglobulin (Ig)E), the six
 CC polypeptides are not explicitly identified in the specification. Also
 CC included are a composition comprising an antibody that specifically binds
 CC to a polypeptide at least 80% identical to (SI)-(S6), an antibody that
 CC specifically binds to equine IgE made by the process of immunising an
 CC animal with a polypeptide at least 80% identical to (SI)-(S6), making an
 CC antibody that specifically binds to equine IgE (involving immunising an
 CC animal with a composition further comprising an isolated polypeptide (the
 CC amino acid sequence of the polypeptide is at least 80% identical to (SI)-
 CC (S6)), and collecting antiserum from the animal) and a kit for detection
 CC of equine IgE in a biological sample comprising the antibody and means
 CC for detecting specific binding of the antibody to equine IgE. The
 CC antibody is useful for detecting equine IgE protein in a biological
 CC sample (serum) which involves contacting the sample with the antibody,
 CC thus forming an antigen/antibody complex, and detecting the presence or
 CC absence of the antigen/antibody complex. The antibody and antigen are
 CC immobilised on a solid surface. The antibody is labelled such that the
 CC complex can be detected. The complex is detected using a second labelled
 CC antibody. The peptides are useful for generating antibodies specific for
 CC IgE which can serve as a diagnostic test for allergy. The present
 CC sequence is a Horse immunoglobulin E, IgE, heavy chain immunogenic
 CC peptide from the middle portion of the C2 region.
 CC
 CC Sequence 15 AA;

Query Match 81.2%; Score 78; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IDGKRVDEQFPQHG 14
 |||||
 2 IDGKRVDEQFPQHG 15

Db

RESULT 5
 ABP96585
 ID ABP96585 standard; protein; 569 AA.
 XX
 AC ABP96585;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Horse IgE heavy chain amino acid sequence SEQ ID NO:30.
 XX
 KW Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
 KW immune response; major histocompatibility complex; MHC; immunogenic;
 KW antiallergic; antiaesthetic; immunosuppressive; vasoactive; cytostatic;
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy;
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
 KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
 KW urticaria hives.
 XX
 OS Equus caballus.
 XX
 PN WO2003015716-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 08-AUG-2002; 2002WO-US026986.
 XX
 PR 13-AUG-2001; 2001US-0312120P.
 PA (IGET-) IGE THERAPEUTICS INC.
 P1 Chen SA, Yang Y, Barankiewicz T, Chen Z;
 XX
 DR WPI; 2003-268242/26.
 XX
 PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL, response
 PT against IgE, by identifying peptide eliciting CTL response to IgE
 PT peptides naturally presented by major histocompatibility complex class I
 PT protein.
 XX
 PS Example 7; Page 157-160; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
 CC E (IgE), comprising providing a test peptide (T) suspected of being able
 CC to bind to major histocompatibility complex (MHC) class I molecule, and
 CC evaluating (T) for ability to elicit in a mammal a CTL response to
 CC naturally processed and presented IgE peptides, where a peptide that
 CC induces such a response is identified. Also described are compositions:
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC IgE peptides. C1-3 have antiallergic, antiaesthetic, immunosuppressive,
 CC vasoactive, dermatological, antiinflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against IgE, and in
 CC vaccine. C1-3 can be used for modulating an IgE-mediated condition such as
 CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as
 CC IgE-mediated atopic hypersensitivity condition. IgE-mediated non-atopic
 CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria

CC hives). The present sequence represents an IgE heavy chain amino acid
CC sequence, which is given in an example from the present invention
XX
SQ Sequence 569 AA;

Query Match 65.6%; Score 63; DB 6; Length 569;
Best Local Similarity 66.7%; Pred. No. 0.31;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGVLVK 18
|:|||||:|:
Db 291 IEGQKVDQFPPTQASMKQ 308

RESULT 6
ADCC0951
ID ADC0951 standard; protein; 616 AA.

XX ADC0951;

XX 04-DEC-2003 (first entry)

XX Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 996.

XX enterohaemorrhagic; anti-bacterial.

XX Escherichia coli; O157:H7.

XX JF2002355074-A.

XX 10-DEC-2002.

XX 24-JAN-2002; 2002JP-00015959.

XX 24-JAN-2001; 2001JP-00112010.

XX (UYTS-) UNIV TSUKUBA.

XX WPI; 2003-451640/43.

XX Enterohaemorrhagic Escherichia coli O157:H7-specific nucleic acid molecule
PT and a polypeptide and its use, a polypeptide, a vector and a host cell.

XX Claim 3; SEQ ID NO 996; 2067bp; Japanese.

XX The invention relates to a novel enterohaemorrhagic Escherichia coli
CC O157:H7-specific nucleic acid molecule. A polynucleotide of the invention
CC has anti-bacterial activity. The polypeptide can be used in detection
CC and/or treatment of O157:H7 infection. The nucleotide sequence of the
CC genome of Enterohaemorrhagic E. coli O157:H7 was determined. The present
CC sequence represents an E. coli O157:H7-specific polypeptide of the
XX invention.

XX Sequence 616 AA;

Query Match 51.0%; Score 49; DB 7; Length 616;
Best Local Similarity 50.0%; Pred. No. 58;
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

Qy 4 QKVDQFPQ-HGVLK 17
|:|||||:|:
Db 58 QKIDEPPELTHGLIK 73

RESULT 7

ABU27912
ID ABU27912 standard; protein; 504 AA.

XX AC ABU27912;

XX 19-JUN-2003 (first entry)

XX Protein encoded by prokaryotic essential gene #13439.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX Enterobacter cloacae.

XX NC0200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002MO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948893.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Hasebeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RN, Xu HH;
XX WPI; 2003-029926/02.

XX N-PSDB; ACA31782.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 55836; 1766bp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 504 AA;

Query Match 46.9%; Score 45; DB 6; Length 504;
Best Local Similarity 53.3%; Pred. No. 2e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGVL 15
|:|||||:|:
Db 315 IDGKRVYIQKPAHAI 329

```
RESULT 8
ABB64268
ID ABB64268 standard; protein; 685 AA.
XX
XX ABB64268;
AC
XX 26-MAR-2002 (first entry)
DT
XX Drosophila melanogaster polypeptide SEQ ID NO 19596.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PMD, Myers EW;
XX WPI; 2001-656660/75.
XX DR N-PSDB; ABL08371.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Discloure; SEQ ID NO 19596; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
XX sequences (AB101840-AB16175) and the encoded proteins (AB57737-
XX AB12072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 685 AA;
SQ
Query Match 46.9%; Score 45; DB 4; Length 685;
Best Local Similarity 53.3%; Pred. NO. 2.9e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Oy 3 GQKVDQFPQHGVLVK 17
|||
:|:|||||
Db 577 GQVGSNSTPFGVLVK 591
|||
:|:|||||

RESULT 9
ADA33876
ID ADA33876 standard; protein; 1512 AA.
XX
XX ADA33876;
AC
XX 20-NOV-2003 (first entry)
DT
XX Acinetobacter baumannii protein #1037.
XX
XX Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
XX plant biocontrol agent.
XX
```

```
OS Acinetobacter baumannii.
XX
XX US6562958-B1.
XX
XX 13-MAY-2003.
XX
XX 04-JUN-1999; 99US-00328352.
XX
XX 09-JUN-1998; 98US-0088701P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Breton G, Bush D;
XX
XX WPI; 2003-576092/54.
XX DR N-PSDB; ADA29750.
XX
XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
XX for diagnosing a bacterial disease, as components of antibacterial
XX vaccines, as targets for antibacterial drugs, or as biocontrol agents for
XX plants.
XX
XX Example; SEQ ID NO 5163; 328pp; English.
XX
XX The invention relates to isolated Acinetobacter baumannii nucleic acids.
XX The A. baumannii nucleic acids and polypeptides are useful as reagents
XX for diagnosing a bacterial disease, as components of antibacterial
XX vaccines, as targets for antibacterial drugs, to detect the presence of
XX A. baumannii and other Acinetobacter species in a sample, in screening
XX compounds for the ability to interfere with the A. baumannii life cycle
XX or to inhibit A. baumannii infection, and as biocontrol agents for
XX plants. The present sequence represents the amino acid sequence of an A.
XX baumannii protein.
XX
XX Sequence 1512 AA;
SQ
Query Match 46.9%; Score 45; DB 6; Length 1512;
Best Local Similarity 50.0%; Pred. NO. 6.9e+02;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
Oy 3 GQKVDQFPQHGVLVKQ 18
|||
:|:|||||
Db 328 GDRTPDPLMPSHGVLVSQ 343
|||
:|:|||||

RESULT 10
ABR53009
ID ABR53009 standard; protein; 1536 AA.
XX
XX ABR53009;
AC
XX 20-JUN-2003 (first entry)
DT
XX Protein sequence #SEQ ID 883.
XX
XX Multiprotein complex; eukaryote; drug target; diagnosis.
XX
XX Saccharomycetes cerevisiae.
XX
XX EP1258494-A1.
XX PN
XX 20-NOV-2002.
XX PD
XX 20-DEC-2001; 2001EP-00130253.
XX
XX 15-MAY-2001; 2001EP-00111774.
XX PR
XX (CELL-) CELLZOME AG.
XX PA
XX Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;
XX Marzloch W, Schultz JD, Superti-Furga GD;
XX WPI; 2003-250078/25.
XX
```

	Query Match	Similarity	Score	DB	Length
Best Local	8	53.3%	Pred. No. 7e+02	3	Indels 0; Gaps 0;
Matches	8	Conservative	3	Mismatches	4; Indels 0; Gaps 0;
Qy	1	IDGQKVDGEQFPQHG	15		
db	1370	IDGTEVDEDFSPDEGI	1384		

CC	proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or prevention of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).
SQ	Sequence 1536 AA;
OY	Query Match 46.9%; Score 45; DB 7; Length 1536; Best Local Similarity 53.3%; Pred. No. 7e+02; Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0 1 IDGKRVDEQFPQHCL 15 :: : :-:GVDEDFSPSGI 1384
ID	ABG05706 standard; protein, 128 AA.
AC	ABG05706;
DT	13-FEB-2002 (first entry)
XX	Novel human diagnostic protein #5697.
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
OS	Homo sapiens.
PV	WO200175067-A2.
PD	11-OCT-2001.
PF	30-MAR-2001; 2001WO-US0008631.
PR	31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.
PA	(HYSE-) HYSEQ INC.
PI	Dymanac RT, Liu C, Tang YT;
DR	WPI: 2001-639362/73. N-P8DB; AAS69893.
PT	New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
PS	Claim 20; SEQ ID NO 36065; 103bp; English.
CC	The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

Sequence 128 AA;
SQ

Query Match 45.8%; Score 44; DB 4; Length 128;
Best Local Similarity 52.9%; Pred. No. 63;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 2 DGGKVDGQPPQHGVLKQ 18
Db 60 DPQRPESQSPVHGLVQR 76

RESULT 13
ABG05705
ID ABG05705 standard; protein; 159 AA.
XX
AC ABG05705;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #5696.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PE 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dymnac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS69892.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 36064; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (II) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostic as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

Sequence 159 AA;
SQ

Query Match 45.8%; Score 44; DB 4; Length 159;
Best Local Similarity 52.9%; Pred. No. 80;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 2 DGGKVDGQPPQHGVLKQ 18
Db 91 DPQRPESQSPVHGLVQR 107

RESULT 14
AAU65086
ID AAU65086 standard; protein; 369 AA.
XX
AC AAU65086;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #25982.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PE 20-APR-2001; 2001WO-US012865.
XX
PR 21-APR-2000; 2000US-0199047P.
PR 02-JUN-2000; 2000US-0208841P.
PR 07-JUL-2000; 2000US-0216747P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
DR WPI; 2001-616774/71.
DR N-PSDB; AAS59658.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
PS Claim 3; SEQ ID NO 26281; 1069pp; English.
XX
CC Sequences AAU9105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the

CC presence or absence of *P. acnes* in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for *P. acnes* proteins. These antibodies can be used to
 CC downregulate expression and activity of *P. acnes* polypeptides and
 CC therefore treat *P. acnes* infections. The antibodies may also be used as
 CC diagnostic agents for determining *P. acnes* presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 369 AA;

QY 3 GQXVDEQFPOH 13
 Db 267 GRDIDDQFPRH 277

Query Match 45.8%; Score 44; DB 4; Length 369;
 Best Local Similarity 54.5%; Pred. No. 2.1e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

RESULT 15
 ABM61605 A standard; protein; 369 AA.
 XX
 AC ABM61605;
 XX
 DT 20-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes transporter-related polypeptide #26281.
 XX
 KM Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 XX immunostimulant; immune response; vaccine.
 OS Propionibacterium acnes.
 XX
 PN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032727.
 XX
 PR 15-OCT-2001; 2001US-00978825.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Mitcham JL, Skeiky YAM, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vallieve-Douglas J;
 XX
 DR WPI; 2003-381789/36.
 DR N-PDB; ACF64587.
 XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a *P. acnes* protein.
 XX
 PS Claim 3k; SEQ ID NO 26281; 1481bp; English.
 XX
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of *P. acnes* polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a *P. acnes*
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising *P. acnes* polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or

CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of *P. acnes* in a
 CC patient; and a method for inhibiting the development of *P. acnes* in a
 CC patient. The *P. acnes* polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a *P. acnes*
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against *P. acnes*, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a specifically claimed polypeptide which is predicted
 CC to be encoded by an ORF (open reading frame) contained within the *P.*
 CC acnes polynucleotides of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 369 AA;

QY 3 GQXVDEQFPOH 13
 Db 267 GRDIDDQFPRH 277

Query Match 45.8%; Score 44; DB 6; Length 369;
 Best Local Similarity 54.5%; Pred. No. 2.1e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Search completed: December 12, 2005, 20:30:32
 Job time : 99.6034 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: December 12, 2005, 19:23:41 ; Search time 24.5172 Seconds
(without alignments)
60.699 Million cell updates/sec

Title: US-10-758-165A-11

Perfect score: 96

Sequence: 1 IDGQKVDEQFPQHGLVKQ 18

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents, AA: *
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/BCTUS_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	47.9	195	2	US-09-248-796A-19566
2	45	46.9	1512	2	US-09-328-352-5163
3	45	46.9	1536	2	US-09-487-558B-322
4	43	44.8	612	2	US-09-252-991A-25727
5	42	43.8	137	2	US-08-961-083-40
6	42	43.8	137	2	US-09-536-784-40
7	42	43.8	137	2	US-09-765-271-40
8	42	43.8	137	2	US-09-765-272A-40
9	42	43.8	185	2	US-09-583-110-5222
10	42	43.8	194	2	US-09-107-433-5104
11	42	43.8	228	2	US-09-134-000C-6247
12	42	43.8	359	1	US-08-307-382-2
13	42	43.8	359	1	US-08-366-779-2
14	42	43.8	359	1	US-08-478-727-2
15	42	43.8	359	1	US-08-473-508-2
16	42	43.8	359	1	US-08-789-936-2
17	42	43.8	359	1	US-08-833-610-6
18	42	43.8	359	2	US-08-834-033A-16
19	42	43.8	359	2	US-08-934-254-2
20	42	43.8	359	2	US-09-377-452-6
21	42	43.8	359	2	US-09-685-775-2
22	42	43.8	363	2	US-09-108-020-44
23	42	43.8	363	2	US-09-685-296-44
24	42	43.8	590	2	US-09-489-039A-8178
25	41	42.7	297	2	US-09-248-796A-25364
26	41	42.7	381	2	US-09-248-796A-17552
27	41	42.7	394	2	US-09-252-991A-32539

28	41	42.7	535	2	US-09-589-733C-18	Sequence 18, Appl
29	41	42.7	536	2	US-09-258-031C-77	Sequence 77, Appl
30	40.5	42.2	246	2	US-09-543-681A-8212	Sequence 8212, Ap
31	40	41.7	230	2	US-09-252-991A-25914	Sequence 25914, A
32	40	41.7	344	2	US-09-252-991A-30083	Sequence 30083, A
33	40	41.7	666	2	US-09-270-767-46736	Sequence 46736, A
34	39.5	41.1	79	2	US-08-951-871-2	Sequence 23915, A
35	39.5	41.1	912	1	US-08-951-871-2	Sequence 21451, A
36	39	40.6	195	2	US-09-252-991A-21451	Sequence 21451, A
37	39	40.6	271	1	US-08-152-019A-28	Sequence 28, Appl
38	39	40.6	336	1	US-07-667-276A-8	Sequence 8, Appl
39	39	40.6	411	2	US-09-134-000C-3961	Sequence 3961, Ap
40	39	40.6	416	2	US-09-134-000C-6248	Sequence 6248, Ap
41	39	40.6	463	2	US-09-198-452A-115	Sequence 115, App
42	39	40.6	468	2	US-09-438-185A-100	Sequence 100, App
43	39	40.6	505	2	US-09-252-991A-29343	Sequence 29343, A
44	39	40.6	510	2	US-09-270-767-46399	Sequence 46399, A
45	39	40.6	1725	2	US-09-562-702A-20	Sequence 20, Appl

ALIGNMENTS

```
RESULT 1
US-09-248-796A-19566
; Sequence 19566, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; NUMBER OF SEQ ID NOS: 19566
; SEQ ID NO 19566
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19566

Query Match      47.9%; Score 46; DB 2; Length 195;
Best Local Similarity 55.0%; Pred. No. 4.1;
Matches 11; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY      1 IDGQKVDEQF--PQHGLVKQ 18
       :|||||:||||:
Db      34 MDGQKVDVLLPQHGLVKQ 53

RESULT 2
US-09-328-352-5163
; Sequence 5163, Application US/09328352
; Patent No. 6362958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5163
; LENGTH: 1512
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5163

Query Match      46.9%; Score 45; DB 2; Length 1512;
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Best Local Similarity 50.0%; Pred. No. 64;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 3 GQKVDQEPFHGLVQ 18
Db 328 GDRTPDPLMPKGLVSQ 343

RESULT 3
US-09-487-558B-322
; Sequence 322, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Bueby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.130
; CURRENT APPLICATION NUMBER: US/09/487,558B
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 322
; LENGTH: 1536
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-322

Query Match 46.9%; Score 45; DB 2; Length 1536;
Best Local Similarity 53.3%; Pred. No. 65;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 IDGQKVDQEPFHGL 15
Db 1370 IDGTEVDEFEPSFEG 1384

RESULT 4
US-09-252-991A-25727
; Sequence 25727, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25727
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25727

Query Match 44.8%; Score 43; DB 2; Length 612;
Best Local Similarity 44.4%; Pred. No. 50;

Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 IDGQKVDQEPFHGLVQ 18
Db 401 VDGKSVGEPSFGKGMVQ 418

RESULT 5
US-08-961-083-40
; Sequence 40, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-40

Query Match 43.8%; Score 42; DB 2; Length 137;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 IDGQKVDQEPQ 12
Db 93 IDGKTEVGEFPQ 104

RESULT 6
US-09-536-784-40
; Sequence 40, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA


```

RESULT 9
US-09-583-110-5222
; Sequence 5222, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5222
; LENGTH: 185
; TYPE: PR1
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5222

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Query Match	43.8%	Score 42	DB 2	Length 185
Best Local Similarity	66.7%	Pred. No. 19		
Matches	8	Conservative	1	Mismatches 3
				Indels 0
				Gaps 0
QY	1	IDGQKVDGEQFPQ	12	
Db	112	IQGKLTVEQFPQ	123	

RESULT 10
 US-09-107-433-5104
 Sequence 5104, Application US/09107433
 Patent No. 6800744
 GENERAL INFORMATION:
 APPLICANT: Lynn A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
 SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
 THERAPEUTICS
 NUMBER OF SEQUENCES: 5206
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02354
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: <Unknown>
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: <Unknown>
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,433
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085131
 FILING DATE: May 12, 1998
 APPLICATION NUMBER: 60/051553
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Arinello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 5104:

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?      SEQUENCE CHARACTERISTICS:
?          LENGTH: 194 amino acids
?          TYPE: amino acid
?          TOPOLOGY: linear
?          MOLECULE TYPE: protein
?          HYPOTHETICAL: YES
?          ORIGINAL SOURCE:
?              ORGANISM: Streptococcus pneumoniae
?
?      FEATURE:
?          NAME/KEY: misc_feature
?          LOCATION: (B) LOCATION 1...194
?      SEQUENCE DESCRIPTION: SEQ ID NO: 5104:
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US-09-107-433-5104

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[illegible]

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RESULT 11
US-09-134-000C-6247
; Sequence 6247, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucetre-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR APPLICATION NUMBER: 1998-08-13
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6247
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-6247

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Query Match	43.8%	Score 42	DB 2	Length 228
Best Local Similarity	87.5%	Pred. No.	24	
Matches	7	Conservative	1	Mismatches 0
				Gaps 0

QY	10	FPQHGVLK	17
		:	
Db	174	FPQHGVLK	181

```

1 RESULT 12
2 US-08-307-382-2
3 Sequence 2, Application US/08307382
4 Patent No. 5552306
5
6 GENERAL INFORMATION:
7
8 APPLICANT: Thomas, Terry L.
9
10 APPLICANT: Reddy, Avutu S.
11
12 APPLICANT: Nuccio, Michael
13
14 APPLICANT: Freyshtet, Georges L.
15
16 TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
17
18 TITLE OF INVENTION: ACID BY A DELTA 6-DESATURASE
19
20 NUMBER OF SEQUENCES: 3
21
22 CORRESPONDENCE ADDRESS:
23
24 ADDRESSEE: Scully, Scott, Murphy & Presser
25
26 STREET: 400 Garden City Plaza
27
28 CITY: Garden City
29
30 STATE: New York
31
32 COUNTRY: United States
33
34 ZIP: 11530
35
36 COMPUTER READABLE FORM:
37

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US-08-366-779-2
Sequence 2, Application US/08366779
Patent No. 5614393
GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
APPLICANT: Reddy, Avutu S.
APPLICANT: Nuccio, Michael
APPLICANT: Freysbittel, Georges L.
APPLICANT: Numbers, Andrew N.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
TITLE OF INVENTION: DELTA 6-DESATURASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,779
FILING DATE: 30-DEC-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,727
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,362
FILING DATE: 14-SEP-1994
APPLICATION NUMBER: US 07/817,919
FILING DATE: 08-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: McNuley, William E.
REGISTRATION NUMBER: 22,606
REFERENCE/DOCKET NUMBER: 83832
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-478-727-2

```

QY 4 QKVD EQF PQHGLVKQ 18
| : || | : || | : :
Db 21 QRVDA YFAEHGLTQR 35

```

1      RESULT 15
2      US-08-473-508-2
3      Sequence 2, Application US/08473508
4      Patent No. 5689050
5      GENERAL INFORMATION:
6      APPLICANT: Thomas, Terry L.
7      APPLICANT: Reddy, Avutu S.
8      APPLICANT: Nuccio, Michael
9      APPLICANT: Freyshtet, Georges L.
10     TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
11     TITLE OF INVENTION: ACID BY A DELTA 6-DESATURASE
12     NUMBER OF SEQUENCES: 3
13     CORRESPONDENCE ADDRESS:
14     ADDRESSEE: Scully, Scott, Murphy & Presser
15     STREET: 400 Garden City Plaza
16     CITY: Garden City
17     STATE: New York
18     COUNTRY: United States
19     ZIP: 11530
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Floppy disk
22     COMPUTER: IBM PC compatible
23     OPERATING SYSTEM: PC-DOS/MS-DOS
24     SOFTWARE: Patent in Release #1.0, Version #1.25
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/08/473,508
27     FILING DATE: 07-JUN-1995
28     CLASSIFICATION: 800
29     PRIOR APPLICATION DATA:
30     APPLICATION NUMBER: US 08/307,382
31     FILING DATE: 14-SEP-1994
32     APPLICATION NUMBER: US 07/817,919
33     FILING DATE: 08-JAN-1992
34     ATTORNEY/AGENT INFORMATION:
35     NAME: McNulty, William B.
36     REGISTRATION NUMBER: 22,606
37     REFERENCE/DOCKET NUMBER: 83832
38     TELECOMMUNICATION INFORMATION:
39     TELEPHONE: (516) 742-4343
40     TELEFAX: (516) 742-4366
41     TELEX: 230 901 SANS UR
42     INFORMATION FOR SEQ ID NO: 2:
43     SEQUENCE CHARACTERISTICS:
44     LENGTH: 359 amino acids
45     TYPE: amino acid
46     TOPOLOGY: linear
47     MOLECULE TYPE: protein
48     US-08-473-508-2

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Query Match	43.8%	Score 42	DB 1	Length 359
Best Local Similarity	46.7%	Pred. No. 40		
Matches	7	Conservative	4	Mismatches
			4	Indels
			0	Gaps
QY	4	OKUDEQPPQHGKVKO	18	
	: :	: :	:	
Db	21	QRVDAYFAEHHGTOR	35	

Search completed: December 12, 2005, 19:37:07
Job time : 25.5172 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:33:42 ; Search time 80.3793 Seconds
(without alignments)
93.568 Million cell updates/sec

Title: US-10-758-165a-11
Perfect score: 96
Sequence: 1 IDGQKVDQFPQHGLVKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	US-10-758-165-11	Sequence 11, Appl
2	96	100.0	424	US-10-451-078-2	Sequence 2, Appl
3	96	100.0	424	US-10-451-078-4	Sequence 4, Appl
4	78	81.2	15	US-10-052-788-5	Sequence 5, Appl
5	63	65.6	569	US-10-214-524-30	Sequence 30, Appl
6	45	46.9	178	US-10-424-599-146307	Sequence 146307,
7	45	46.9	504	US-10-282-122A-55836	Sequence 55836, A
8	45	46.9	685	US-11-097-143-19596	Sequence 19596, A
9	45	46.9	1536	US-09-801-368-322	Sequence 322, App
10	44	45.8	89	US-10-424-599-205669	Sequence 205669,
11	44	45.8	128	US-10-450-763-36065	Sequence 36065, A
12	44	45.8	130	US-10-424-599-145103	Sequence 145103,
13	44	45.8	159	US-10-450-763-36064	Sequence 36064, A
14	44	45.8	421	US-10-437-963-159933	Sequence 154933,
15	44	45.8	421	US-10-238-075-1472	Sequence 1472, Ap
16	43.5	44.3	718	US-10-017-161-784	Sequence 784, App
17	43	44.8	121	US-10-425-115-187877	Sequence 187877,
18	43	44.8	146	US-10-425-114-46519	Sequence 46519, A
19	43	44.8	149	US-10-425-115-210792	Sequence 210792,
20	43	44.8	152	US-10-425-114-42340	Sequence 42340, A
21	43	44.8	316	US-10-922-282-12	Sequence 12, Appl
22	43	44.8	325	US-10-425-114-37611	Sequence 37611, A
23	43	44.8	346	US-10-425-114-39826	Sequence 39826, A
24	43	44.8	356	US-10-922-282-30	Sequence 30, Appl
25	43	44.8	366	US-10-425-114-37769	Sequence 37769, A
26	43	44.8	371	US-10-425-114-48824	Sequence 48824, A
27	43	44.8	374	US-10-767-701-45372	Sequence 45372, A

28	43	44.8	374	4	US-10-425-115-216179	Sequence 216179,
29	43	44.8	374	4	US-10-425-115-216182	Sequence 216182,
30	43	44.8	375	4	US-10-767-701-42582	Sequence 42582, A
31	43	44.8	398	4	US-10-425-115-300080	Sequence 300080,
32	43	44.8	403	4	US-10-425-114-40459	Sequence 40459, A
33	43	44.8	403	4	US-10-425-114-57233	Sequence 57233, A
34	43	44.8	409	4	US-10-425-114-46619	Sequence 46619, A
35	43	44.8	434	4	US-10-425-114-67344	Sequence 67344, A
36	43	44.8	605	4	US-10-437-963-169342	Sequence 169342,
37	42	43.8	84	4	US-10-424-599-157014	Sequence 157014,
38	42	43.8	137	3	US-09-765-272-40	Sequence 40, Appl
39	42	43.8	137	6	US-11-106-649-40	Sequence 40, Appl
40	42	43.8	185	5	US-10-472-928-1980	Sequence 1980, Ap
41	42	43.8	191	4	US-10-474-776-661	Sequence 661, App
42	42	43.8	194	5	US-10-617-320-5104	Sequence 5104, Ap
43	42	43.8	199	4	US-10-282-122A-46126	Sequence 46126, A
44	42	43.8	218	4	US-10-369-493-2768	Sequence 2768, Ap
45	42	43.8	232	4	US-10-425-114-51771	Sequence 51771, A

ALIGNMENTS

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RESULT 1
US-10-758-165-11
; Sequence 11, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-11

Query Match      100.0%; Score 96; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 8,66-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 IDGQKVDQFPQHGLVKQ 18
|||||
DB      1 IDGQKVDQFPQHGLVKQ 18

RESULT 2
US-10-451-078-2
; Sequence 2, Application US/10451078
; Publication No. US20040115764A1
; GENERAL INFORMATION:
; APPLICANT: Leibold, Wolfgang
; APPLICANT: Bettina, Wagner
; APPLICANT: Radbruch, Andreas
; TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the
; TITLE OF INVENTION: Heavy Chain of an Equine IgE Allotype, Recombinant
; TITLE OF INVENTION: Immunoglobulin Obtained Using Them and Corresponding
; TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use
; FILE REFERENCE: 0310017aa
; CURRENT APPLICATION NUMBER: US/10/451,078
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: PCT/DE01/04810
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 100 64 415.5
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
```

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SEQ ID NO 2
LENGTH: 424
TYPE: PRT
ORGANISM: Equus caballus
FEATURE:
NAME/KEY: Domain
LOCATION: (1)..(97)
OTHER INFORMATION: CH1 domain, IGE allotype a
FEATURE:
NAME/KEY: Domain
LOCATION: (98)..(205)
OTHER INFORMATION: CH2 domain, IGE allotype a
FEATURE:
NAME/KEY: Domain
LOCATION: (206)..(312)
OTHER INFORMATION: CH3 domain, IGE allotype a
FEATURE:
NAME/KEY: Domain
LOCATION: (313)..(424)
OTHER INFORMATION: CH4 domain, IGE allotype a
US-10-451-078-2
```

```
Query Match
Best Local Similarity 100.0%; Score 96; DB 4; Length 424;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 IDGQKVDQFPQHGVLVKQ 18
Db 145 IDGQKVDQFPQHGVLVKQ 162
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```
RESULT 3
US-10-451-078-4
Sequence 4, Application US/10451078.
```

```
Publication No. US20040115764A1
```

```
GENERAL INFORMATION:
```

```
APPLICANT: Leibold, Wolfgang
```

```
APPLICANT: Bettina, Wagner
```

```
APPLICANT: Radbruch, Andreas
```

```
TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the
```

```
TITLE OF INVENTION: Heavy Chain of an Equine IGE Allotype, Recombinant
```

```
TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use
```

```
FILE REFERENCE: 03100177a
```

```
CURRENT APPLICATION NUMBER: US/10/451, 078
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```
CURRENT FILING DATE: 2003-12-24
```

```
PRIOR APPLICATION NUMBER: PCT/DE01/04810
```

```
PRIOR FILING DATE: 2001-12-20
```

```
PRIOR APPLICATION NUMBER: DE 100 64 415.5
```

```
NUMBER OF SEQ ID NOS: 7
```

```
SOFTWARE: PatentIn version 3.2
```

```
SEQ ID NO 4
```

```
LENGTH: 424
```

```
TYPE: PRT
```

```
ORGANISM: Equus caballus
```

```
FEATURE:
```

```
NAME/KEY: Domain
```

```
LOCATION: (1)..(97)
```

```
OTHER INFORMATION: CH1 domain, IGE allotype b
```

```
FEATURE:
```

```
NAME/KEY: Domain
```

```
LOCATION: (98)..(205)
```

```
OTHER INFORMATION: CH2 domain, IGE allotype b
```

```
FEATURE:
```

```
NAME/KEY: Domain
```

```
LOCATION: (206)..(312)
```

```
OTHER INFORMATION: CH3 domain, IGE allotype b
```

```
FEATURE:
```

```
NAME/KEY: Domain
```

```
LOCATION: (313)..(424)
```

```
OTHER INFORMATION: CH4 domain, IGE allotype b
```

```
US-10-451-078-4
```

```
Query Match
Best Local Similarity 100.0%; Score 96; DB 4; Length 424;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 IDGQKVDQFPQHGVLVKQ 18
Db 145 IDGQKVDQFPQHGVLVKQ 162
```

```
RESULT 4
US-10-052-788-5
Sequence 5, Application US/10052788
```

```
Publication No. US2003008731A1
```

```
GENERAL INFORMATION:
```

```
APPLICANT: Gershwin, Laurel J.
```

```
APPLICANT: Pettigrew, Howard David
```

```
APPLICANT: Kalina, Warren V.
```

```
TITLE OF INVENTION: The Regents of the University of California
```

```
TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
```

```
FILE REFERENCE: 023070-121000US
```

```
CURRENT APPLICATION NUMBER: US/10/052, 788
```

```
CURRENT FILING DATE: 2001-11-08
```

```
NUMBER OF SEQ ID NOS: 6
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```
SOFTWARE: PatentIn Ver. 2.1
```

```
SEQ ID NO 5
```

```
LENGTH: 15
```

```
TYPE: PRT
```

```
ORGANISM: Artificial Sequence
```

```
FEATURE:
```

```
OTHER INFORMATION: Description of Artificial Sequence:epsilon peptide
```

```
OTHER INFORMATION: P5, middle portion of C2 of equine IGE epsilon
```

```
OTHER INFORMATION: heavy chain
```

```
US-10-052-788-5
```

```
Query Match
Best Local Similarity 100.0%; Score 78; DB 4; Length 15;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 IDGQKVDQFPQHG 14
Db 2 IDGQKVDQFPQHG 15
```

```
RESULT 5
US-10-214-524-30
```

```
Sequence 30, Application US/10214524
```

```
Publication No. US20030073142A1
```

```
GENERAL INFORMATION:
```

```
APPLICANT: Chen, Swei-Shen Alex
```

```
APPLICANT: Yang, Yong-Min
```

```
APPLICANT: Barankiewicz, Theresa J.
```

```
APPLICANT: Chen, Zhong
```

```
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
```

```
FILE REFERENCE: IGE-00101.P.1.1
```

```
CURRENT APPLICATION NUMBER: US/10/214, 524
```

```
CURRENT FILING DATE: 2002-08-08
```

```
PRIOR APPLICATION NUMBER: 60/312,120
```

```
PRIOR FILING DATE: 2001-08-13
```

```
NUMBER OF SEQ ID NOS: 61
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```
SOFTWARE: PatentIn version 3.1
```

```
SEQ ID NO 30
```

```
LENGTH: 569
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```
TYPE: PRT
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```
ORGANISM: Horse (Equus caballus)
```

```
US-10-214-524-30
```

```
Query Match
Best Local Similarity 65.6%; Score 63; DB 4; Length 569;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 IDGQKVDQFPQHGVLVKQ 18
```

Db 291 IEGQKRVDEQFPQASMKQ 308

RESULT 6

US-10-424-599-146307
; Sequence 146307, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 146307
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_103132C.1.dep
US-10-424-599-146307

Query Match Best Local Similarity 46.9%; Score 45; DB 4; Length 178;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IDGQKRVDEQFPQHG 14
:|||||:
Db 152 VDSNVVAPQFPQHG 165

RESULT 7

US-10-282-122A-55836
; Sequence 55836, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55836
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-10-282-122A-55836

Query Match Best Local Similarity 46.9%; Score 45; DB 4; Length 504;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKRVDEQFPQHGL 15
:|||||:
Db 315 IDGERVDIQFPAHAI 329

RESULT 8
US-11-097-143-19596
; Sequence 19596, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CLO00728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19596
; LENGTH: 685
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-19596

Query Match Best Local Similarity 46.9%; Score 45; DB 6; Length 685;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GQKRVDEQFPQHGLVK 17
:|||||:
Db 577 GQVGSNSYPEHGLVK 591

RESULT 9
US-09-801-368-322
; Sequence 322, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:

```

; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 322
; LENGTH: 1536
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-322
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Query Match          46.9%; Score 45; DB 3; Length 1536;
Best Local Similarity 53.3%; Pred. No. 3.4e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DGQKVDQFPQHG 15
Db 1370 IDGTEVDEFEFSPBGI 1384

RESULT 10
US-10-424-599-205669
; Sequence 205669, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 205669
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(89)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_27747C.1.pep
US-10-424-599-205669
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Query Match          45.8%; Score 44; DB 4; Length 89;
Best Local Similarity 58.3%; Pred. No. 21;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GQKVDQFPQHG 14
Db 46 GIKKDDKMPQHG 57
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```

RESULT 11
US-10-450-763-36065
; Sequence 36065, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 36065
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(128)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-36065
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Query Match          45.8%; Score 44; DB 5; Length 128;
Best Local Similarity 52.9%; Pred. No. 32;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 DGQKVDQFPQHG 18
Db 60 DPGRRQSPVHG 76
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```

RESULT 12
US-10-424-599-145103
; Sequence 145103, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 145103
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_102046C.1.pep
US-10-424-599-145103
```

```

Query Match          45.8%; Score 44; DB 4; Length 130;
Best Local Similarity 69.2%; Pred. No. 32;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GQKVDQFPQHG 15
Db 65 GQLQAEHFPQHG 77
```

```

RESULT 13
US-10-450-763-36064
; Sequence 36064, Application US/10450763
```

```

; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 36064
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(159)
; OTHER INFORMATION: xaa = X or * as defined in Table 2
US-10-450-763-36064

Query Match          45.8%; Score 44; DB 5; Length 159;
Best Local Similarity 52.9%; Pred. No. 40;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      2 DGQKVDQFPQHGVLKQ 18
      |||:|||||:
Db      91 DQQRREQSPVHGVLQR 107

RESULT 14
US-10-437-963-154933
; Sequence 154933, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 154933
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_54746C.1.pcp
US-10-437-963-154933

Query Match          45.8%; Score 44; DB 4; Length 387;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      6 VDEQFPQHGVL 15
      ::|||:|:
Db      302 IESFPQHGVL 311

RESULT 15
US-10-238-075-1472
; Sequence 1472, Application US/10238075

```

```

; Publication No. US20030148324A1
; GENERAL INFORMATION:
; APPLICANT: I.N.S.E.R.M.
; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat
; TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of thei
; FILE REFERENCE: BLANDINE
; CURRENT APPLICATION NUMBER: US/10/238,075
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 0003145
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1472
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-238-075-1472

Query Match          45.8%; Score 44; DB 4; Length 421;
Best Local Similarity 43.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 7; Mismatches 0; Indels 2; Gaps 1;

QY      4 QKVDQFPQ--HGVLK 17
      ||::|||:|:|:|:
Db      58 QKLEDFEPFTHGLIR 73

Search completed: December 12, 2005, 20:19:25
Job time : 80.3793 secs

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; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
; OS:11-074-176-4

```

Query Match	38.5%	Score 37	DB 7	Length 423
Best Local Similarity	37.5%	Pred. No. 26		
Matches	6	Conservative	5	Mismatches 5; Indels 0; Gaps 0;

```
QY      1 IDGQKVDEQFPQHLV 16
          ::|||:|::
Db     379 VDGKRVDDVASLHSL 394
```

```

RESULT 3
US-10-467-657-84
: Sequence 84. Application US/10467657
: Publication No. US20050260581A1
: GENERAL INFORMATION:
: APPLICANT: CHIRON Spa
: APPLICANT: FONTANA Maria Rita
: APPLICANT: PIZZA Mariagrazia
: APPLICANT: MASIGNANI Vega
: APPLICANT: MONACI Elisabetta
: TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/10/0467,657
: CURRENT FILING DATE: 2003-08-11
: PRIOR APPLICATION NUMBER: GB-0103424.8
: PRIOR FILING DATE: 2001-02-12
: NUMBER OF SEQ ID NOS: 9218
: SOFTWARE: SeqWin99, version 1.04
: SEQ ID NO 84
: LENGTH: 2004
: TYPE: PRT
: ORGANISM: Neisseria gonorrhoeae
: US-10-467-657-84

```

Query Match	38.5%	Score 37;	DB 6;	Length 2004;
Best Local Similarity	46.7%	Pred. No. 1.6e+02;		
Matches	7;	Conservative	3;	Mismatches 5;
				Indels 0;
				Gaps 0;

```
OY      1 IDGQKVD EQFPQHGL 15
          :||:| :| | |
Db      1618 VDGKKYE EGFDRQL 16
```

```

RESULT 4
US-10-467-657-6332
Sequence 6332, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Eliaabette
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 6332
LENGTH: 2004
TYPE: PR1

```

US-10-467-657-6322

Query Match	38.5%	Score 37;	DB 6;	Length 2004;
Best Local Similarity	46.7%	Pred. No. 1.6e+02;		
Matches	7;	Conservative	3;	Mismatches 5;
			Indels	0;
			Gaps	0;

```
QY      1 IDGQKNDGEQFPQHGL 15
          :||:|:|:|
Db     1618 VDGKRYEEGFDDQRL 1632
```

```

RESULT 5
US-11-054-515-2449
; Sequence 2449, Application US/11054515
; Publication No. US20050235532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/5580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2449
; LENGTH: 14
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-054-515-2449

```

Query Match	37.5%;	Score 36;	DB 7;	Length 14;
Best Local Similarity	100.0%;	Pred. No. 0.72;		
Matches	6;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

Qy	10	FPQHG	15
Db	7	FPQHG	12

RESULT 6
US-11-054-515-774
; Sequence 774, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyss
; FILE REFERENCE: PF52313
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18


```
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 774
/ LENGTH: 249
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-774
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```
Query Match          37.5% Score 36; DB 7; Length 249;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      10 PPOHGL 15
       |||||
Db      105 PPOHGL 110
```

```
RESULT 7
US-10-793-626-2454
/ Sequence 2454, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMBERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU34800S
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2454
/ LENGTH: 359
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2454
```

```
Query Match          37.5% Score 36; DB 6; Length 359;
Best Local Similarity 41.2%; Pred. No. 32;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
```

```
OY      1 IDGKRVDEQFPOHGLV 17
       :|||:|:|:|:|
Db      65 LDFTGIDIDFKNSGLIK 81
```

```
RESULT 8
US-10-467-657-3816
/ Sequence 3816, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
```

```
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqMan99, version 1.04
/ SEQ ID NO 3816
/ LENGTH: 445
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3816
```

```
Query Match          37.5% Score 36; DB 6; Length 445;
Best Local Similarity 57.1%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
OY      3 GOKRVDEQFPOHGLV 16
       |||||
Db      398 GKCDVEFGVHGV 411
```

```
RESULT 9
US-10-793-626-2212
/ Sequence 2212, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMBERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU34800S
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2212
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2212
```

```
Query Match          37.0% Score 35.5; DB 6; Length 122;
Best Local Similarity 41.2%; Pred. No. 11;
Matches 7; Conservative 5; Mismatches 4; Indels 1; Gaps 1;
```

```
OY      1 IDGKRVDEQFPOHGLV 16
       :|||:|:|:|:|
Db      52 LNKKTLKMIPEHGLV 68
```

```
RESULT 10
US-10-793-626-1922
/ Sequence 1922, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMBERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU34800S
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1922
/ LENGTH: 179
```

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-1922

Query Match 37.0%; Score 35.5; DB 6; Length 179;
Best Local Similarity 41.2%; Pred. No. 17;
Matches 7; Conservative 5; Mismatches 4; Indels 1; Gaps 1;

QY 1 IDGQKVDQFPQH-GLV 16
DB 38 LMGKRLKRMIPHEGLV 54

RESULT 11
US-10-485-517-166
Sequence 166, Application US/10485517
Publication No. US20050256299A1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Foster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629WO
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: PatentIn version 3.1
SEQ ID NO 166
LENGTH: 375
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-485-517-166

Query Match 37.0%; Score 35.5; DB 6; Length 375;
Best Local Similarity 44.4%; Pred. No. 41;
Matches 8; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 2 DGQKVDQF-----POHG 14
DB 242 DGRKAGEFPFAGANPMHG 259

RESULT 12
US-10-793-626-3082
Sequence 3082, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P03480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3082
LENGTH: 724
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3082

Query Match 37.0%; Score 35.5; DB 6; Length 724;
Best Local Similarity 44.4%; Pred. No. 88;
Matches 8; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 2 DGQKVDQF-----POHG 14
DB 591 DGRKAGEFPFAGANPMHG 608

RESULT 13
US-11-129-143-111
Sequence 111, Application US/11129143
Publication No. US20050266518A1
GENERAL INFORMATION:
APPLICANT: BERRY, Alan
APPLICANT: BRETZEL, Werner
APPLICANT: HUMBELIN, Markus
APPLICANT: LOPEZ-ULIBARRI, Rual
APPLICANT: MAYER, Anne F.
APPLICANT: YELISEEV, Alexei A.
TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
FILE REFERENCE: C38435/121966
CURRENT APPLICATION NUMBER: US/11/129,143
CURRENT FILING DATE: 2005-05-13
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PatentIn version 3.1
SEQ ID NO 111
LENGTH: 358
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-11-129-143-111

Query Match 36.5%; Score 35; DB 7; Length 358;
Best Local Similarity 26.7%; Pred. No. 47;
Matches 4; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHGL 15
DB 333 VDKEKIDYDWTKHGI 347

RESULT 14
US-10-131-826A-498
Sequence 498, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Flivaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gunney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P0330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113

Search completed: December 12, 2005, 20:19:49
Job time : 2.94828 secs

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/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059122
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059184
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059352
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 498
/ LENGTH: 444
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-131-826A-498
```

```
Query Match          36.5%; Score 35; DB 6; Length 444;
Best Local Similarity 35.7%; Pred. No. 60;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
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```
QY      5 KVDQEPQHGIVKQ 18
         ||:::|::|
Db      341 KLDQKYMHEHLRQ 354
```

```
RESULT 15
US-11-071-580-1
/ Sequence 1, Application US/11071580
/ Publication No. US20050260708A1
/ GENERAL INFORMATION:
/ APPLICANT: INCYTE GENOMICS, INC.
/ APPLICANT: YUE, Henry
/ APPLICANT: TANG, Y. Tom
/ APPLICANT: BANDMAN, Olga
/ APPLICANT: LAL, Preeti
/ APPLICANT: BAUGHN, Mariah R.
/ APPLICANT: AZIMZAI, Yaida
/ APPLICANT: LU, Dyung Aina M.
/ APPLICANT: YANG, Junming
/ TITLE OF INVENTION: PROTEASES AND PROTEASE INHIBITORS
/ FILE REFERENCE: PF-0727 PCT
/ CURRENT APPLICATION NUMBER: US/11/071,580
/ CURRENT FILING DATE: 2005-03-04
/ PRIOR APPLICATION NUMBER: 60/147,986
/ PRIOR FILING DATE: 1999-08-09
/ PRIOR APPLICATION NUMBER: 60/160,807
/ PRIOR FILING DATE: 1999-10-21
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PERL Program
/ SEQ ID NO 1
/ LENGTH: 444
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No: 088718CD1
US-11-071-580-1
```

```
Query Match          36.5%; Score 35; DB 7; Length 444;
Best Local Similarity 35.7%; Pred. No. 60;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      5 KVDQEPQHGIVKQ 18
         ||:::|::|
Db      341 KLDQKYMHEHLRQ 354
```

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Best Local Similarity 50.0%; Pred. No. 3.4;
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;
QY 4 QKVDQFPQ--HGLVX 17
|||::|||:||||:
Db 58 QKIDEPPELTHGLIK 73

RESULT 3
JC7557
lipidosis - mouse
N:Alternate names: lipidosis-related protein
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C:Accession: J07557
R:Morita-Sato, A.; Hida, A.; Inagawa-Ogashiwa, M.; Wade, M.R.; Sugiyama, K.; Shimizu, J.
Biochem. Biophys. Res. Commun. 279, 62-68, 2000
A:Title: Novel acyl-CoA synthetase in adrenoleukodystrophy target tissues.
A:Reference number: J07557; MUID: 20563802; PMID:1112418
A:Contents: Brain
A:Accession: J07557
A:Molecule type: mRNA
A:Residues: 1-721 <MOR>
A:Cross-references: UNIPROT:Q99PUS; UNIPARC:UPI000017A518
C:Comment: This protein possesses long-chain acyl-CoA synthetase activity and catalyzes
the impairment of fatty acid metabolism in X-linked adrenoleukodystrophy. This
in human X-linked adrenoleukodystrophy.
C:Keywords: adrenoleukodystrophy

Query Match 49.0%; Score 47; DB 2; Length 721;
Best Local Similarity 53.3%; Pred. No. 8.9;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQGL 15
|||::|||:||||:
Db 44 IDGQTLKESKSHGL 58

RESULT 4
AG3034
inositol monophosphatase family protein (imported) - Agrobacterium tumefaciens (strain C
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AG3034
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McCell
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743153
A:Accession: AG3034
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-262 <KOR>
A:Cross-references: UNIPROT:Q8U945; UNIPARC:UPI0000164892; GB:AE008689; PIDN:AAL44693.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3885
A:Map position: linear chromosome
C:Superfamily: suppressor protein subB

Query Match 47.9%; Score 46; DB 2; Length 262;
Best Local Similarity 54.5%; Pred. No. 4.2;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 6 VDEQFPQHGILV 16
::|:|||||:
Db 59 IEEFPPQHGIL 69

. RESULT 5

E98251
similar to mlib1779.29 (probable monophosphatase gene) in mycobacterium leprae [imported]
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: E98251

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: E98251

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-297 <KOR>
A:Cross-references: UNIPROT:Q8U945; UNIPARC:UPI00000237F; GB:AE007870; PIDN:AAK89535.1;
C:Genetics:
A:Gene: AGR L 1926
A:Map position: linear chromosome
C:Superfamily: suppressor protein subB

Query Match 47.9%; Score 46; DB 2; Length 297;
Best Local Similarity 54.5%; Pred. No. 4.8;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 6 VDEQFPQHGILV 16
::|:|||||:
Db 94 IEEFPPQHGIL 104

RESULT 6
RG8V33
regulatory protein SIN3 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein O2385; protein YOL004W
C:Species: Saccharomyces cerevisiae
C:Date: 30-Sep-1991 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: S66686; A36381; A41957; S12068; S22283
R:Hughey, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66685
A:Accession: S66686
A:Molecule type: DNA
A:Residues: 1-1536 <HUG>
A:Cross-references: UNIPROT:P22579; UNIPARC:UPI0000052F61; EMBL:Z74746; NID:G1419766; PII
A:Experimental source: strain S288C
R:Wang, H.; Clark, I.; Nicholson, P.R.; Herxkowitz, I.; Stillman, D.J.
Mol. Cell. Biol. 10, 5927-5936, 1990
A:Title: The Saccharomyces cerevisiae SIN3 gene, a negative regulator of HO, contains for
A:Reference number: A36381; MUID:91042523; PMID:2233725
A:Accession: A36381
A:Molecule type: DNA
A:Residues: 1-510, 'AQ', 511-1536 <WAN>
A:Cross-references: UNIPARC:UPI0000168DAF; GB:M36822; NID:G172093; PIDN:AAA34839.1; PID:G
R:Vidal, M.; Strich, R.; Eposito, R.E.; Gaber, R.F.
Mol. Cell. Biol. 11, 6306-6316, 1991
A:Title: RPD1 (SIN3/UME3) is required for maximal activation and repression of diverse y
A:Reference number: A41957; MUID:92049361; PMID:1944290
A:Accession: A41957
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 227-285,414-441, 'DE',444-472,667-725,1140-1200 <VID>
A:Cross-references: UNIPARC:UPI0000174911; UNIPARC:UPI0000174912; UNIPARC:UPI0000174913;
C:Genetics:
A:Gene: SCD:SIN3; SD11; UME4; RPD1; MIPS:YOL004W
A:Cross-references: SGD:S0005364; MIPS:YOL004W
A:Map position: 15L
C:Superfamily: regulatory protein SIN3
C:Keywords: nucleus; transcription regulation
F;480-519/Region: glutamine-rich

Query Match 46.9%; Score 45; DB 1; Length 1536;
Best Local Similarity 53.3%; Pred. No. 46;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 IDGQKVDQFPQHGL 15
|||:|||||:
Db 1370 IDGTEVDEBFSPGSI 1384

RESULT 7

T42322
hypothetical protein - phage SPPI
C:Species: phage SPPI
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T42322
R:Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A:Title: The complete nucleotide sequence and functional organization of Bacillus subtilis
A:Reference number: 222137; MUID:98094274; PMID:9434185
A:Accession: T42322
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-105 <ALD>
A:Cross-references: UNIPROT:O48482; UNIPARC:UPI000009B161; EMBL:X97918; PIDN:CAA6529.1

Query Match 44.8%; Score 43; DB 2; Length 105;
Best Local Similarity 50.0%; Pred. No. 4.9;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 1 IDGQKVDQFPQHGLVKQ 18
|||:|||||:
Db 5 INGOKIGEMFIERGRVDQ 22

RESULT 8

G83358
probable ATP-binding component of ABC transporter PA2294 [imported] - Pseudomonas aerugi
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: G83358
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lam,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G83358
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-284 <STO>
A:Cross-references: UNIPROT:O91111; UNIPARC:UPI00000C5650; GB:AE004655; GB:AE004091; NID
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2294

Query Match 44.8%; Score 43; DB 2; Length 284;
Best Local Similarity 44.4%; Pred. No. 15;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Oy 1 IDGQKVDQFPQHGLVKQ 18
|||:|||||:
Db 73 VDGSRVGEPSFGKRVFQ 90

RESULT 9

H86717
hypothetical protein yhfB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86717
R:Boletín, A.; Winkler, P.; Mauger, S.; Jallón, O.; Malarme, K.; Weissenbach, J.; Ehrh
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: H86717
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-654 <STO>
A:Cross-references: UNIPROT:O9CH17; UNIPARC:UPI00000C68D4; GB:AE005176; PID:G12723660; P
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: yhfB

Query Match 44.8%; Score 43; DB 2; Length 654;
Best Local Similarity 43.8%; Pred. No. 39;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy 1 IDGQKVDQFPQHGLV 16
|||:|||||:
Db 441 IDHRRDDDFEHALL 456

RESULT 10

D95115
thioredoxin family protein [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: D95115
R:Retellin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: D95115
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-185 <KUR>
A:Cross-references: UNIPROT:O97R36; UNIPARC:UPI0000051693; GB:AE005672; PIDN:AAK75117.1,
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI000

Query Match 43.8%; Score 42; DB 2; Length 185;
Best Local Similarity 46.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 IDGQKVDQFPQ 12
|||:|||||:
Db 112 IQGKTEVQFPQ 123

RESULT 11

H97984
conserved hypothetical protein spr0904 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: H97984
R:Hoshino, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.,
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: H97984
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-191 <KUR>
A:Cross-references: UNIPROT:O8DQ10; UNIPARC:UPI00000E3552; GB:AE007317; PIDN:AAK99708.1,
C:Genetics:
A:Gene: spr0904

Query Match 43.8%; Score 42; DB 2; Length 191;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 IDGQKVDQFPQ 12
|||:|||||:

A;Description: cDNA encoding the *Pisum sativum* mitochondrial pyruvate dehydrogenase E1b

Search completed: December 12, 2005, 20:42:53
Job time : 17.2069 secs

Search completed: December 12, 2005, 20:42:53
Job time : 17.2069 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:41 ; Search time 97.7586 Seconds
(without alignments)
129.907 Million cell updates/sec

Title: US-10-758-165A-11
Perfect score: 96
Sequence: 1 IDGQKVDQEPQHGLVKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	53.1	1089	2	Q8VQF9_XENBV
2	50.5	52.6	1008	2	Q5GR68_ALCXH
3	50	52.1	271	2	Q4LMX1_9MRK
4	50	52.1	283	2	Q88RC3_PSEPK
5	49	51.0	616	2	Q8X7U6_ECO57
6	48	50.0	345	2	Q61Y77_CABR
7	47	49.0	721	2	Q99PUS_MOUSE
8	47	49.0	724	2	Q6ZQ79_MOUSE
9	46	47.9	239	2	Q87979_BOBR
10	46	47.9	239	2	Q7W262_BOBR
11	46	47.9	262	2	Q80945_AGR75
12	46	47.9	273	2	Q74BV7_GEOSL
13	46	47.9	297	2	Q7CTJ2_AGR75
14	46	47.9	408	2	Q8CLM8_YERPE
15	46	47.9	447	2	Q51J08_MAGGR
16	46	47.9	606	2	Q664Y3_YERPS
17	46	47.9	1164	2	Q6SLC8_COCH
18	45	46.9	201	2	Q75B28_ASHGO
19	45	46.9	342	2	Q5KY10_GEOKA
20	45	46.9	694	2	Q9GZ15_GEOSL
21	45	46.9	783	2	Q7KUY7_DROME
22	45	46.9	840	2	Q9VXL1_DROME
23	45	46.9	970	2	Q4GZAB_YTRYP
24	45	46.9	1536	1	SIN3_YEAST
25	44	45.8	169	2	Q8DKM9_SYNEL
26	44	45.8	282	2	Q65WBI_MANSML
27	44	45.8	376	2	Q54LC6_DICDI
28	44	45.8	386	2	Q6TKU8_ECOLI
29	44	45.8	501	2	Q6ABQ0_PROAC
30	44	45.8	524	2	Q4NMW4_9DELT
31	44	45.8	615	2	Q7N9G7_PHOHL

32	44	45.8	617	2	Q72NZ2_LEPIC
33	44	45.8	617	2	Q8F7H8_LEPIN
34	44	45.8	864	2	Q5AZZ9_ASPERILLUS
35	44	45.8	916	2	Q5B315_ASPERILLUS
36	44	45.8	1517	2	Q4T2E2_TETNG
37	44	45.8	105	2	Q48482_BPSPP
38	44	45.8	131	2	Q7RH83_PLAYO
39	43	44.8	201	2	Q8R7E4_THETN
40	43	44.8	235	2	Q71123_BRARE
41	43	44.8	284	2	Q91111_PSEAE
42	43	44.8	314	1	HAT7_ABRTH
43	43	44.8	363	2	Q7Q3M5_ANOGA
44	43	44.8	373	2	Q9ZQY3_MAIZE
45	43	44.8	374	2	Q9ZQY1_MAIZE

ALIGNMENTS

RESULT 1					
ID	Q8VQF9_XENBV	PRELIMINARY;	PRT;	1089 AA.	
AC	Q8VQF9;				
DT	01-MAR-2002 (TrEMBLrel. 20, Created)				
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)				
DE	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)				
GN	Peptide synthetase Xpsa.				
OS	Name=xpsa;				
OC	Xenorhabdus bovienii.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OX	NCBI_TaxID=40576;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=1228;				
RA	Pinon R.A., Thomas C.J.,				
RL	Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.				
DR	EMBL; AF455810; AAL57599.1; -; Genomic DNA.				
DR	HSSP; P14687; 1AMU.				
DR	GO; GO:0048037; F:cofactor binding; IEA.				
DR	GO; GO:0018874; F:ligase activity; IEA.				
DR	GO; GO:0008152; P:metabolism; IEA.				
DR	InterPro; IPR010071; AA_adenyl_dom.				
DR	InterPro; IPR009081; ACP_like.				
DR	InterPro; IPR008873; AMP-bind.				
DR	InterPro; IPR001242; Condensatn.				
DR	InterPro; IPR006163; Phosphateth_bind.				
DR	Pfam; PF00501; AMP-binding; 1.				
DR	Pfam; PF00668; Condensation; 2.				
DR	Pfam; PF00550; PP-binding; 1.				
DR	PRINTS; PR00154; AMPBINDING.				
DR	TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.				
DR	PROSITE; PS50075; ACP_DOMAIN; 1.				
DR	PROSITE; PS00455; AMP_BINDING; 1.				
SQ	SEQUENCE 1089 AA; 122986 MW; FF42C1A12506CBF9 CRC64;				
Query Match					
		53.1%;	Score 51;	DB 2;	Length 1089;
		Best Local Similarity 52.9%;	Pred. No. 26;		
		Matches 9;	Conservative 2;	Mismatches 6;	Indels 0;
				Gaps 0;	
Qy	2	DGQKVDQEPQHGLVKQ	18		
Db	470	DNKTKDKEPQHGLVHQ	486		
RESULT 2					
ID	Q5GR68_ALCXH	PRELIMINARY;	PRT;	1008 AA.	
AC	Q5GR68;				
DT	10-MAY-2005 (TrEMBLrel. 30, Created)				
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)				
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)				
DE	Transposase.				

```

GN Name=tnpA;
OS Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxydans).
OG Plasmid pAB1.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Achromobacter.
OX NCBI_TaxID=85698;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB;
RA Jencova V., Strnad H., Chodora Z., Ulbrich P., Hickey W.J., Paces V.;
RT "Chlorocatechol catabolic enzymes from Achromobacter xylosoxydans
RT AB.";
RL Int. Biodeterior. Biodegradation 54:175-181(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AB;
RA Jencova V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ515144; CA147903.1; -; Genomic_DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004803; F:Transposase activity; IEA.
DR GO; GO:0006313; P:DNA transposition; IEA.
DR InterPro; IPR002513; Transposase_7.
DR Pfam; PF01526; Transposase_7; 1.
KM plasmid.
SQ SEQUENCE 1008 AA; 114816 MW; A9F92682878061E5 CRC64;

Query Match 52.6%; Score 50.5; DB 2; Length 1008;
Best Local Similarity 45.5%; Pred. No. 30;
Matches 10; Conservative 3; Mismatches 0; Indels 9; Gaps 1;

Qy 1 IDGQKVDQFPQHGVLVQ 13
Db 516 VDGKQLLTETAEKVDSEFPQH 537

RESULT 3
Q4LMX1_9BURK PRELIMINARY; PRT; 271 AA.
AC Q4LMX1;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE ABC transporter.
GN ORFNames=Bcen2424DRAFT_2386;
OS Burkholderia cenocepacia H12424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RA US DOE Joint Genome Institute (JGI-PGP);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hamon N., Israeli S., Plutnick S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RA US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT H12424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
SQ SEQUENCE 271 AA; 29686 MW; E9976DF67E02527 CRC64;

Query Match 52.1%; Score 50; DB 2; Length 271;

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Best Local Similarity 50.0%; Pred. No. 9.1;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGVLVQ 18
Db 85 VDEGRVDRPHPRDGLVFQ 102

RESULT 4
Q88RC3_PSEPK PRELIMINARY; PRT; 283 AA.
AC Q88RC3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Nitrate ABC transporter, ATP-binding protein, putative.
GN OrderedCusNames=PP0209;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22423050; PubMed=12534463;
RX DOI=10.1046/j.1462-2920.2002.00366.x;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson M.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzaz A., Uteerback T.R., Rizzo M., Lee K., Kosack D., Meestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hohnselt J., Straetz M., Heim S.,
RA Kewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuenmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AE016774; AAN65842.1; -; Genomic_DNA.
DR HSSP; Q9YGA6; 1G29.
DR TIGR; PP0209; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016867; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Membrane; Nucleotide-binding;
KW Transport.
SQ SEQUENCE 283 AA; 31651 MW; DA1B21FCA2223A4A CRC64;

Query Match 52.1%; Score 50; DB 2; Length 283;
Best Local Similarity 55.6%; Pred. No. 9.5;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFPQHGVLVQ 18
Db 73 VDGQPVDPSPQRCGMVFQ 90

RESULT 5
Q8X7U6_ECOS7 PRELIMINARY; PRT; 616 AA.
AC Q8X7U6; 07AH17;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE No significant matches (Hypothetical protein EC80229).

```

GN OrderedLocuNames=Ec80229, z0260;
OS *Escherichia coli* O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
RN (1)
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL93 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Riese D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackert J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamoustis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.",
RL Nature 409:529-533(2001).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shingawa H.;
RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:111-22(2001).
RN (3)
DR EMBL, AE005174; AAG54529.1; -; Genomic_DNA.
DR EMBL, BA000007; BAB3652.1; -; Genomic_DNA.
DR PIR, E85508; E85508.
DR PIR, E90657; E90657.
DR InterPro: IPR010272; DUF879; bac.
DR Pfam: PF05947; DUF879; 1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 616 AA; 7185 MW; 1FBC0A5128341E30 CRC64;

Query Match 51.0%; Score 49; DB 2; Length 616;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 8; Conservative 6; Mismatches 0; Indels 2; Gaps 1;

QY 4 OKVDEQFPQ--HGLVYK 17
||:||||:||||:
DB 58 OKIEDPEFPELTHGLIK 73

RESULT 6
ID 061Y77 CAEBR PRELIMINARY; PRT; 345 AA.
AC 061Y77-
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG03674.
GN Name=CBG03674;
OS *Caenorhabditis briggsae*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Felodermatidae; Caenorhabditis.
NCBI_TaxID=6238;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, CAC0100016; CAC0129.1; -; Genomic_DNA.
DR GO, GO:0004263; F:chymotrypsin activity; IEA.
DR GO, GO:0004295; F:trypsin activity; IEA.
DR GO, GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001254; Peptidase_S1_S6.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam, PF00089; Trypsin, 1.
DR PRINTS, PR00722; CHYMOTRYPSIN.
DR SMART, SM00020; TYP_SPC_1.
DR PROSITE, PS50240; TRYPSIN_DOM; 1.

KW Hypothetical protein.
SQ SEQUENCE 345 AA; 38450 MW; 744C79ED3DB0408D CRC64;

Query Match 50.0%; Score 48; DB 2; Length 345;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 IDGKRVDEQFPQHG 14
:||||:||||:
DB 80 VSGKRVDEQFPVQHG 93

RESULT 7
ID 099PUS MOUSE PRELIMINARY; PRT; 721 AA.
AC 099PUS-
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Lipidosis-related protein Lipidosin (Mus musculus 2 days pregnant
adult female oviduct cDNA, RIKEN full-length enriched library",
DE clone: E230019603 product: lipidosis-related protein lipidosin, full
insert sequence).
GN Name=Lpd; Synonyms=lpd;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=20563802; PubMed=11112418; DOI=10.1006/dbrc.2000.3897;
RA Moriya-Sato A., Hida A., Inagawa-Ogasawa M., Wada M.R., Sugiyama K.,
RA Shimizu J., Yabuki T., Seyama Y., Hashimoto N.;
RT "Novel acyl-CoA synthetase in adrenoleukodystrophy target tissues.";
RL Biochem. Biophys. Res. Commun. 279:62-68(2000).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN (3)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Pleistmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.W., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,
RA Blake J., Botfield D., Boujunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.D., Bult C., Fletcher C., Fujita M., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta R., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN (4)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,


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CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
DR EMBL: AK129179; BAC97989.1; -; mRNA.
DR MGI: MGI:2385656; Lpd.
DR GO: GO:0003824; F: catalytic activity; IEA.
DR GO: GO:0008152; F: metabolism; IEA.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 1.
DR PRINTS: PR00154; AMPBINDING.
DR PROSITE: PS00455; AMP BINDING; 1.
FT NON TER
SQ SEQUENCE 724 AA; 80795 MW; 3E5875777B7E5560 CRC64;

Query Match
Best Local Similarity 49.0%; Score 47; DB 2; Length 724;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 IDGQKVDQFPQHG 15
Db 47 IDGQTLKSPSHGL 61

RESULT 9
O87979 BORBR PRELIMINARY; PRT; 239 AA.
AC O87979;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein BblP51.06.
GN Name=BblP51.06;
OS Bordetella bronchiseptica (Alcaligenes bronchiseptica).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxId=518;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CN7635E;
RX MEDLINE=99346157; PubMed=10417135;
RA Preston A., Allen A.G., Cadisch J., Thomas R., Stevens K.,
RA Churcher C.M., Badcock K.L., Parkhill J., Barrett B., Maskell D.J.,
RA "Genetic Basis for lipopolysaccharide O-antigen biosynthesis in
RA Bordetella.";
RT Infect. Immun. 67:3763-3767(1999).
DR EMBL: AJ007747; CA07645.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 239 AA; 27358 MW; 79CE20279B9C08C2 CRC64;

Query Match
Best Local Similarity 53.8%; Score 46; DB 2; Length 239;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 3 GQKVDQFPQHG 15
Db 182 GQYDEKFPFRHGI 194

RESULT 10
O7W262 BORPA PRELIMINARY; PRT; 239 AA.
AC O7W262;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein wBmp.
GN Name=wBmp; OrderedLocustNames=BPP0129;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxId=519;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12822 / ATCC BAA-587;
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RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Atkin R., Baker S., Basham D., Bason N., Chevreton I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leach S., Moul S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL: BX640423; CAE39870.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 239 AA; 27359 MW; F5AC4AB7759C0622 CRC64;

Query Match
Best Local Similarity 47.9%; Score 46; DB 2; Length 239;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 3 GQKVDQFPQHG 15
Db 182 GQYDEKFPFRHGI 194

RESULT 11
O8U945 AGRTS PRELIMINARY; PRT; 262 AA.
AC O8U945;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Inositol monophosphatase family protein.
GN OrderedLocustNames=Atu3885;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxId=176299;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Dupont;
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Sebubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
RA Chen Y., Paulsen I.T., Bisen J.A., Karp P.D., Bove D. St.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kuyavin T., Levy R., Li M.-J., McClelland B., Palmeri A.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Kreppan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
DR EMBL: AE009319; AAL44693.1; -; Genomic_DNA.
DR PIR: AG3034;
DR PIR: E98251; E98251.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0004437; F:inositol or phosphatidylinositol phosphatase. . .; IEA.
DR InterPro: IPR011809; His_9_proposed.
DR InterPro: IPR000760; Inositol_P.
DR Pfam: PF00459; Inositol_P_1.
DR PRODOM: PD023420; Inositol_P_1.
DR TIGRPFAM: TIGR02067; his_9_proposed; 1.
DR PROSITE: PS00629; IMP_1; 1.
KW Complete proteome.
SQ SEQUENCE 262 AA; 28813 MW; 5E7607DC3A3E431D CRC64;

Query Match
Best Local Similarity 47.9%; Score 46; DB 2; Length 262;
```

Best Local Similarity 54.5%; Pred. No. 41;
Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VDEQPOHGLV 16
:::|||||:
Db 59 IEEFPQHGIL 69

RESULT 12

074BV7 GEOSL PRELIMINARY; PRT; 273 AA.

DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Transport-associated domain protein.

GN OrderedLocustNames=GSU1925;

OS Geobacter sulfurreducens.

OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;

OC Geobacteraceae; Geobacter.

OX NCBI_TaxID=35554;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PCA / ATCC 51573;

RX PubMed=14671304; DOI=10.1126/science.1088727;

RA Heldeberg J.F., Wu D., Ward N.L., Beaman M.J., Dodson R.J.,

RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,

RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,

RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forbarger H.A.,

RA Van Aken S.E., Lovley D.R., Fraser C.M.;

RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface

RT environments."

RL Science 302:1967-1969(2003).

DR EMBL; AEO17180; AAR35301.1; -, Genomic_DNA.

DR TIGR; GSU1925; -, Genomic_DNA.

DR InterPro; IPR007055; TAD.

DR Pfam; PF04972; BON; 1.

DR PROSITE; PS50914; BON; 1.

KM Complete proteome.

SO SEQUENCE 273 AA; 31128 MW; 0449EB5A7B1A346 CRC64;

Query Match 47.9%; Score 46; DB 2; Length 273;

Best Local Similarity 44.4%; Pred. No. 43;

Matches 8; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 IDGKXVDEQPOHGLV 18
:::|||||:
Db 30 VDGKRIAEIAPRYGLDKE 47

RESULT 13

07CTU2 AGRTS PRELIMINARY; PRT; 297 AA.

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DE AGR_L_1926P.

GN OrderedLocustNames=AGR_L_1926;

OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.

OX NCBI_TaxID=176299;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Cereon;

RX MEDLINE=1608551; PubMed=11743194; DOI=10.1126/science.1066803;

RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,

RA Houtz B., Goldman B.S., Cao Y., Akenazi M., Halling C., Mullin L.,

RA Houtz K., Gordon J., Vandin M., Tatchouk O., Epp A., Liu F.,

RA Wolfram C., Allinger W., Doughy D., Scott C., Lappas C., Markelz B.,

RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,

RA Cielo C., Slater S.;

RT "Genome sequence of the plant pathogen and biotechnology agent

RT Agrobacterium tumefaciens C58."

RL Science 294:2323-2328(2001).

DR EMBL; AEO08295; AAK89535.1; -, Genomic DNA.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR GO; GO:0004437; F:inositol or phosphatidylinositol phosphatase. . .; IEA.

DR InterPro; IPR011809; His_9_proposed.

DR InterPro; IPR000760; Inositol P.

DR Pfam; PF00459; Inositol P. 1.

DR PRINTS; PR00378; INOSPHTRASE.

DR Prodom; PD023420; Inositol P. 1.

DR TIGRFAMs; TIGR02067; his_9_proposed; 1.

DR PROSITE; PS00629; IMP_1; 1.

SO SEQUENCE 297 AA; 33042 MW; 83E08201E4508B1E CRC64;

Query Match 47.9%; Score 46; DB 2; Length 297;

Best Local Similarity 54.5%; Pred. No. 47;

Matches 6; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VDEQPOHGLV 16
:::|||||:
Db 94 IEEFPQHGIL 104

RESULT 14

08CLW8 YERPE

ID 08CLW8 YERPE PRELIMINARY; PRT; 408 AA.

AC 08CLW8;

DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DE Hypothetical.

GN OrderedLocustNames=Y0040;

OS Yersinia pestis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Yersinia.

OX NCBI_TaxID=632;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=KIMS / Biovar Medisevalis;

RX MEDLINE=22137863; PubMed=12142430;

RA DOI=10.1128/JB.184.16.4601-4611.2002;

RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,

RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,

RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,

RA Perry R.D.;

RT "Genome sequence of Yersinia pestis KIM."

RL J. Bacteriol. 184:4601-4611(2002).

DR EMBL; AEO13605; AAM83635.1; -, Genomic_DNA.

DR InterPro; IPR010272; DUF879_bac.

DR Pfam; PF05947; DUF879; 1.

KM Hypothetical protein.

SO SEQUENCE 408 AA; 46728 MW; 7E02D4E0003D39DB CRC64;

Query Match 47.9%; Score 46; DB 2; Length 408;

Best Local Similarity 53.3%; Pred. No. 66;

Matches 8; Conservative 5; Mismatches 0; Indels 2; Gaps 1;

Qy 4 QXVDEQPOHGLV 16
:::|||||:
Db 57 EXIDDQFPELTHGL 71

RESULT 15

051J08 MAGGR

ID 051J08 MAGGR PRELIMINARY; PRT; 447 AA.

AC 051J08;

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Hypothetical protein.
 GN ORFNames=MG09895.4;
 OS Magnaporthe grisea 70-15.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
 CX NCBI_taxid=242507;

RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=70-15;
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Alt-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Arachchi H., Armbruster J., Bachantang P., Baldwin J., Barry A.,
 RA Bayul T., Biltsheteyn B., Bloom T., Biye J., Boguslavskiy L.,
 RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheahatang Y., Citroen M.,
 RA Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorrie L., Dufley N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Garin G., Gnerre S.,
 RA Gnrke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Horan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamel M., Kamat A., Kamysseis W., Karlsson E.,
 RA Kells C., Kieu A., Kismet P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-coh K., Liu X., Lokitsang T., Lokitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marabella R., Maru K., Matthews C., Mancini E.,
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Menus L.,
 RA Mesirov J., Mihailev A., Minova T., Mikkelsen T., Mienga V., Moru K.,
 RA Moses J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Rector R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schubach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnuez C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stebson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tenzing P., Testaye S., Theodore J., Thoulitsang Y., Topham K.,
 RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Zander E.;
 RT "The genome sequence of Magnaporthe grisea."
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL: AACU01001744; EAA46674.1; -, Genomic_DNA.
 DR Hypothetical protein.
 KW SEQUENCE 447 AA; 48757 MW; 9BD8DC0B87A2F1CB CRC64;

Query Match 47.9%; Score 46; DB 2; Length 447;
 Best Local Similarity 40.7%; Pred. No. 72;
 Matches 11; Conservative 4; Mismatches 2; Indels 10; Gaps 1;

OY 2 DGQ-----KVDEQFPQHGIVKQ 18
 ||| :||| :||| :||| :|||
 Db 27 DGQTTVTKSTSDDELDDQEPGTGIVKQ 53

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:53:01 ; Search time 181 Seconds
(without alignments)
41.268 Million cell updates/sec

Title: US-10-758-165A-16
Perfect score: 83
Sequence: 1 EDGQVMDVLDSTASTTQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 808799

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*
9: Geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	17	8	ADRI0616 Human IGE
2	51	61.4	13	3	AAB25916 PI mimoto
3	51	61.4	13	3	AAB25914 PI mimoto
4	51	61.4	13	3	AAB25917 PI mimoto
5	51	61.4	13	3	AAB20872 Antialler
6	51	61.4	13	4	AAB51028 IGE pep1
7	51	61.4	13	4	AAB16642 Peptide P
8	51	61.4	13	4	AAB16639 Peptide P
9	51	61.4	13	4	AAB16641 Peptide P
10	51	61.4	13	5	AAB700312 Human IGE
11	51	61.4	13	5	AAB700224 Human IGE
12	51	61.4	13	5	AAB700226 Human IGE
13	51	61.4	16	5	AAB700542 Human IGE
14	51	61.4	9	3	AAB25907 IGE C-peps
15	47	56.6	9	3	AAB20867 Immunoglo
16	47	56.6	9	4	AAB51023 IGE pep1
17	47	56.6	9	4	AAB16632 Peptide P
18	47	56.6	9	5	AAB700217 Human IGE
19	47	56.6	9	7	ADE10893 Chimeric
20	47	56.6	9	7	ADM39798 N meningi
21	47	56.6	9	8	ADG64140 Recombina
22	47	56.6	9	8	ADP73528 Immunoglo
23	47	56.6	9	8	ADRI2820 Human IGE
24	47	56.6	10	3	AAB25929 PI mimoto

25	47	56.6	10	4	AAU16654 Peptide P
26	47	56.6	10	5	ABJ00228 Human IGE
27	47	56.6	10	6	AAE35062 Immunoglo
28	47	56.6	10	7	ADE10902 Chimeric
29	47	56.6	10	7	ADM39807 N meningi
30	47	56.6	10	8	ADG64149 Recombina
31	47	56.6	10	8	ADP73537 Immunoglo
32	47	56.6	10	8	ADRI2829 Human IGE
33	47	56.6	14	5	ABJ00540 Human IGE
34	43	51.8	9	6	AAE35076 Human Imm
35	42	50.6	9	6	AAE35082 Human Imm
36	41	49.4	10	6	AAE35057 Immunoglo
37	37	44.6	13	5	ABJ00541 Human IGE
38	34	41.0	7	3	AAB25923 PI mimoto
39	34	41.0	7	4	AAU16648 Peptide P
40	34	41.0	7	5	ABJ00227 Human IGE
41	34	41.0	17	6	ADA23403 Alzheimer
42	34	41.0	17	7	ADD23080 Breast ca
43	33	39.8	17	4	AAU68511 Human Exp
44	33	39.8	17	4	AAU68255 Human Bre
45	33	39.8	17	4	AAU68364 Human Bre

ALIGNMENTS

```

RESULT 1
ID ADR10616 standard; peptide, 17 AA.
XX
AC ADR10616;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 16.
XX
KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW human.
XX
OS Homo sapiens.
XX
PN WO2004065936-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.
XX
(UNNC-) UNIV NORTH CAROLINA STATE.
XX
Hammerberg B;
XX
WPI; 2004-593545/57.
XX
PT Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
Example 6; Page 9; 14pp; English.
XX
The present invention relates to a novel monoclonal antibody (I) that
specifically binds to a mammalian IGE epitope, where the epitope is
between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
(CC (I) is useful for testing an allergen reactivity of an IGE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

```

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IgE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IgE. The present sequence is the
CC human IgE 3.76 recognition site.

XX Sequence 17 AA;

Query Match 100.0%; Score 83; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVLDSTASTQ 17
Db 1 EDGQVMDVLDSTASTQ 17

RESULT 2
AAB25916
ID AAB25916 standard; peptide; 13 AA.

AC AAB25916;

DT 05-JAN-2001 (first entry)

DE P1 mimotope peptide P15P SEQ ID NO:10.

XX Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;
KM allergic disease; immunophylaxis; immunotherapy; antiallergic;
KM immunosuppressive; vaccine; histamine release inhibitor; immunogen;
KM allergy; atopy.

XX Homo sapiens.

PN W0200050460-A1.

PD 31-AUG-2000.

PF 22-FEB-2000; 2000WO-EP001455.

PR 25-FEB-1999; 99GB-00004405.

PR 29-MAR-1999; 99GB-00007151.

PR 07-MAY-1999; 99GB-00010537.

PR 07-MAY-1999; 99GB-00010538.

PR 07-AUG-1999; 99GB-00018594.

PR 07-AUG-1999; 99GB-00018603.

PR 07-SEP-1999; 99GB-00021046.

PR 07-SEP-1999; 99GB-00021047.

PR 29-OCT-1999; 99GB-00025619.

PR 23-NOV-1999; 99GB-00027698.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
(PEPT-) PEPTIDE THERAPEUTICS LTD.

PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;
PI Randall R, Turnell WG, Van Mechelen MP, Vinals Y De Basolese;

XX WPI; 2000-572073/53.

PT Peptides useful for treating, preventing and ameliorating allergic
PT diseases, comprising an isolated surface exposed group of a specific
PT domain from immunoglobulin E.

DR Disclosure; Page 9; 129pp; English.

XX The present invention describes a peptide (I) comprising an isolated
CC surface exposed group/epitope (EI) of C-epsilon-2 domain (D) of
CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an
CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)
CC for treating allergies comprising (II); (3) a ligand (IV) capable of
CC recognising EI; (4) a pharmaceutical composition (PC) comprising (IV);
CC (5) a peptide (1a) capable of being recognised by (IV); (6) an immunogen
CC (1ia) comprising (1a); and (7) producing (III) by producing (II). (I) can

CC have antiallergic and immunosuppressive activities, and can be used as a
CC vaccine and histamine release inhibitor. (I), (II) and (III) are useful
CC in medicine and in the manufacture of medicaments for treating and
CC preventing allergies. (IV) is useful for identifying mimotopes of P1, in
CC medicine and also in manufacturing medicaments for treating allergies.

CC (1) is useful in diagnostics and in the affinity purification of
CC circulating anti-IgE antibodies from blood. (1), (II) and PC are useful
CC for treating a patient susceptible to or suffering from allergies. (IV)
CC is also useful in diagnosing atopy. AAB25907 to AAB26099 represent
CC peptide sequences which are used in the exemplification of the present
CC invention

XX Sequence 13 AA;

Query Match 61.4%; Score 51; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDL 10
Db 3 EDGQVMDVDL 12

RESULT 3
AAB25914
ID AAB25914 standard; peptide; 13 AA.

AC AAB25914;

DT 05-JAN-2001 (first entry)

DE P1 mimotope peptide PT15 SEQ ID NO:8.

XX Epitope; mimotope; human; immunoglobulin E; IgE; C-epsilon-2 domain;
KM allergic disease; immunophylaxis; immunotherapy; antiallergic;
KM immunosuppressive; vaccine; histamine release inhibitor; immunogen;
KM allergy; atopy.

XX Homo sapiens.

PN W0200050460-A1.

PD 31-AUG-2000.

PF 22-FEB-2000; 2000WO-EP001455.

PR 25-FEB-1999; 99GB-00004405.

PR 29-MAR-1999; 99GB-00007151.

PR 07-MAY-1999; 99GB-00010537.

PR 07-MAY-1999; 99GB-00010538.

PR 07-AUG-1999; 99GB-00018594.

PR 07-AUG-1999; 99GB-00018603.

PR 07-SEP-1999; 99GB-00021046.

PR 07-SEP-1999; 99GB-00021047.

PR 29-OCT-1999; 99GB-00025619.

PR 23-NOV-1999; 99GB-00027698.

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
(PEPT-) PEPTIDE THERAPEUTICS LTD.

PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;
PI Randall R, Turnell WG, Van Mechelen MP, Vinals Y De Basolese;

XX WPI; 2000-572073/53.

PT Peptides useful for treating, preventing and ameliorating allergic
PT diseases, comprising an isolated surface exposed group of a specific
PT domain from immunoglobulin E.

PS Claim 14; Page 9; 129pp; English.

XX The present invention describes a peptide (I) comprising an isolated
CC surface exposed group/epitope (EI) of C-epsilon-2 domain (D) of

CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an
 CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)
 CC for treating allergies comprising (II); (3) a ligand (IV) capable of
 CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);
 CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen
 CC (IIa) comprising (Ia); and (7) producing (III) by producing (II). (I) can
 CC have anti-allergic and immunosuppressive activities, and can be used as a
 CC vaccine and histamine release inhibitor. (I), (II) and (III) are useful
 CC in medicine and in the manufacture of medicaments for treating and
 CC preventing allergies. (IV) is useful for identifying mitotopes of P1, in
 CC medicine and also in manufacturing medicaments for treating allergies.
 CC (I) is useful in diagnosis and in the affinity purification of
 CC circulating anti-IgE antibodies from blood. (I), (III) and PC are useful
 CC for treating a patient susceptible to or suffering from allergies. (IV)
 CC is also useful in diagnosing atopy. AAB25907 to AAB26099 represent
 CC peptide sequences which are used in the exemplification of the present
 CC invention

CC Sequence 13 AA;
 CC
 CC SQ

Query Match 61.4%; Score 51; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.063; Mismatches 0; Gaps 0;
 Matches 10; Conservative 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDL 10
 |||||
 Db 3 EDGQVMDVDL 12

RESULT 4
 AAB25917
 ID AAB25917 standard; peptide; 13 AA.
 AC AAB25917;
 DT 05-JAN-2001 (first entry)
 DE P1 mimotope peptide P15q SEQ ID NO:11.
 XX
 KW Epitope; mimotope; human; immunoglobulin E; IgE; C-epitlon-2 domain;
 KW allergic disease; immunotrophylaxis; immunotherapy; antiallergic;
 KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;
 KW allergy; atopy.
 XX
 OS Homo sapiens.
 XX
 PN WO200050460-A1.
 XX
 PD 31-AUG-2000.
 XX
 PF 22-FEB-2000; 2000WO-EP001455.
 XX
 PR 25-FEB-1999; 99GB-00004405.
 PR 29-MAR-1999; 99GB-00007151.
 PR 07-MAY-1999; 99GB-00010537.
 PR 07-MAY-1999; 99GB-00010538.
 PR 07-AUG-1999; 99GB-00018594.
 PR 07-AUG-1999; 99GB-00018603.
 PR 07-SEP-1999; 99GB-00021046.
 PR 07-SEP-1999; 99GB-00021047.
 PR 29-OCT-1999; 99GB-00025619.
 PR 23-NOV-1999; 99GB-00027698.
 XX
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
 XX
 PI Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;
 PI Randall R, Turnell WG, Van Mechelen MP, Vinals Y De Baasolac;
 XX
 DR WPI; 2000-572073/53.
 XX
 PT Peptides useful for treating, preventing and ameliorating allergic
 PT diseases, comprising an isolated surface exposed group of a specific

PT domain from immunoglobulin E.
 XX
 XX Claim 14; Page 9; 129pp; English.
 XX
 CC The present invention describes a peptide (I) comprising an isolated
 CC surface exposed group/epitope (E1) of C-epitlon-2 domain (D) of
 CC immunoglobulin E (IgE), or its mimotope. Also described are: (1) an
 CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)
 CC for treating allergies comprising (II); (3) a ligand (IV) capable of
 CC recognising E1; (4) a pharmaceutical composition (PC) comprising (IV);
 CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen
 CC (IIa) comprising (Ia); and (7) producing (III) by producing (II). (I) can
 CC have anti-allergic and immunosuppressive activities, and can be used as a
 CC vaccine and histamine release inhibitor. (I), (II) and (III) are useful
 CC in medicine and in the manufacture of medicaments for treating and
 CC preventing allergies. (IV) is useful for identifying mitotopes of P1, in
 CC medicine and also in manufacturing medicaments for treating allergies.
 CC (I) is useful in diagnosis and in the affinity purification of
 CC circulating anti-IgE antibodies from blood. (I), (III) and PC are useful
 CC for treating a patient susceptible to or suffering from allergies. (IV)
 CC is also useful in diagnosing atopy. AAB25907 to AAB26099 represent
 CC peptide sequences which are used in the exemplification of the present
 CC invention

CC Sequence 13 AA;
 CC
 CC SQ

Query Match 61.4%; Score 51; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.063; Mismatches 0; Gaps 0;
 Matches 10; Conservative 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDL 10
 |||||
 Db 3 EDGQVMDVDL 12

RESULT 5
 AAB20872
 ID AAB20872 standard; peptide; 13 AA.
 AC AAB20872;
 DT 03-JAN-2001 (first entry)
 DE Antiallergy peptide mimotope sequence SEQ ID NO:10.
 XX
 KW Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier;
 KW prostate cancer; Haemophilus influenzae; vaccine; infectious disease;
 KW malaria; cytostatic; antiallergic; nootropic; neuroprotective;
 KW protozoacide; Alzheimer's disease; allergy.
 XX
 OS Homo sapiens.
 XX
 PN WO200050077-A1.
 XX
 PD 31-AUG-2000.
 XX
 PF 22-FEB-2000; 2000WO-EP001457.
 XX
 PR 25-FEB-1999; 99GB-00004405.
 PR 25-FEB-1999; 99GB-00004408.
 PR 25-FEB-1999; 99GB-00004412.
 PR 13-AUG-1999; 99GB-00019260.
 XX
 PA (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Coste M, Lobet Y, Van-Mechelen MP, Verriest C;
 XX
 DR WPI; 2000-572040/53.
 XX

PT Immunogens and vaccine comprising the immunogen useful for preventing and
PT treating infectious diseases e.g. malaria and chronic disease e.g.
PT cancer, comprises peptide and carrier from protein D of influenzae.
XX
XX
PS Claim 10; Page 38; 53pp; English.
XX
CC The present invention describes an immunogen (I) comprising a peptide
CC (1a) and a carrier (1b) derived from protein D of Haemophilus influenzae
CC or its fragment. Also described are: (1) a vaccine comprising (I), and an
CC excipient; (2) preparation of (I), comprising conjugating a peptide to
CC protein D or its fragment; and (3) preparation of a vaccine of (1),
CC comprising formulating (I) with an excipient. (I) has cytostatic,
CC antiallergic, neutrotropic, neuroprotective and protozoacide activities. (I)
CC and the vaccine are useful for the manufacture of a medicament for
CC preventing and treating infectious diseases such as malaria or chronic
CC disease such as cancer, Alzheimer's disease or allergy in a patient.
CC Unlike prior art immunogens, (I) induces high levels of antipeptide
CC immune responses while inducing a moderate humoral response against the
CC carrier. The present sequence represents a specifically claimed mimotope
CC peptide sequence, which can be used in an immunogen of the present
CC invention
XX
XX Sequence 13 AA;
SQ
Query Match 61.4%; Score 51; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 EDGQVMDVDL 10
Db 3 EDGQVMDVDL 12
RESULT 6
AAB51028
ID AAB51028 standard; peptide; 13 AA.
XX
AC AAB51028;
XX
DT 21-MAR-2001 (first entry)
XX
DE IGE peptide #6.
XX
KW Vaccine; immunoglobulin E; IGE; anti-allergy.
XX
OS Mammalia.
XX
PN WO200074716-A2.
XX
PD 14-DEC-2000.
XX
PF 06-JUN-2000; 2000MO-EP005164.
XX
PR 08-JUN-1999; 99GB-00013327.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Prieels J;
XX
DR WPI; 2001-091150/10.
XX
PT New vaccine comprising allergy peptides linked by an inert carrier,
PT useful for boosting an anti-allergy immune response in an individual
PT susceptible to an allergic response.
XX
PS Claim 5; Page 20; 26pp; English.
XX
CC The present invention relates to a composition comprising allergy
CC peptides linked by an inert carrier. The allergy peptides are derived
CC from immunoglobulin E (IGE) or IGE receptor. The present peptide is one
CC such peptide from IGE. The composition is useful as a vaccine or for
CC manufacturing a medicament for the prophylaxis or treatment of allergy.
CC In particular, for boosting an anti-allergy immune response in an

CC individual susceptible to an allergic response
XX
XX Sequence 13 AA;
SQ
Query Match 61.4%; Score 51; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 EDGQVMDVDL 10
Db 3 EDGQVMDVDL 12
RESULT 7
AAU16642
ID AAU16642 standard; peptide; 13 AA.
XX
AC AAU16642;
XX
DT 07-NOV-2001 (first entry)
XX
DE Peptide P15q derived as mimotope of Cepsilon2 region of human IGE.
XX
KW Human; linkage technology; conjugated compound; carrier vehicle; epitope;
KW Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E; IGE mediated disease;
KW antibody response.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN WO200145745-A2.
XX
PD 28-JUN-2001.
XX
PF 21-DEC-2000; 2000MO-GB004935.
XX
PR 21-DEC-1999; 99GB-00030233.
XX
PR 22-FEB-2000; 2000GB-00004096.
XX
PR 22-AUG-2000; 2000GB-00020707.
XX
PR 22-AUG-2000; 2000GB-00020708.
XX
PA (ACAM-) ACAM-BIS RES LTD.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Flynn N, Johnson T;
XX
DR WPI; 2001-521967/57.
XX
PT A linkage comprising an immunogenic conjugate useful treatment of IGE
PT mediated diseases.
XX
PS Example 4; Page 21; 48pp; English.
XX
CC The present invention relates to linkage methodology for use in the
CC conjugation of compounds (e.g. peptides) to carrier vehicles (e.g.
CC macromolecules, polymers, dendrimers, proteins) to produce biological and
CC immunological constructs. The invention provides a method for linking an
CC epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a
CC pharmaceutical composition or a vaccine. The invention describes peptides
CC derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4
CC regions of human immunoglobulin E (IGE) which are used to produce
CC conjugated compounds. The compounds or compositions of the invention are
CC useful in the manufacture of a medicament for the treatment of IGE
CC mediated diseases. The invention allows for controlled conjugation of a
CC peptide epitope (antigen) to a protein so as to form an immunogenic
CC conjugate which may be able to raise a protective antibody response in an
CC animal or human patient. AAU16632-AAU16913 represent peptides derived
CC from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human
CC IGE
XX
SQ Sequence 13 AA;
Query Match 61.4%; Score 51; DB 4; Length 13;

ID ABJ00312 standard; peptide; 13 AA.
XX
AC ABJ00312;
XX
DT 02-SEP-2002 (first entry)
XX
DE Human IGE cyclic immunogenic peptide SEQ ID NO: 96.
XX
KM Immunogen; human; IGE; immunoglobulin E; allergy; thio-ether linkage;
KW vaccine; antiallergic; cyclic.
XX
OS Homo sapiens.
XX
PN WO200216409-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-EP009576.
XX
PR 22-AUG-2000; 2000GB-00020717.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
PI Friede M, Mason S, Turnell WG, Vinals Y Baeso1sc;
XX WPI; 2002-489648/52.
DR
PT Conjugate for use in vaccine for treatment of allergy, comprises
PT disulfide bridge cyclized peptide and immunogenic carrier.
XX
PS Claim 4; Page 11; 45pp; English.
XX
CC The present invention relates to conjugates suitable for use in vaccines,
CC where the conjugate comprises a disulphide bridge cyclised peptide and an
CC immunogenic carrier. The vaccines can be used in the treatment of
CC allergies. The present sequence is a cyclic peptide immunogen derived
CC from human immunoglobulin E (IGE) suitable for use in the invention
XX
SQ Sequence 13 AA;
XX
Query Match 61.4%; Score 51; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EDGQVMDVDL 10
Db 3 EDGQVMDVDL 12
XX
RESULT 11
ABJ00224
ID ABJ00224 standard; peptide; 13 AA.
XX
AC ABJ00224;
XX
DT 02-SEP-2002 (first entry)
XX
DE Human IGE immunogenic peptide SEQ ID NO: 8.
XX
KM Immunogen; human; IGE; immunoglobulin E; allergy; thio-ether linkage;
KW vaccine; antiallergic.
XX
OS Homo sapiens.
XX
PN WO200216409-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-EP009576.
XX
PR 22-AUG-2000; 2000GB-00020717.
XX

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
PI Friede M, Mason S, Turnell WG, Vinals Y Baeso1sc;
XX WPI; 2002-489648/52.
DR
XX
XX Conjugate for use in vaccine for treatment of allergy, comprises
PT disulfide bridge cyclized peptide and immunogenic carrier.
XX
PS Claim 4; Page 9; 45pp; English.
XX
CC The present invention relates to conjugates suitable for use in vaccines,
CC where the conjugate comprises a disulphide bridge cyclised peptide and an
CC immunogenic carrier. The vaccines can be used in the treatment of
CC allergies. The present sequence is a peptide immunogen derived from human
CC immunoglobulin E (IGE) suitable to be cyclised and used in the invention
XX
SQ Sequence 13 AA;
XX
Query Match 61.4%; Score 51; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EDGQVMDVDL 10
Db 3 EDGQVMDVDL 12
XX
RESULT 12
ABJ00226
ID ABJ00226 standard; peptide; 13 AA.
XX
AC ABJ00226;
XX
DT 02-SEP-2002 (first entry)
XX
DE Human IGE immunogenic peptide SEQ ID NO: 10.
XX
KM Immunogen; human; IGE; immunoglobulin E; allergy; thio-ether linkage;
KW vaccine; antiallergic.
XX
OS Homo sapiens.
XX
PN WO200216409-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-EP009576.
XX
PR 22-AUG-2000; 2000GB-00020717.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
PI Friede M, Mason S, Turnell WG, Vinals Y Baeso1sc;
XX WPI; 2002-489648/52.
DR
XX
XX Conjugate for use in vaccine for treatment of allergy, comprises
PT disulfide bridge cyclized peptide and immunogenic carrier.
XX
PS Claim 4; Page 9; 45pp; English.
XX
CC The present invention relates to conjugates suitable for use in vaccines,
CC where the conjugate comprises a disulphide bridge cyclised peptide and an
CC immunogenic carrier. The vaccines can be used in the treatment of
CC allergies. The present sequence is a peptide immunogen derived from human
CC immunoglobulin E (IGE) suitable to be cyclised and used in the invention
XX
SQ Sequence 13 AA;
XX
Query Match 61.4%; Score 51; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGQVMDVDL 10
DB 3 EDGQVMDVDL 12

RESULT 13

ABJ00542 ID ABJ00542 standard; peptide; 16 AA.

XX AC ABJ00542;

DT 02-SEP-2002 (first entry)

DE Human IGE cyclic immunogenic peptide SEQ ID NO: 326.

XX KW Immunogen; human; IGE; immunoglobulin E; allergy; thio-ether linkage;
XX KV vaccine; anti-allergic; cyclic.

XX OS Homo sapiens.

XX PN WO200216409-A2.

XX PD 28-FEB-2002.

XX PE 17-AUG-2001; 2001WO-EP009576.

XX PR 22-AUG-2000; 2000GB-00020717.

XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
(PEPT-) PEPTIDE THERAPEUTICS LTD.

XX P1 Friede M, Mason S, Turnell WG, Vinals Y BassolsC;

XX DR WPI; 2002-489648/52.

PT Conjugate for use in vaccine for treatment of allergy, comprises
PT disulfide bridge cyclized peptide and immunogenic carrier.

XX PS Claim 4; Page 16; 45pp; English.

CC The present invention relates to conjugates suitable for use in vaccines,
CC where the conjugate comprises a disulfide bridge cyclised peptide and an
CC immunogenic carrier. The vaccines can be used in the treatment of
CC allergies. The present sequence is a cyclic peptide immunogen derived
CC from human immunoglobulin E (IGE) suitable for use in the invention

XX SQ Sequence 16 AA;

Query Match 61.4%; Score 51; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGQVMDVDL 10
DB 3 EDGQVMDVDL 12

RESULT 14

AAB25907 ID AAB25907 standard; peptide; 9 AA.

XX AC AAB25907;

DT 05-JAN-2001 (first entry)

DE IGE C-epsilon-2 domain surface exposed epitope peptide P1 SEQ ID NO:1.

XX KW Epitope; mimotope; human; immunoglobulin E; IGE; C-epsilon-2 domain;
KW allergic disease; immunotherapy; anti-allergic;
KW immunosuppressive; vaccine; histamine release inhibitor; immunogen;

KW allergy; atopy.

XX OS Homo sapiens.

XX PN WO200050460-A1.

XX PD 31-AUG-2000.

XX PF 22-FEB-2000; 2000WO-EP001455.

XX PR 25-FEB-1999; 99GB-00004405.

XX PR 29-MAR-1999; 99GB-00007151.

XX PR 07-MAY-1999; 99GB-00010537.

XX PR 07-MAY-1999; 99GB-00010538.

XX PR 07-AUG-1999; 99GB-00018594.

XX PR 07-AUG-1999; 99GB-00018603.

XX PR 07-SEP-1999; 99GB-00021046.

XX PR 07-SEP-1999; 99GB-00021047.

XX PR 29-OCT-1999; 99GB-00025619.

XX PR 23-NOV-1999; 99GB-00027698.

XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
(PEPT-) PEPTIDE THERAPEUTICS LTD.

XX P1 Dyson M, Friede M, Greenwood J, Hewitt E, Lamont A, Mason S;
Randall R, Turnell WG, Van Mechelen MP, Vinals Y De BassolsC;

XX DR WPI; 2000-572073/53.

XX PT Peptides useful for treating, preventing and ameliorating allergic
XX diseases, comprising an isolated surface exposed group of a specific
XX domain from immunoglobulin E.

XX PS Claim 2; Page 5; 129pp; English.

CC The present invention describes a peptide (I) comprising an isolated
CC surface exposed group/epitope (EI) of C-epsilon-2 domain (D) of
CC immunoglobulin E (IGE), or its mimotope. Also described are: (1) an
CC immunogen (II) for treating allergy comprising (I); (2) a vaccine (III)
CC for treating allergies comprising (II); (3) a ligand (IV) capable of
CC recognising EI; (4) a pharmaceutical composition (PC) comprising (IV);
CC (5) a peptide (Ia) capable of being recognised by (IV); (6) an immunogen
CC (IIa) comprising (Ia); and (7) producing (III) by producing (II). (I) can
CC have anti-allergic and immunosuppressive activities, and can be used as a
CC vaccine and histamine release inhibitor. (I), (II) and (III) are useful
CC in medicine and in the manufacture of medicaments for treating and
CC preventing allergies. (IV) is useful for identifying mimotopes of PI, in
CC medicine and also in manufacturing medicaments for treating allergies.

CC (I) is useful in diagnostics and in the affinity purification of
CC circulating anti-IGE antibodies from blood. (I), (III) and PC are useful
CC for treating a patient susceptible to or suffering from allergies. (IV)
CC is also useful in diagnosing atopy. AAB25907 to AAB26099 represent
CC peptide sequences which are used in the exemplification of the present
XX invention

XX SQ Sequence 9 AA;

Query Match 56.6%; Score 47; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EDGQVMDVD 9
DB 1 EDGQVMDVD 9

RESULT 15

AAB20867 ID AAB20867 standard; peptide; 9 AA.

XX AC AAB20867;

DT 03-JAN-2001 (first entry)

```

XX Immunoglobulin E epitope immunogenic peptide SEQ ID NO:5.
DE
XX
XX Immunoglobulin E; IgE; immunogenic; immunogen; Protein D; carrier;
KM prostate cancer; Haemophilus influenzae; vaccine; infectious disease;
KM malaria; cytostatic; antiallergic; nootropic; neuroprotective;
KM protozoacide; Alzheimer's disease; allergy.
XX
OS Homo sapiens.
XX
XX WO200050077-A1.
XX
XX
XX 31-AUG-2000.
XX
XX
XX 22-FEB-2000; 2000WO-EP001457.
XX
XX
XX 25-FEB-1999; 99GB-00004405.
XX
XX 25-FEB-1999; 99GB-00004408.
XX
XX 25-FEB-1999; 99GB-00004412.
XX
XX 13-AUG-1999; 99GB-00019260.
XX
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX
XX Coeste M, Lobet Y, Van-Mechelen MP, Verriest C;
XX
XX WPI; 2000-572040/53.
XX
XX
XX Immunogens and vaccine comprising the immunogen useful for preventing and
PT treating infectious diseases e.g. malaria and chronic disease e.g.
XX cancer, comprises peptide and carrier from protein D of influenzae.
XX
XX
XX Claim 9; Page 37; 53pp; English.
XX
XX
XX The present invention describes an immunogen (I) comprising a peptide
CC (Ia) and a carrier (Ib) derived from protein D of Haemophilus influenzae
CC or its fragment. Also described are: (1) a vaccine comprising (I), and an
CC excipient; (2) preparation of (I), comprising conjugating a peptide to
CC protein D or its fragment; and (3) preparation of a vaccine of (I),
CC comprising formulating (I) with an excipient. (I) has cytostatic,
CC antiallergic, nootropic, neuroprotective and protozoacide activities. (I)
CC and the vaccine are useful for the manufacture of a medicament for
CC preventing and treating infectious diseases such as malaria or chronic
CC disease such as cancer, Alzheimer's disease or allergy in a patient.
CC Unlike prior art immunogens, (I) induces high levels of antipeptide
CC immune responses while inducing a moderate humoral response against the
CC carrier. The present sequence represents a specifically claimed
CC immunoglobulin E (IgE) epitope immunogenic peptide sequence, which can be
CC used in an immunogen of the present invention
XX
XX
XX Sequence 9 AA:
SQ

```

```

Query Match          56.6%; Score 47; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EDGQVMDVD 9
   |||||
Db 1 EDGQVMDVD 9

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Search completed: December 12, 2005, 22:08:38
Job time : 182 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:24:05 ; Search time 45 Seconds
(without alignments)
31.233 Million cell updates/sec

Title: US-10-758-165A-16
Perfect score: 83
Sequence: 1 EDQGVMDVDTASTTQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 201056

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*

- 1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/RECOMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.8	14	2	US-08-526-136-25	Sequence 25, Appl
2	28	33.7	7	US-09-842-164A-12	Sequence 12, Appl
3	28	33.7	10	US-08-447-411-46	Sequence 46, Appl
4	28	33.7	10	US-08-662-227-3	Sequence 3, Appl
5	28	33.7	10	US-09-017-947-3	Sequence 3, Appl
6	28	33.7	10	US-09-925-442-3	Sequence 3, Appl
7	28	33.7	13	US-08-162-081B-13	Sequence 13, Appl
8	28	33.7	13	US-08-780-872-13	Sequence 13, Appl
9	28	33.7	13	US-09-085-957-13	Sequence 13, Appl
10	28	33.7	16	PCT-US91-02942-91	Sequence 91, Appl
11	27	32.5	10	US-08-724-548-28	Sequence 28, Appl
12	27	32.5	10	US-07-978-674B-28	Sequence 28, Appl
13	27	32.5	12	US-09-238-448-8	Sequence 8, Appl
14	27	32.5	14	US-09-010-317-60	Sequence 60, Appl
15	27	32.5	15	US-08-906-769-179	Sequence 179, Appl
16	27	32.5	15	US-08-906-616-179	Sequence 179, Appl
17	27	32.5	15	US-08-639-075A-179	Sequence 179, Appl
18	27	32.5	15	US-09-004-731-68	Sequence 68, Appl
19	27	32.5	15	US-09-012-431-179	Sequence 179, Appl
20	27	32.5	15	US-08-749-699-68	Sequence 68, Appl
21	27	32.5	15	US-09-012-692-179	Sequence 179, Appl
22	27	32.5	15	US-08-906-613-179	Sequence 68, Appl
23	27	32.5	15	US-09-004-729-68	Sequence 68, Appl
24	27	32.5	15	US-09-071-252-33	Sequence 33, Appl
25	26	31.3	10	US-09-010-317-73	Sequence 73, Appl
26	26	31.3	10	US-09-010-317-74	Sequence 74, Appl
27	26	31.3	12	US-08-617-929-32	Sequence 32, Appl

28	26	31.3	14	1	US-08-617-929-31	Sequence 31, Appl
29	26	31.3	14	2	US-09-010-317-103	Sequence 103, Appl
30	26	31.3	15	1	US-08-528-057-18	Sequence 18, Appl
31	26	31.3	16	1	US-08-845-926-20	Sequence 20, Appl
32	26	31.3	16	2	US-09-351-226-20	Sequence 20, Appl
33	26	31.3	17	2	US-10-394-960-72	Sequence 72, Appl
34	25	30.1	9	2	US-08-724-548-29	Sequence 11, Appl
35	25	30.1	10	2	US-07-978-674B-29	Sequence 29, Appl
36	25	30.1	10	2	US-09-743-467-12	Sequence 12, Appl
37	25	30.1	13	1	US-08-463-115-102	Sequence 102, Appl
38	25	30.1	13	1	US-08-465-388-102	Sequence 102, Appl
39	25	30.1	14	1	US-08-480-793-1	Sequence 1, Appl
40	25	30.1	14	4	PCT-US92-05825A-1	Sequence 1, Appl
41	25	30.1	15	2	US-08-912-560-3	Sequence 9, Appl
42	25	30.1	16	2	US-09-914-831-9	Sequence 4, Appl
43	24	28.9	10	1	US-08-198-962-4	Sequence 4, Appl
44	24	28.9	10	1	US-08-682-412B-4	Sequence 4, Appl
45	24	28.9	10	1	US-08-682-412B-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-526-136-25
; Sequence 25, Application US/08526136
; Patent No. 6107089
; GENERAL INFORMATION:
; APPLICANT: Towle, Christine A. et al.
; TITLE OF INVENTION: ANNEXIN XI
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,136
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,036
; FILING DATE:
; APPLICATION NUMBER: 07/837,775
; FILING DATE: February 13, 1992
; APPLICATION NUMBER: 07/764,465
; FILING DATE: September 23, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/099001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELETYPE: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; US-08-526-136-25
Query Match 39.8%; Score 33; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EDGQWMDVDL 10
| | | : | |
Db 1 EDGSVIDVEL 10

RESULT 2

US-09-842-164A-12
; Sequence 12, Application US/09842164A
; Patent No. 6544754
; GENERAL INFORMATION:
; APPLICANT: INOYE, SATOSHI
; TITLE OF INVENTION: LUCIFERASE AND PHOTOPROTEIN
; FILE REFERENCE: 206497US0
; CURRENT APPLICATION NUMBER: US/09/842,164A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: JP 2000-125053
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Oplophorus graciliorostis
US-09-842-164A-12

Query Match 33.7%; Score 28; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GQWMDVD 9
| | | : | |
Db 1 GDVMDMD 7

RESULT 3

US-08-447-411-46
; Sequence 46, Application US/08447411
; Patent No. 5773243
; GENERAL INFORMATION:
; APPLICANT: FRITZINGER, DAVID C.
; APPLICANT: BREDEHORST, REINHARD
; APPLICANT: VOGEL, CARL-WILHELM
; TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,411
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/043,747
; FILING DATE: 07-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5773243man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-101-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UK

; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-447-411-46

Query Match 33.7%; Score 28; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EDGQWMDVDL 10
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Db 1 EDGFIADSDI 10

RESULT 4

US-08-662-227-3
; Sequence 3, Application US/08662227
; Patent No. 5922320
; GENERAL INFORMATION:
; APPLICANT: VOGEL, CARL-WILHELM
; APPLICANT: BREDEHORST, REINHORST
; APPLICANT: KOCK, MICHAEL
; APPLICANT: FRITZINGER, DAVID
; TITLE OF INVENTION: RECOMBINANT PROCVF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/662,227
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1126-0107-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-662-227-3

Query Match 33.7%; Score 28; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EDGQWMDVDL 10
| | | : | |
Db 1 EDGFIADSDI 10

RESULT 5

US-09-017-947-3
; Sequence 3, Application US/09017947

Patent No. 6303754
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
ADDRESS: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,947
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/662,227
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-017-947-3

Query Match 33.7%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGQVMDVDL 10
DB 1 EDGFADSDI 10

RESULT 6
US-09-925-442-3
Sequence 3, Application US/0925442
Patent No. 6607897
GENERAL INFORMATION:
APPLICANT: VOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORST
APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
ADDRESS: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/925,442
FILING DATE: 10-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/017,947
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-925-442-3

Query Match 33.7%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGQVMDVDL 10
DB 1 EDGFADSDI 10

RESULT 7
US-08-162-081B-13
Sequence 13, Application US/08162081B
Patent No. 5824492
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph; Otsu, Masayuki; Panayiotu, George; Volina,
APPLICANT: Stefano; Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felde & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-162-081B-13

Query Match 33.7%; Score 28; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EDGQVMDVD 9
:||||: :|
Db 1 DDGQLPHID 9

RESULT 8
US-08-780-872-13
Sequence 13, Application US/08780872
Patent No. 5846824
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
APPLICANT: Stefano; Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
TITLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,872
FILING DATE: 09-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-780-872-13

Query Match 33.7%; Score 28; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EDGQVMDVD 9
:||||: :|

Db 1 DDGQLPHID 9

RESULT 9
US-09-085-957-13
Sequence 13, Application US/09085957
Patent No. 6274327
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
APPLICANT: Stefano; Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
TITLE OF INVENTION: THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,957
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/780,872
FILING DATE: 09-JAN-1997
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-085-957-13

Query Match 33.7%; Score 28; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EDGQVMDVD 9
:||||: :|
Db 1 DDGQLPHID 9

RESULT 10
PCT-US91-02942-91
Sequence 91, Application PC/TUS9102942
GENERAL INFORMATION:
APPLICANT: ROTHLEIN, ROBERT
APPLICANT: ADAIR, JOHN R
APPLICANT: ATHWAL, DILJEET S
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Keseler, Goldstein & Fox

STREET: 1225 Connecticut Ave. NW Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02942
FILING DATE: 19910429
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9009549.8
FILING DATE: 27-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1011.0586600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 466-0800
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-02942-91

Query Match 33.7%; Score 28; DB 4; Length 16;
Best Local Similarity 53.8%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQVMDVLDSTAST 15
Db 2 GCGTIVTVSSAST 14

RESULT 11
US-08-724-548-28
Sequence 28, Application US/08724548
Patent No. 5830637
GENERAL INFORMATION:
APPLICANT: Frank, Ronald
APPLICANT: Galer, Sinan
TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF
TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR
TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL
TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND
TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE
NUMBER OF INVENTION: PROCESS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joseph T. Eisele
ADDRESSEE: Kane, Daisimer, Sullivan, Kurucz,
ADDRESSEE: Levy, Eisele and Richard
STREET: 711 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10017-4059
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" DISKETTE
COMPUTER: IBM-XT COMPATIBLE
OPERATING SYSTEM: DOS 3.3:
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,548
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/978,674
FILING DATE: 03/22/93
ATTORNEY/AGENT INFORMATION:
NAME: EISELE, JOSEPH T.
REGISTRATION NUMBER: 25,331
REFERENCE/DOCKET NUMBER: 2727-68 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 687-6000
TELEFAX: (212) 682-3485
TELEX: (212) 426767
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: Peptide
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE: Internal fragment
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
ORGANELLE:
IMMEDIATE SOURCE:
US-08-724-548-28

Query Match 32.5%; Score 27; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EDGQVMDVDL 10
Db 1 DDGGLDXDL 10

RESULT 12
US-07-978-674B-28
Sequence 28, Application US/07978674B
Patent No. 6040423
GENERAL INFORMATION:
APPLICANT: Frank, Ronald
APPLICANT: Galer, Sinan
TITLE OF INVENTION: PROCESS FOR THE RAPID SYNTHESIS OF
TITLE OF INVENTION: SUPPORT-BOUND OR FREE PEPTIDES OR
TITLE OF INVENTION: OLIGONUCLEOTIDES, A FLAT MATERIAL
TITLE OF INVENTION: PREPARED THEREWITH AND ITS USE AND
TITLE OF INVENTION: A DEVICE FOR CARRYING OUT THE
NUMBER OF INVENTION: PROCESS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joseph T. Eisele
ADDRESSEE: Kane, Daisimer, Sullivan, Kurucz,
ADDRESSEE: Levy, Eisele and Richard
STREET: 711 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10017-4059
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" DISKETTE
COMPUTER: IBM-XT COMPATIBLE
OPERATING SYSTEM: DOS 3.3:
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/978,674B
FILING DATE:
CLASSIFICATION:

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: FILING DATE: 03/22/93
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: EISELE, JOSEPH T.
: REGISTRATION NUMBER: 25,331
: REFERENCE/DOCKET NUMBER: 2727-68 PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 687-6000
: TELEFAX: (212) 682-3485
: TELEX: (212) 426767
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 residues
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: LINEAR
: MOLECULE TYPE: Peptide
: HYPOTHEetical:
: ANTI-SENSE:
: FRAGMENT TYPE: Internal fragment
: ORIGINAL SOURCE:
: ORGANISM:
: STRAIN:
: INDIVIDUAL ISOLATE:
: DEVELOPMENTAL STAGE:
: HAPLOTYPE:
: TISSUE TYPE:
: CELL LINE:
: ORGANELLES:
: IMMEDIATE SOURCE:
: US-07-978-674B-28

Query Match      32.5%; Score 27; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 EDGQVMDVDL 10
Db      1 DDGPGLDXDL 10

RESULT 13
US-09-238-448-8
: Sequence 8, Application US/09238448
: Patent No. 6238925
: GENERAL INFORMATION:
: APPLICANT: Sampson, Hugh A.
: TITLE OF INVENTION: Method for Determining Likelihood of Developing
: FILE REFERENCE: HS 100
: CURRENT APPLICATION NUMBER: US/09/238,448
: CURRENT FILING DATE: 1999-01-28
: EARLIER APPLICATION NUMBER: 60/073,171
: EARLIER FILING DATE: 1998-01-30
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 8
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-238-448-8

Query Match      32.5%; Score 27; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVM 6
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Db      5 EDGKVM 10

RESULT 14
US-09-010-317-60
: Sequence 60, Application US/09010317
: Patent No. 6685943
: GENERAL INFORMATION:
: APPLICANT: Hook, Magnus
: APPLICANT: Patti, Joseph M.
: APPLICANT: House-Pompeo, Karen L.
: APPLICANT: Speziale, Pietro
: APPLICANT: John, Danny
: APPLICANT: McGavin, Martin J.
: TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN COMPOSITIONS
: NUMBER OF SEQUENCES: 105
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Arnold, White & Durkee
: STREET: P.O. Box 4433
: CITY: Houston
: STATE: TX
: COUNTRY: USA
: ZIP: 77210-4433
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/010,317
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/036,139
: FILING DATE: 21-JAN-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Hibler, David W.
: REGISTRATION NUMBER: 41,071
: REFERENCE/DOCKET NUMBER: TAMK.189
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 512-418-3000
: TELEFAX: 512-474-7577
: INFORMATION FOR SEQ ID NO: 60:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 14 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
US-09-010-317-60

Query Match      32.5%; Score 27; DB 2; Length 14;
Best Local Similarity 25.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy      1 EDGQVMDVDLST 12
Db      1 QGQNVIDIDFDS 12

RESULT 15
US-08-906-769-179
: Sequence 179, Application US/08906769
: Patent No. 6077687
: GENERAL INFORMATION:
: APPLICANT: Grieve, Robert B.
: APPLICANT: Rushlow, Keith E.
: APPLICANT: Wu Hunter, Shirley
: APPLICANT: Frank, Glenn R.
: APPLICANT: Stiegler, Gary
: APPLICANT: Gaines, Patrick J.
: APPLICANT: Silver, Gary
```

TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Rose & McInloch
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,769
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 179:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-906-769-179

Query Match 32.5%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 DVDLIST 12
|||:
6 DVDIST 11

Search completed: December 12, 2005, 21:52:52
Job time : 46 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:46:41 ; Search time 159 Seconds

(without alignments)
44.674 Million cell updates/sec

Title: US-10-758-165A-16

Perfect score: 83

Sequence: 1 EDGQVMDVLDLSTASTTQ 17

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 345637

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*

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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	17	US-10-758-165-16	Sequence 16, Appl
2	51	61.4	13	US-10-362-527-8	Sequence 8, Appl
3	51	61.4	13	US-10-362-527-10	Sequence 10, Appl
4	51	61.4	13	US-10-362-527-96	Sequence 96, Appl
5	51	61.4	13	US-11-005-794-8	Sequence 8, Appl
6	51	61.4	13	US-11-005-794-10	Sequence 10, Appl
7	51	61.4	13	US-11-005-794-11	Sequence 11, Appl
8	51	61.4	13	US-10-362-527-326	Sequence 326, App
9	47	56.6	9	US-10-082-014-273	Sequence 273, App
10	47	56.6	9	US-10-372-076-127	Sequence 127, App
11	47	56.6	9	US-10-362-527-1	Sequence 1, Appl
12	47	56.6	9	US-10-732-862A-141	Sequence 141, App
13	47	56.6	9	US-10-677-074-127	Sequence 127, Appl
14	47	56.6	9	US-11-005-794-1	Sequence 1, Appl
15	47	56.6	10	US-10-144-188-60	Sequence 60, Appl
16	47	56.6	10	US-10-082-014-282	Sequence 282, App
17	47	56.6	10	US-10-372-076-136	Sequence 136, App
18	47	56.6	10	US-10-362-527-12	Sequence 12, App
19	47	56.6	10	US-10-732-862A-150	Sequence 150, App
20	47	56.6	10	US-10-677-074-136	Sequence 136, App
21	47	56.6	10	US-11-005-794-23	Sequence 23, App
22	47	56.6	14	US-10-362-527-334	Sequence 324, App
23	41	49.4	10	US-10-144-188-55	Sequence 55, App
24	37	46.6	13	US-10-362-527-325	Sequence 325, App
25	34	41.0	7	US-10-362-527-11	Sequence 11, Appl
26	34	41.0	7	US-11-005-794-17	Sequence 17, Appl
27	33	39.8	17	US-09-988-493-175	Sequence 175, App

28	33	39.8	17	4	US-10-014-340-12	Sequence 12, Appl
29	33	39.8	17	4	US-10-014-340-500	Sequence 500, App
30	33	39.8	17	4	US-10-700-340-4	Sequence 4, Appl
31	33	39.8	17	5	US-10-652-779-62	Sequence 62, Appl
32	31	37.3	14	4	US-10-308-128-112	Sequence 112, App
33	29	34.9	10	3	US-09-572-270A-1084	Sequence 1084, App
34	29	34.9	10	3	US-09-572-270A-1086	Sequence 1086, App
35	29	34.9	11	4	US-10-362-527-49	Sequence 49, Appl
36	29	34.9	11	6	US-11-005-794-104	Sequence 36, Appl
37	29	34.9	14	4	US-10-137-867-36	Sequence 147, App
38	29	34.9	14	4	US-10-308-128-147	Sequence 101, App
39	29	34.9	16	3	US-09-791-378-101	Sequence 326, App
40	29	34.9	16	3	US-09-791-378-326	Sequence 230, App
41	29	34.9	16	3	US-09-826-290-230	Sequence 341, App
42	29	34.9	16	3	US-09-826-290-341	Sequence 398, App
43	29	34.9	16	3	US-09-826-290-398	Sequence 48, Appl
44	29	34.9	16	3	US-09-791-383-48	Sequence 48, Appl
45	29	34.9	16	3	US-09-791-389-48	Sequence 48, Appl

ALIGNMENTS

```
RESULT 1
US-10-758-165-16
; Sequence 16, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758.165
; PRIOR FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: US 60/440.472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-758-165-16

Query Match      100.0%; Score 83; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVLDLSTASTTQ 17
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DB      1 EDGQVMDVLDLSTASTTQ 17

RESULT 2
US-10-362-527-8
; Sequence 8, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals y De Bascoles, Carloca
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362.527
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
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; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-527-8

Query Match          61.4%; Score 51; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVDL 10
        |||||
Db       3 EDGQVMDVDL 12

RESULT 3
US-10-362-527-10
; Sequence 10, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals y De Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-527-10

Query Match          61.4%; Score 51; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVDL 10
        |||||
Db       3 EDGQVMDVDL 12

RESULT 4
US-10-362-527-96
; Sequence 96, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals y De Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Artificial variant of Homo sapiens IGE peptide
US-10-362-527-96

Query Match          61.4%; Score 51; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVDL 10
        |||||
Db       3 EDGQVMDVDL 12

RESULT 5
US-11-005-794-8
; Sequence 8, Application US/11005794
; Publication No. US20050214285A1
; GENERAL INFORMATION:
; APPLICANT: Dyson, Michael
; APPLICANT: Friede, Martin
; APPLICANT: Greenwood, Judyley
; APPLICANT: Hewitt, Ellen
; APPLICANT: Lamont, Alan
; APPLICANT: Mason, Sean
; APPLICANT: Randall, Roger
; APPLICANT: Turnell, William Gordon
; APPLICANT: Van Mechelen, Marcelle Paullette
; APPLICANT: Vinals y de Bassols, Carlota
; TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
; TITLE OF INVENTION: C-Epsilon-2 Domain of IGE, Antagonists Thereof, and Their
; TITLE OF INVENTION: Therapeutic Uses
; FILE REFERENCE: B45172
; CURRENT APPLICATION NUMBER: US/11/005,794
; CURRENT FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US/09/914,088
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: GB 9904405.9
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: GB 9907151.6
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: GB 9910537.1
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9910538.9
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9918594.4
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918603.3
; PRIOR FILING DATE: 1999-08-07
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric
US-11-005-794-8

Query Match          61.4%; Score 51; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVDL 10
        |||||
Db       3 EDGQVMDVDL 12

RESULT 6
US-11-005-794-10
; Sequence 10, Application US/11005794
; Publication No. US20050214285A1
; GENERAL INFORMATION:
; APPLICANT: Dyson, Michael
```

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; APPLICANT: Friede, Martin
; APPLICANT: Greenwood, Judithy
; APPLICANT: Hewitt, Ellen
; APPLICANT: Lamont, Alan
; APPLICANT: Mason, Sean
; APPLICANT: Randall, Roger
; APPLICANT: Turnell, William Gordon
; APPLICANT: Van Mechelen, Marcelle Paulette
; APPLICANT: Vinals y de Bassols, Carlota
; TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
; TITLE OF INVENTION: C-Epsilon-2 Domain of IGF, Antagonists Thereof, and Their
; TITLE OF INVENTION: Therapeutic Uses
; FILE REFERENCE: B45172
; CURRENT APPLICATION NUMBER: US/11/005,794
; PRIOR FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US/09/914,088
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: GB 9904405.9
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: GB 9907151.6
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: GB 9910537.1
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9910538.9
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9918594.4
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918603.3
; PRIOR FILING DATE: 1999-08-07
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric
US-11-005-794-10

Query Match      61.4%; Score 51; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVMDVDL 10
Db      3 EDGQVMDVDL 12

RESULT 7
US-11-005-794-11
; Sequence 11, Application US/11005794
; Publication No. US20050214285A1
; GENERAL INFORMATION:
; APPLICANT: Dyson, Michael
; APPLICANT: Friede, Martin
; APPLICANT: Greenwood, Judithy
; APPLICANT: Hewitt, Ellen
; APPLICANT: Lamont, Alan
; APPLICANT: Mason, Sean
; APPLICANT: Randall, Roger
; APPLICANT: Turnell, William Gordon
; APPLICANT: Van Mechelen, Marcelle Paulette
; APPLICANT: Vinals y de Bassols, Carlota
; TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
; TITLE OF INVENTION: C-Epsilon-2 Domain of IGF, Antagonists Thereof, and Their
; FILE REFERENCE: B45172
; CURRENT APPLICATION NUMBER: US/11/005,794
; PRIOR FILING DATE: 2004-12-07
; PRIOR APPLICATION NUMBER: US/09/914,088
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: GB 9904405.9
; PRIOR FILING DATE: 1999-02-25
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; PRIOR APPLICATION NUMBER: GB 9907151.6
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: GB 9910537.1
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9910538.9
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: GB 9918594.4
; PRIOR FILING DATE: 1999-08-07
; PRIOR APPLICATION NUMBER: GB 9918603.3
; PRIOR FILING DATE: 1999-08-07
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric
US-11-005-794-11

Query Match      61.4%; Score 51; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVMDVDL 10
Db      3 EDGQVMDVDL 12

RESULT 8
US-10-362-527-326
; Sequence 326, Application US/10362527
; Publication No. US20040030106A1
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Mason, Sean
; APPLICANT: Turnell, William Gordon
; APPLICANT: Vinals y de Bassols, Carlota
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
; FILE REFERENCE: B45236
; CURRENT APPLICATION NUMBER: US/10/362,527
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/EP01/09576
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: GB 0020717.5
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial variant of Homo sapiens IGF peptide
US-10-362-527-326

Query Match      61.4%; Score 51; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVMDVDL 10
Db      3 EDGQVMDVDL 12

RESULT 9
US-10-082-014-273
; Sequence 273, Application US/10082014
; Publication No. US20030185858A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
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FILE REFERENCE: ICC-130.0 4564/85124
CURRENT APPLICATION NUMBER: US/10/082,014
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/930,915
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn version 3.1
SEQ ID NO 273
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-082-014-273

Query Match      56.6%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVD 9
Db      1 EDGQVMDVD 9

RESULT 10
US-10-372-076-127
Sequence 127, Application US/10372076
Publication No. US20030198645A1
GENERAL INFORMATION:
APPLICANT: Page, Mark
APPLICANT: Friede, Martin
TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
FILE REFERENCE: 4564/87179
CURRENT APPLICATION NUMBER: US/10/372,076
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 10/080,299
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/082,014
PRIOR FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.2
SEQ ID NO 127
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-372-076-127

Query Match      56.6%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVD 9
Db      1 EDGQVMDVD 9

RESULT 11
US-10-362-527-1
Sequence 1, Application US/10362527
Publication No. US20040030106A1
GENERAL INFORMATION:
APPLICANT: Friede, Martin
APPLICANT: Mason, Sean
APPLICANT: Turnell, William Gordon
APPLICANT: Vinals y De Bassols, Carlota
TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
FILE REFERENCE: B45236
CURRENT APPLICATION NUMBER: US/10/362,527
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: PCT/EP01/09576
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: GB 0020717.5
PRIOR FILING DATE: 2000-08-22
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NUMBER OF SEQ ID NOS: 328
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-362-527-1

Query Match      56.6%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVD 9
Db      1 EDGQVMDVD 9

RESULT 12
US-10-732-862A-141
Sequence 141, Application US/10732862A
Publication No. US20040146524A1
GENERAL INFORMATION:
APPLICANT: ASHLEY, BIRKETT J.
APPLICANT: Lyons, Katelynne J.
APPLICANT: Jay, Haron J.
TITLE OF INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES
FILE REFERENCE: ICC-136.0 (4564-88881)
CURRENT APPLICATION NUMBER: US/10/732,862A
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: US 60/432,123
PRIOR FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 10/274,616
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 10/080,299
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US 10/082,014
PRIOR FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 455
SOFTWARE: PatentIn version 3.2
SEQ ID NO 141
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-732-862A-141

Query Match      56.6%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVD 9
Db      1 EDGQVMDVD 9

RESULT 13
US-10-677-074-127
Sequence 127, Application US/10677074
Publication No. US20040156863A1
GENERAL INFORMATION:
APPLICANT: Friede, Martin
APPLICANT: Schmidt, Annette Elisabeth
APPLICANT: Seiber, Detlef
TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
FILE REFERENCE: 4564/87179
CURRENT APPLICATION NUMBER: US/10/677,074
CURRENT FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: 10/372,076
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/080,299
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/082,014
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;; PRIOR FILING DATE: 2002-02-22
;; NUMBER OF SEQ ID NOS: 308
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 127
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-677-074-127

Query Match 56.6%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9
 |||||
Db 1 EDGQVMDVD 9

RESULT 14
US-11-005-794-1
; Sequence 1, Application US/11005794
; Publication No. US20050214285A1
; GENERAL INFORMATION:
; APPLICANT: Dyson, Michael
; APPLICANT: Friede, Martin
; APPLICANT: Greenwood, Judith
; APPLICANT: Hewitt, Ellen
; APPLICANT: Lamont, Alan
; APPLICANT: Mason, Sean
; APPLICANT: Randall, Roger
; APPLICANT: Turnell, William Gordon
; APPLICANT: Van Mechelen, Marcelle Paulette
; APPLICANT: Vinals y de Bassols, Carlota
TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
TITLE OF INVENTION: C-Epsilon-2 Domain of IgE, Antagonists Thereof, and Their
FILE REFERENCE: B45172
CURRENT APPLICATION NUMBER: US/11/005,794
CURRENT FILING DATE: 2004-12-07
PRIOR APPLICATION NUMBER: US/09/914,088
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: GB 9904405.9
PRIOR FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: GB 9907151.6
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: GB 9910537.1
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: GB 9910538.9
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: GB 9918594.4
PRIOR FILING DATE: 1999-08-07
PRIOR APPLICATION NUMBER: GB 9918603.3
NUMBER OF SEQ ID NOS: 193
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric
US-11-005-794-1

Query Match 56.6%; Score 47; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVD 9
 |||||
Db 1 EDGQVMDVD 9

RESULT 15

US-10-144-188-60
; Sequence 60, Application US/10144188
; Publication No. US20030170212A1
; GENERAL INFORMATION:
; APPLICANT: Cai, Zeling
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; APPLICANT: Shi, Weixing
; APPLICANT: Kong, Yan
; APPLICANT: Degraw, Juli
TITLE OF INVENTION: Ex-Vivo Priming For Generating Cytotoxic T Lymphocytes Specific
TITLE OF INVENTION: For No. US20030170212A1-Tumor Antigens To Treat Autoimmune And A
FILE REFERENCE: PRI0010 ORT-1627
CURRENT APPLICATION NUMBER: US/10/144,188
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 60/291,300
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.2
SEQ ID NO 60
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide antigen
US-10-144-188-60

Query Match 56.6%; Score 47; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QVMDVLDSTA 13
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Db 1 QVMDVLDSTA 10

Search completed: December 12, 2005, 22:05:13
Job time : 160 secs

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OM protein - protein search, using SW model

Run on: December 12, 2005, 21:52:16 ; Search time 11 Seconds
(without alignments)
8.630 Million cell updates/sec

Title: US-10-758-165A-16

Perfect score: 83

Sequence: 1 EDGQVMDVLDLSTRTTQ 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 9353

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	23	27.7	9	US-11-010-748A-423	Sequence 423, App
2	23	27.7	9	US-11-010-748A-424	Sequence 424, App
3	23	27.7	9	US-11-010-748A-429	Sequence 429, App
4	23	27.7	9	US-11-010-748A-435	Sequence 435, App
5	23	27.7	9	US-11-010-748A-436	Sequence 436, App
6	23	27.7	9	US-11-010-748A-440	Sequence 440, App
7	23	27.7	9	US-11-097-864-475	Sequence 475, App
8	23	27.7	9	US-11-097-912-475	Sequence 475, App
9	23	27.7	15	US-11-106-932-134	Sequence 134, App
10	23	27.7	15	US-11-106-932-134	Sequence 134, App
11	23	27.7	17	US-11-010-748A-418	Sequence 418, App
12	23	27.7	17	US-11-010-748A-430	Sequence 430, App
13	23	27.7	17	US-11-119-249-8	Sequence 8, Appl
14	22	26.5	12	US-11-084-554-4	Sequence 4, Appl
15	22	26.5	12	US-10-986-501-287	Sequence 287, App
16	22	26.5	13	US-10-511-559-1068	Sequence 1068, Ap
17	22	26.5	13	US-10-511-559-1068	Sequence 1069, Ap
18	22	26.5	14	US-10-467-657-8761	Sequence 8761, Ap
19	22	26.5	15	US-10-467-657-8749	Sequence 8749, Ap
20	22	26.5	17	US-11-011-666-7	Sequence 7, Appl
21	21	25.3	9	US-11-010-748A-891	Sequence 891, App
22	21	25.3	9	US-11-010-748A-895	Sequence 895, App
23	21	25.3	9	US-11-010-748A-897	Sequence 897, App
24	21	25.3	9	US-11-010-748A-901	Sequence 901, App
25	21	25.3	9	US-11-010-748A-904	Sequence 904, App

26	21	25.3	9	US-11-097-864-482	Sequence 482, App
27	21	25.3	9	US-11-097-912-482	Sequence 482, App
28	21	25.3	10	US-11-054-515-3180	Sequence 3180, Ap
29	21	25.3	15	US-11-054-515-3083	Sequence 3083, Ap
30	21	25.3	16	US-11-089-764-68	Sequence 69, Appl
31	21	25.3	17	US-11-010-748A-890	Sequence 890, Appl
32	20	24.1	9	US-11-097-864-454	Sequence 454, App
33	20	24.1	9	US-11-097-864-569	Sequence 569, App
34	20	24.1	9	US-11-097-912-454	Sequence 454, App
35	20	24.1	9	US-11-097-912-569	Sequence 569, App
36	20	24.1	10	US-11-097-864-502	Sequence 502, App
37	20	24.1	10	US-11-097-864-510	Sequence 510, App
38	20	24.1	10	US-11-097-864-613	Sequence 613, App
39	20	24.1	10	US-11-097-912-502	Sequence 502, App
40	20	24.1	10	US-11-097-912-540	Sequence 540, App
41	20	24.1	11	US-11-097-912-613	Sequence 613, App
42	20	24.1	11	US-11-054-515-3177	Sequence 3177, Ap
43	20	24.1	12	US-10-467-657-8948	Sequence 8948, Ap
44	20	24.1	13	US-10-511-559-813	Sequence 813, App
45	20	24.1	13	US-10-511-559-886	Sequence 886, App

ALIGNMENTS

```
RESULT 1
US-11-010-748A-423
; Sequence 423, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOIL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 423
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 418
US-11-010-748A-423

Query Match      27.7%  Score 23;  DB 7;  Length 9;
Best Local Similarity 66.7%  Pred. No. 2.8e+04;
Matches 4;  Conservative 1;  Mismatches 1;  Indels 0;  Gaps 0;

QY      1  EDGQVM 6
Db      2  EDGNVL 7

RESULT 2
US-11-010-748A-424
; Sequence 424, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOIL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
```

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; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 424
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 418
; US-11-010-748A-424

Query Match      27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EDGQVM 6
        ||| |
        ||| |
Db      2 EDGNVL 7

RESULT 3
US-11-010-748A-429
; Sequence 429, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: WOLL, Heidrun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 418
; US-11-010-748A-429

Query Match      27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EDGQVM 6
        ||| |
        ||| |
Db      2 EDGNVL 7

RESULT 4
US-11-010-748A-435
; Sequence 435, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: WOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
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; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 435
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 430
; US-11-010-748A-435

Query Match      27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EDGQVM 6
        ||| |
        ||| |
Db      2 EDGNVL 7

RESULT 5
US-11-010-748A-436
; Sequence 436, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: WOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 436
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 430
; US-11-010-748A-436

Query Match      27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EDGQVM 6
        ||| |
        ||| |
Db      2 EDGNVL 7

RESULT 6
US-11-010-748A-440
; Sequence 440, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: WOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
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; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 440
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 430
US-11-010-748A-440

Query Match 27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDGOVM 6
Db 2 EDGNVL 7

RESULT 7
US-11-097-864-475
; Sequence 475, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eld, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 475
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-475

Query Match 27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.8e+04;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 QVMDVLTST 12
Db 1 RVRDVELLT 9

RESULT 8
US-11-097-912-475
; Sequence 475, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Challita-Eld, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204

; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 475
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-475

Query Match 27.7%; Score 23; DB 7; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.8e+04;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 QVMDVLTST 12
Db 1 RVRDVELLT 9

RESULT 9
US-11-106-932-50
; Sequence 50, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-11-106-932-50

Query Match 27.7%; Score 23; DB 7; Length 15;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 DVDLTSTAS 14
Db 7 DTDSKTAS 14

RESULT 10
US-11-106-932-134
; Sequence 134, Application US/11106932
; Publication No. US20050260697A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 134
; LENGTH: 15
; TYPE: PRT

ORGANISM: Homo sapiens
US-11-106-932-134

Query Match 27.7%; Score 23; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 74;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DQGVMDVD 9
|||:
Db 7 DGERVDFD 14

RESULT 11
US-11-010-748A-418

Sequence 418, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:

APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMATTER, Wolfgang
APPLICANT: MOLL, Heidrun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136

CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13

PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13

PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13

NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1

SEQ ID NO 418

LENGTH: 17
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: CD64 peptide fragment
US-11-010-748A-418

Query Match 27.7%; Score 23; DB 7; Length 17;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDQVVM 6
|||:
Db 2 EDGNVL 7

RESULT 12
US-11-010-748A-430

Sequence 430, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:

APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMATTER, Wolfgang
APPLICANT: MOLL, Heidrun

APPLICANT: SCHARR, Burkhard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE

FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13

PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13

PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13

NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1

SEQ ID NO 430

LENGTH: 17
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: CD64 peptide fragment

US-11-010-748A-430

Query Match 27.7%; Score 23; DB 7; Length 17;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDQVVM 6
|||:
Db 2 EDGNVL 7

RESULT 13
US-11-119-249-8

Sequence 8, Application US/1119249
Publication No. US20050261190A1
GENERAL INFORMATION:

APPLICANT: SK Corp.
APPLICANT: Ewha Womans University
APPLICANT: LEE, Kong-Joo

APPLICANT: KIM, Hee-Jung
APPLICANT: CHO, Jeong Woo

APPLICANT: KIM, Eunhee
APPLICANT: SONG, Eun Joo

TITLE OF INVENTION: PAS ASSOCIATED FACTOR 1
FILE REFERENCE: 12120-02USA

CURRENT APPLICATION NUMBER: US/11/119,249
CURRENT FILING DATE: 2005-04-29

PRIOR APPLICATION NUMBER: US 60/566,966
PRIOR FILING DATE: 2004-04-29

PRIOR APPLICATION NUMBER: US 60/590,327
PRIOR FILING DATE: 2004-07-21

NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3

SEQ ID NO 8

LENGTH: 17
TYPE: PRT

ORGANISM: Artificial sequence
FEATURE:

OTHER INFORMATION: Protein spots
US-11-119-249-8

Query Match 27.7%; Score 23; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DLSTA 13
|||:
Db 10 DLSTA 14

RESULT 14
US-11-084-554-4

Sequence 4, Application US/11084554
Publication No. US20050260679A1
GENERAL INFORMATION:

APPLICANT: Kellermann, Syrid-Ai
APPLICANT: Green, Larry L.

APPLICANT: Korvet, Walter
TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN

FILE REFERENCE: ABGENIX.100A
CURRENT APPLICATION NUMBER: US/11/084,554
CURRENT FILING DATE: 2005-03-17

PRIOR APPLICATION NUMBER: 60/554,372
PRIOR FILING DATE: 2004-03-19

PRIOR APPLICATION NUMBER: 60/574,661
PRIOR FILING DATE: 2004-05-24

NUMBER OF SEQ ID NOS: 266
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 12
TYPE: PRT

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 12
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-084-554-4

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Query Match          26.5%; Score 22; DB 7; Length 12;
Best Local Similarity 83.3%; Pred. No. 85;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      10 LSTAST 15
      |||||
Db       4 LSTASS 9

```

```

RESULT 15
US-10-986-501-287
; Sequence 287, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/986,501
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 287
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-287

```

```

Query Match          26.5%; Score 22; DB 6; Length 13;
Best Local Similarity 62.5%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

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QY      5 VMDVDLST 12
      |||||
Db       3 VMDTSRST 10

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Search completed: December 12, 2005, 22:05:30
Job time : 12 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 22:02:32 ; Search time 37 Seconds
(without alignments)
44.208 Million cell updates/sec

Title: US-10-758-165A-16
Perfect score: 83
Sequence: 1 EDGQVMDVLDLSTATTQ 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2991

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	26.5	15	2 PH1631	Ig H chain V-D-J r
2	22	26.5	15	2 S20410	protein kinase (EC
3	22	26.5	17	4 IS1887	hypothetical EWSR1
4	21.5	25.9	16	2 S02473	coat protein VP1 -
5	21	25.3	13	2 B61458	Ig kappa chain V-I
6	21	25.3	13	2 A61458	Ig kappa chain V-I
7	21	25.3	16	2 PI0137	protein kinase, 80
8	20	24.1	10	2 G58501	48k bile/gallblad
9	20	24.1	11	2 PS0259	39k protein 3225 -
10	20	24.1	15	2 S70719	H+-transporting tw
11	20	24.1	15	2 PQ0778	NADH2 dehydrogenas
12	20	24.1	16	2 A42291	tail fiber protein
13	19	22.9	10	2 GXHU1	gastric juice pept
14	19	22.9	12	2 PN0160	ribosomal protein
15	19	22.9	13	2 PQ0491	self-incompatibili
16	19	22.9	13	2 S47381	T-cell antigen rec
17	19	22.9	13	2 D56661	S-locus specific g
18	19	22.9	14	2 PH1332	Ig heavy chain DJ
19	19	22.9	15	2 A18304	heterogeneous ribo
20	19	22.9	15	2 S23487	GTP-binding protei
21	19	22.9	15	2 PH0750	T-cell receptor be
22	19	22.9	17	2 S71864	glutathione transf
23	19	22.9	17	2 S71327	hypothetical prote
24	19	22.9	17	2 D48138	d(TTAGGG)n-binding
25	18	21.7	10	2 C26997	unspecific monooxy
26	18	21.7	12	2 A28856	fructose-bisphosph
27	18	21.7	12	2 PT0216	T-cell receptor be
28	18	21.7	13	2 A33660	osteoclast functio
29	18	21.7	13	2 S66235	sperm motility inh

30	18	21.7	15	2 D38925	seed storage prote
31	18	21.7	15	2 PI0154	glycoprotein - log
32	18	21.7	15	2 A53594	calnexin - mouse (
33	18	21.7	15	2 A26997	unspecific monooxy
34	18	21.7	16	2 C39509	mannose-specific l
35	18	21.7	16	2 S65430	pyrogallol hydroxy
36	18	21.7	17	2 PS0384	Ig heavy chain J r
37	18	21.7	17	2 S58660	H+-transporting tw
38	18	21.7	17	2 S28839	RNA-binding protei
39	18	21.7	17	2 C22595	hemolysin III - A
40	17	20.5	6	2 PT0604	T-cell receptor be
41	17	20.5	6	2 PT0657	T-cell receptor be
42	17	20.5	7	2 PT0543	T-cell receptor be
43	17	20.5	8	2 S21288	lectin - potato (f
44	17	20.5	8	2 A28719	thymic humoral fac
45	17	20.5	10	2 S10926	inhibin beta-A cha

ALIGNMENTS

RESULT 1

PH1631
Ig H chain V-D-J region (clone B-leas 202) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1631
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93101609; PMID:8315387
A:Accession: PH1631
A:Molecule type: DNA
A:Residues: 1-15 <LEV>
A:Cross-References: UNIPARC:UPI000017C699
A:Experimental source: Bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match

Best Local Similarity 26.5%; Score 22; DB 2; Length 15;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DGQVMD 7
Db 9 DGYAMD 14

RESULT 2

S20410
protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)
N:Alternate names: LHCI protein kinase
C:Species: chloroplast Spinacia oleracea (spinach)
C:Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: S20410
R:Gal, A.; Herrmann, R.G.; Iotsepelch, F.; Ohad, I.
FEBS Lett. 298, 33-35, 1992
A>Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cyroc

A:Reference number: S20410; MUID:92183623; PMID:1544419
A:Accession: S20410
A:Molecule type: protein
A:Residues: 1-15 <GAL>
A:Cross-References: UNIPROT:Q9T2K8; UNIPARC:UPI000008E40D

A:Genetics:
A:Genome: chloroplast

C:Function:
A:Description: is responsible for the regulation of energy distribution between photosyn
A>Note: does not exhibit redox-controlled activation
C:Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phosphot

Query Match 26.5%; Score 22; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 DVDLSTAS 14
|:|:|
Db 6 DVEKSTLS 13

RESULT 3

151887
hypothetical EMSRI/FLI1 mutant fusion protein, type 1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C/Accession: 151887
R/Downing, J.R.; Head, D.R.; Parham, D.M.; Douglass, E.C.; Hulsnoff, M.G.; Link, M.P.; Mc
Am, J. Patbol. 143, 1294-1300, 1993
A/Title: Detection of the (11;22)(q24;q12) translocation of Ewing's sarcoma and peripher
A/Reference number: 151887; PMID:9405652; PMID:8238248
A/Accession: 151887
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-17 <DOW>
A/Cross-references: UNIPARC:UPI000011BDE2; GB:S66911; NID:g440935; PIDN:AMB28655.1; PID:
C/Comment: This sequence is the chimeric product of a translocation mutation.
C/Genetics:
A/Gene: EMSRI/FLI1; EMS/FLI-1
A/Map position: 22q12/11q24
C/Keywords: fusion protein

Query Match 26.5%; Score 22; DB 4; Length 17;
Best Local Similarity 36.4%; Pred. No. 1.9e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGQVMVDLS 11
|:|:|
Db 7 DEGPDLIDPS 17

RESULT 4

502473
coat protein VP1 - human poliovirus 1 (fragment)
C/Species: human poliovirus 1
C/Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C/Accession: 502473
R/Martin, A.; Wychowski, C.; Couderc, T.; Craintic, R.; Hogle, J.; Girard, M.
EMBO J. 7, 2839-2847, 1988
A/Title: Engineering a poliovirus type 2 antigenic site on a type 1 capsid results in a
A/Reference number: 502473; PMID:89030650; PMID:2460345
A/Accession: 502473
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-16 <MAR>
A/Cross-references: UNIPROT:Q8QNT2; UNIPROT:Q84871; UNIPROT:Q84866; UNIPROT:Q84865; UNIF

Query Match 25.9%; Score 21.5; DB 2; Length 16;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 6 MDVDLSTASTT 16
|:|:|
Db 1 MTVD-NPASTT 10

RESULT 5

B61458
Ig kappa chain V-1 region (BLA) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C/Accession: B61458
R/Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A/Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-assoc
A/Reference number: A61458; PMID:90039128; PMID:2478651
A/Accession: B61458
A/Status: preliminary
A/Molecule type: protein

A/Residues: 1-13 <BRO>
A/Cross-references: UNIPARC:UPI000017C25D
C/Keywords: heterotetramer; immunoglobulin

Query Match 25.3%; Score 21; DB 2; Length 13;
Best Local Similarity 30.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 DVDLSTASTT 16
|:|:|
Db 1 DIQWTSPTT 10

RESULT 6

A61458
Ig kappa chain V-1 region (BOU) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C/Accession: A61458; PLO156
R/Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A/Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-assoc
A/Reference number: A61458; PMID:90039128; PMID:2478651
A/Accession: A61458
A/Molecule type: protein
A/Residues: 1-13 <BRO>
A/Cross-references: UNIPARC:UPI000017C25E
C/Comment: This protein is one of monoclonal IGM reactive with myeloma-associated glycop
C/Keywords: heterotetramer; immunoglobulin

Query Match 25.3%; Score 21; DB 2; Length 13;
Best Local Similarity 30.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 DVDLSTASTT 16
|:|:|
Db 1 DIQWTSPTT 10

RESULT 7

PL0137
protein kinase, 80K - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 18-Jun-1993
C/Accession: PL0137
R/Decheret, U.; Weber, M.; Weber-Schaeufelen, M.; Wolny, E.
J. Neurochem. 53, 1268-1275, 1989
A/Title: Isolation and partial characterization of an 80,000-dalton protein kinase from t
A/Reference number: PL0137; PMID:89361455; PMID:2769266
A/Accession: PL0137
A/Molecule type: protein
A/Residues: 1-16 <DEC>
A/Cross-references: UNIPARC:UPI0000177D3E
C/Comment: This protein has a novel serine/threonine-specific protein kinase activity.

Query Match 25.3%; Score 21; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 2.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GQVMDVD 9
|:|:|
Db 1 GDEVVDVD 7

RESULT 8

G58501
48K bile/gallbladder stone protein - unidentified bacterium (fragment)
C/Species: unidentified bacterium
C/Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C/Accession: G58501
R/Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A/Description: The proteins of kidney and gallbladder stones.

A:Reference number: A58501
A:Accession: G58501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <BIN>
A:Cross-references: UNIPROT:O7M1C8, UNIPARC:UPI000017ABD6
A:Experimental source: human bile and gallbladder stones
A:Note: 1-Ser and 4-Glu were also found

Query Match 24.1%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EDQGMV 6
|||:
Db 5 EDGKAL 10

RESULT 9

PS0259
39K protein 3225 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
R:Teugita, A.; Kamo, M.
C:Accession: PS0259
Submitted to JIPID, April 1993
A:Reference number: PS0209
A:Accession: PS0259
A:Molecule type: protein
A:Residues: 1-11 <TSU>
A:Cross-references: UNIPARC:UPI000017B102
A:Experimental source: callus
C:Comment: molecular weight 39K, pI 5.7.

Query Match 24.1%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EDQGMV 6
|||:
Db 4 EDGPIV 9

RESULT 10

S70719
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Salmonella typhimurium (fr
C:Species: Salmonella typhimurium
C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 31-Dec-2004
C:Accession: S70719
R:Qi, S.Y.; Li, Y.; Szynski, A.; Giles, I.G.; Moir, A.; O'Connor, C.D.
Mol. Microbiol. 17, 523-531, 1995
A:Title: Salmonella typhimurium responses to a bactericidal protein from human neutroph
A:Reference number: S70719; MUID:96100451; PMID:8559071
A:Accession: S70719
A:Molecule type: protein
A:Residues: 1-15 <OIS>
A:Cross-references: UNIPROT:Q9RFJ3, UNIPROT:Q8XGX4, UNIPARC:UPI000017CDB2
A:Experimental source: strain SL1344
C:Superfamily: H(+)-transporting ATP synthase
C:Keywords: ATP binding; hydrogen ion transport; hydrolase

Query Match 24.1%; Score 20; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 GQVMDV 8
|||:
Db 10 GAVVDV 15

RESULT 11

PD0778
NADH2 dehydrogenase (EC 1.6.99.3) 46K chain - fava bean mitochondrion (fragment)

N:Alternate names: complex I 46K chain; NADH-ubiquinone reductase 46K chain
C:Species: mitochondrion Vicia faba (fava bean)
C>Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 03-Jun-2002
C:Accession: PD0778
R:Leferme, S.; Bonty, M.
Plant Physiol. 102, 435-443, 1993

A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH:
A:Reference number: PD0775; MUID:94151437; PMID:8108509
A:Accession: PD0778
A:Molecule type: protein

A:Residues: 1-15 <LEF>
A:Cross-references: UNIPARC:UPI000017CDAF
C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the th
ranging from 5K to 75K.
C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by
C:Genetics:
A:Genome: mitochondrion
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 24.1%; Score 20; DB 2; Length 15;
Best Local Similarity 37.5%; Pred. No. 3.6e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 EDQGMV 8
|||:
Db 3 DNGDVTDV 10

RESULT 12

A42291
tail fiber protein I - phage P2 (fragment)
C:Species: phage P2
C>Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C:Accession: A42291
R:Haggard-Ljungquist, E.; Halling, C.; Calendar, R.
J. Bacteriol. 174, 1462-1477, 1992
A:Title: DNA sequences of the tail fiber genes of bacteriophage P2: evidence for horizon
A:Reference number: A42291; MUID:92165720; PMID:1531648
A:Accession: A42291
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <HAG>
A:Cross-references: UNIPROT:P26701, UNIPARC:UPI000017A829; GB:M64677

Query Match 24.1%; Score 20; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 3.9e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 DQVMDV 8
|||:
Db 7 DGDVITV 13

RESULT 13

GKHU1
gastric juice peptide - human
C:Species: Homo sapiens (man)
C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 16-Aug-2004
C:Accession: A01628
R:Heathcote, J.G.; Washington, R.J.
Int. J. Protein Res. 2, 117-126, 1970
A:Title: Peptides of normal human gastric juice.
A:Reference number: A01628; MUID:75150568; PMID:5538385
A:Accession: A01628
A:Molecule type: protein
A:Residues: 1-10 <HEA>
A:Cross-references: UNIPROT:P01358, UNIPARC:UPI000012B049
A:Note: a second peptide lacking 1-Leu, but otherwise identical in composition with the
C:Keywords: stomach

Query Match 22.9%; Score 19; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GQVMDVD 9
|:|:|
Db 4 GKVEDSD 10

RESULT 14

PN0160
ribosomal protein S16 - fungus (*Fusarium sporotrichioides*) (fragment)
C/Species: *Fusarium sporotrichioides*
C/Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C/Accession: PN0160
R:Fukaya, N.; Chow, L.P.; Sugiura, Y.; Taugita, A.; Ueno, Y.; Tabuchi, K.
Submitted to JIPID, May 1994
A/Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*
A/Reference number: PN0160
A/Accession: PN0160
A/Molecule type: protein
A/Residues: 1-12 <FUK>
A/Cross-references: UNIPROT:Q7M4Y0, UNIPARC:UPI000017B41C
C/Keywords: protein biosynthesis; ribosome

Query Match 22.9%; Score 19; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 4.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 VMDVD 9
|:|:|
Db 6 VRDVD 10

RESULT 15

PQ0491
self-incompatibility locus glycoprotein delta - wild cabbage (fragment)
C/Species: *Brassica oleracea* (wild cabbage)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C/Accession: PQ0491
R:Gaude, T.; Frilly, A.; Heilmann, P.; Mariac, C.; Rougier, M.; Fobis, I.; Dumas, C.
Plant Cell 5, 75-86, 1993
A/Title: Expression of a self-incompatibility gene in a self-compatible line of *Brassica oleracea*
A/Reference number: J01733; MUID:93177215; PMID:8439745
A/Accession: PQ0491
A/Molecule type: protein
A/Residues: 1-13 <GAU>
A/Cross-references: UNIPROT:Q9SXH5, UNIPROT:Q9SXH7, UNIPROT:Q23846, UNIPROT:Q23837, UNIPROT:Q9SXH4, UNIPROT:Q23833, UNIPROT:Q8S9B2, UNIPROT:Q9SXH6, UNIPROT:Q23834, UNIPROT:Q8W
A/Experimental source: stigma, var. acephala P5751
C/Superfamily: S-locus receptor-like kinase SRK; protein kinase homology; S-locus-specific
C/Keywords: glycoprotein

Query Match 22.9%; Score 19; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 4.5e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 10 LSTASTQ 17
::|:|:|
Db 1 INTLSTE 8

Search completed: December 12, 2005, 22:15:08
Job time : 38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 22:02:21 ; Search time 229 Seconds
(without alignments)
52.375 Million cell updates/sec

Title: US-10-758-165A-16
Perfect score: 83
Sequence: 1 EDGQVMDVLDLASTTQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 10169

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	30.1	10	2	Q70G06_PRVKA
2	25	30.1	15	2	Q9UWH9_9EURY
3	25	30.1	15	2	Q69FJ1_9PLEO
4	24	28.9	14	2	Q69FHS_9PLEO
5	24	28.9	15	1	DNAX_COMAC
6	24	28.9	15	2	Q69FJ3_9PLEO
7	24	28.9	15	2	Q69GDI_9PLEO
8	24	28.9	16	2	Q69G98_9PLEO
9	24	28.9	16	2	Q69GB0_9PLEO
10	24	28.9	16	2	Q69GCS_9PLEO
11	24	28.9	16	2	Q69GC8_9PLEO
12	24	28.9	17	2	Q69GA7_9PLEO
13	23	27.7	15	2	Q85HM7_9PAS
14	23	27.7	16	2	Q9CTB2_MOUSE
15	23	27.7	17	2	Q71IF7_LACDL
16	23	27.7	17	2	Q9QV75_9MURI
17	23	27.7	17	2	Q9QVK3_9MURI
18	22	26.5	13	2	Q7TE19_9CIOS
19	22	26.5	13	2	Q7TE20_9CIOS
20	22	26.5	13	2	Q7TE21_9CIOS
21	22	26.5	13	2	Q7TE22_9CIOS
22	22	26.5	14	1	GRF75_CANPA
23	22	26.5	15	2	Q9T2K8_SPIOI
24	22	26.5	16	2	Q69F17_9PLEO
25	22	26.5	17	2	Q9HDO6_CANRU
26	21	25.3	10	2	Q9LSW6_LIBAC
27	21	25.3	11	2	Q9R1N6_MOUSE
28	21	25.3	13	2	Q7TE26_9CIOS
29	21	25.3	13	2	Q7TE28_9CIOS
30	21	25.3	13	2	Q7TE30_9CIOS
31	21	25.3	13	2	Q7TE32_9CIOS

32	21	25.3	13	2	Q7TE34_9CIOS
33	21	25.3	13	2	Q7TE36_9CIOS
34	21	25.3	13	2	Q7TE38_9CIOS
35	21	25.3	13	2	Q7TE40_9CIOS
36	21	25.3	13	2	Q7TE42_9CIOS
37	21	25.3	13	2	Q7TE44_9CIOS
38	21	25.3	13	2	Q7TE46_9CIOS
39	21	25.3	13	2	Q7TE48_9CIOS
40	21	25.3	13	2	Q7TE50_9CIOS
41	21	25.3	13	2	Q7TE52_9CIOS
42	21	25.3	13	2	Q7TE54_9CIOS
43	21	25.3	13	2	Q7TE56_9CIOS
44	21	25.3	13	2	Q7TE58_9CIOS
45	21	25.3	13	2	Q7TE60_9CIOS

ALIGNMENTS

```

RESULT 1
Q70G06_PRVKA PRELIMINARY; PRT; 10 AA.
ID Q70G06_PRVKA PRELIMINARY; PRT; 10 AA.
AC Q70G06;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DE ORF1.2 protein (Fragment).
OS Pseudorabies virus (strain Kaplan) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=33703;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Kaplan;
RX PubMed=14671123; DOI=10.1128/JVI.78.1.424-440.2004;
RA Klupp B.G., Hengartner C.J., Mettenleiter T.C., Enquist L.W.;
RT "Complete, annotated sequence of the pseudorabies virus genome.";
RL J. Virol. 78:424-440(2004).
DR EMBL; AJ581560; CAB46335.1; -; Genomic_DNA.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1006 MW; D276B4C1A8640B02 CRC64;

Query Match 30.1%; Score 25; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 3.1e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 MDVLISTAS 14
Db 1 MDVERTAA 9

RESULT 2
Q9UWH9_9EURY PRELIMINARY; PRT; 15 AA.
ID Q9UWH9_9EURY PRELIMINARY; PRT; 15 AA.
AC Q9UWH9;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DE Aldhyde ferredoxin oxidoreductase (Fragment).
OS Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=35749;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=ES-1;
RX MEDLINE=95370155; PubMed=7642503;
RA Heider J., Ma K., Adams M.W.;
RT "Purification, characterization, and metabolic function of tungsten-
containing aldehyde ferredoxin oxidoreductase from the
RT hyperthermophilic and proteolytic archaeon Thermococcus strain ES-1.";
RL J. Bacteriol. 177:4757-4764(1995).
SQ SEQUENCE 15 AA; 1750 MW; 0441670278198619 CRC64;

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Query Match 30.1%; Score 25; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 4.7e+03;
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQVMDVDLST 12
 DB 6 GKLRVNLTT 15

RESULT 3
 069FJ1_9PLEO PRELIMINARY; PRT; 15 AA.

AC 069FJ1;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Stenphylium solani.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stenphylium.
 OX NCBI_TaxID=110364;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=EGS41-135;
 RA Inderbitzin P., Berbee M.L.;
 RT "Mating type gene evolution in Pleospora, the sexual state of Stenphylium."
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY339855; AAR0451.1; -, Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1547 MW; 84F7BEBAD16DF45 CRC64;

Query Match 30.1%; Score 25; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 4.7e+03;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 DVDLSTASTQ 17
 DB 3 DIIPIINGTQ 13

RESULT 4
 069FH5_9PLEO PRELIMINARY; PRT; 14 AA.

AC 069FH5;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Stenphylium callisteph.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stenphylium.
 OX NCBI_TaxID=119932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NO 0536;
 RA Inderbitzin P., Berbee M.L.;
 RT "Mating type gene evolution in Pleospora, the sexual state of Stenphylium."
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY339863; AAR0467.1; -, Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1401 MW; CSF7BFCD169F5D CRC64;

Query Match 28.9%; Score 24; DB 2; Length 14;
 Best Local Similarity 36.4%; Pred. No. 6.5e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 DVDLSTASTQ 17
 DB 3 DIIPIINGTQ 13

DB 2 DIIPIINGTQ 12

RESULT 5
 DNAX COMAC STANDARD; PRT; 15 AA.

AC P81709;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Chaperone protein dnax (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) (Fragment).
 GN Name-dnax;
 OS Comamonas acidovorans (Pseudomonas acidovorans).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Comamonadaceae; Delftia.
 OX NCBI_TaxID=80866;
 RN [1]
 RP PROTEIN SEQUENCE, AND INDUCTION.
 RC STRAIN=MCI;
 RX PubMed=15073309; DOI=10.1099/mic.0.26774-0;
 RA Bendoric D., Davidson I., Babel W.;
 RT "Regulation of catabolic enzymes during long-term exposure of Delftia acidovorans MCI to chlorophenox herbicides";
 RL Microbiology 150:1005-1014(2004).
 CC -1- FUNCTION: Acts as a chaperone (By similarity).
 CC -1- INDUCTION: By stress conditions e.g. heat shock, and by the herbicide dichlorprop [(R)-2-(2,4-dichlorophenoxy)propionate].
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 CC HAMAP: MF_00332; -, 1.
 DR InterPro: IPR001023; Hsp70.
 DR Pfam: PF00012; HSP70; 1.
 DR PROSITE: PS00297; HSP70_1; 1.
 DR PROSITE: PS00329; HSP70_2; PARTIAL.
 DR PROSITE: PS01036; HSP70_3; PARTIAL.
 KW ATP-binding; Chaperone; Direct protein sequencing; Heat shock;
 KW Nucleotide-binding.
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1513 MW; 28EAD48F7526C40F CRC64;

Query Match 28.9%; Score 24; DB 1; Length 15;
 Best Local Similarity 25.0%; Pred. No. 7e+03;
 Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 QVMDVDLST 15
 DB 1 KIIGIDGTNS 12

RESULT 6
 069FJ3_9PLEO PRELIMINARY; PRT; 15 AA.

AC 069FJ3;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Stenphylium sarciniforme.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stenphylium.
 OX NCBI_TaxID=119934;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=EGS38-121;
 RA Inderbitzin P., Berbee M.L.;
 RT "Mating type gene evolution in Pleospora, the sexual state of

```

RT   Stenphyllum.";
RL   Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
DR   EMBL; AY339854; AAR04449.1; -; Genomic_DNA.
KW   Hypothetical protein..1
FT   NON_TER
SQ   SEQUENCE 15 AA; 1533 MW; 84EF1D8AD166DF45 CRC64;

Query Match
Best Local Similarity 28.9%; Score 24; DB 2; Length 15;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY   7 DVDLSTASTTQ 17
      |::|::|
      3 DIEVPTINGTQ 13

Db

RESULT 7
Q69GDI_9PLEO
ID   Q69GDI_9PLEO PRELIMINARY; PRT; 15 AA.
AC   Q69GDI;
DT   25-OCT-2004 (TREMBLrel. 28, Created)
DT   25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE   Hypothetical protein (Fragment).
OS   Stenphyllum sp. EGS08-174.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC   Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stenphyllum.
OC   NCBI_TaxId=234989;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=EGS 08-174;
RA   Inderbitzin P., Berbee M.L.;
RT   "Mating type gene evolution in Pleospora, the sexual state of
RT   Stenphyllum."
RL   Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
DR   EMBL; AY335169; AAR00951.1; -; Genomic_DNA.
KW   Hypothetical protein..1
FT   NON_TER
SQ   SEQUENCE 15 AA; 1533 MW; 84EF1D8AD166DF45 CRC64;

Query Match
Best Local Similarity 28.9%; Score 24; DB 2; Length 15;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY   7 DVDLSTASTTQ 17
      |::|::|
      3 DIEVPTINGTQ 13

Db

RESULT 8
Q69G98_9PLEO
ID   Q69G98_9PLEO PRELIMINARY; PRT; 16 AA.
AC   Q69G98;
DT   25-OCT-2004 (TREMBLrel. 28, Created)
DT   25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Pleospora sp. P337.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC   Pleosporales; Pleosporaceae; Pleospora.
OC   NCBI_TaxId=234982;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=P337;
RA   Inderbitzin P., Berbee M.L.;
RT   "Mating type gene evolution in Pleospora, the sexual state of
RT   Stenphyllum."
RL   Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
DR   EMBL; AY335180; AAR00984.1; -; Genomic_DNA.
KW   Hypothetical protein..1
FT   NON_TER
SQ   SEQUENCE 16 AA; 1662 MW; 54D36D8AD166DF07 CRC64;

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Query Match
Best Local Similarity 28.9%; Score 24; DB 2; Length 16;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY   7 DVDLSTASTTQ 17
      |::|::|
      4 DIEVPTINGTQ 14

Db

RESULT 9
Q69GB0_9PLEO
ID   Q69GB0_9PLEO PRELIMINARY; PRT; 16 AA.
AC   Q69GB0;
DT   25-OCT-2004 (TREMBLrel. 28, Created)
DT   25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Pleospora etumina.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC   Pleosporales; Pleosporaceae; Pleospora.
OC   NCBI_TaxId=235069;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=EGS 29-099;
RA   Inderbitzin P., Berbee M.L.;
RT   "Mating type gene evolution in Pleospora, the sexual state of
RT   Stenphyllum."
RL   Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
DR   EMBL; AY335176; AAR00972.1; -; Genomic_DNA.
KW   Hypothetical protein..1
FT   NON_TER
SQ   SEQUENCE 16 AA; 1632 MW; 54CF1D8AD166DF07 CRC64;

Query Match
Best Local Similarity 28.9%; Score 24; DB 2; Length 16;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY   7 DVDLSTASTTQ 17
      |::|::|
      4 DIEVPTINGTQ 14

Db

RESULT 10
Q69GCS_9PLEO
ID   Q69GCS_9PLEO PRELIMINARY; PRT; 16 AA.
AC   Q69GCS;
DT   25-OCT-2004 (TREMBLrel. 28, Created)
DT   25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Stenphyllum sp. EGS48-089.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC   Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stenphyllum.
OC   NCBI_TaxId=235021;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=EGS 48-089;
RA   Inderbitzin P., Berbee M.L.;
RT   "Mating type gene evolution in Pleospora, the sexual state of
RT   Stenphyllum."
RL   Submitted (JUL-2003) to the EMBL/Genbank/DBJ databases.
DR   EMBL; AY335171; AAR00957.1; -; Genomic_DNA.
KW   Hypothetical protein..1
FT   NON_TER
SQ   SEQUENCE 16 AA; 1632 MW; 54CF1D8AD166DF07 CRC64;

Query Match
Best Local Similarity 28.9%; Score 24; DB 2; Length 16;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY   7 DVDLSTASTTQ 17
      |::|::|
      4 DIEVPTINGTQ 14

Db

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RESULT 11
ID 069GC8_9PLEO PRELIMINARY; PRT; 16 AA.
AC 069GC8;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Stenphylium sp. EG548-074.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Stenphylium.
OX NCBI_TaxID=235018;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EGS 48-074;
RA Inderbitzin P., Berbee M.L.;
RT "Matling type gene evolution in Pleospora, the sexual state of
RT Stenphylium."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY35170; AAR0954.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 16 AA; 1632 MW; 54CF1D8AD16DF07 CRC64;

Query Match 28.9%; Score 24; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. No. 7.5e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 DVDLSTASTQ 17
DB 4 DIEVPTINGTQ 14

RESULT 12
ID 069GA7_9PLEO PRELIMINARY; PRT; 17 AA.
AC 069GA7;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Pleospora paludiscripti.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Pleospora.
OX NCBI_TaxID=235070;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=EGS 31-016;
RA Inderbitzin P., Berbee M.L.;
RT "Matling type gene evolution in Pleospora, the sexual state of
RT Stenphylium."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY35177; AAR0975.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 17 AA; 1733 MW; 38C9DD8AD16DF07 CRC64;

Query Match 28.9%; Score 24; DB 2; Length 17;
Best Local Similarity 36.4%; Pred. No. 7.9e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 DVDLSTASTQ 17
DB 5 DIEVPTINGTQ 15

RESULT 13
ID 085HM7_9PASS PRELIMINARY; PRT; 15 AA.
AC 085HM7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)

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DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE ATPase subunit 8 (Fragment).
OS Name=ATP8;
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Motacillidae; Motacilla.
OX NCBI_TaxID=228286;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=22745498; PubMed=12859633;
RX DOI=10.1046/j.1365-294X.2003.01883.x;
RA Odeen A., Bjorklund M.;
RT "Dynamics in the evolution of sexual traits: losses and gains";
RT radiation and convergence in yellow wagtails (Motacilla flava).";
RL Mol. Ecol. 12:2113-2130(2003).
DR EMBL; AY259472; AAP20723.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON TER 1
SQ SEQUENCE 15 AA; 1768 MW; 85F1FD232395861 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1e+04;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 LSTASTT 16
DB 2 LTPSTT 8

RESULT 14
ID 09CTB2_MOUSE PRELIMINARY; PRT; 16 AA.
AC 09CTB2;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:110033N23 product:nitrogen fixation gene 1 (S.
DE cerevisiae), full insert sequence. (Fragment).
GN Name=Nfs1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RX Kawai T., Shinagawa A., Shibata K., Yoshino W., Itoh M., Ishii Y.,
RX Aizawa K., Hara A., Fukunishi Y., Kono H., Adachi U., Fukuda S.,
RX Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RX Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RX Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RX Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RX Schirml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RX Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RX Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RX Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RX Guernicich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RX Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombaerts P.,

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RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=whole body;
RA The FANTOM Consortium,
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kikunai T., Tashiro H., Itoh M.,
RA Suni N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Mochizuki M.,
RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Aizawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishi Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL, AK004077; BAB3157.1; -; mRNA.
DR MGI; MGI:1316706; Nfsl.
DR GO; GO:0005615; C:extracellular space; TRS.
DR GO; GO:0005759; C:mitochondrial matrix; IDA.
FT NON TER 1
SO SEQUENCE 16 AA; 1881 MW; 029ECFC9BC205263 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 16;
Best Local Similarity 35.3%; Pred. No. 1.1e+04;
Matches 6; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

OY 1 EDGQVMDVLDSTASTTQ 17
Db :||:|:|:|
3 QDG---IDLKSIKWTQ 15

RESULT 15
O71IF7_LACDL
ID O71IF7_LACDL PRELIMINARY; PRT; 17 AA.
AC O71IF7;

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DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Glycylserine kinase (EC 2.7.1.30) (Fragment).
OS Lactobacillus delbrueckii (subsp. lactis).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=29397;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 4797;
RA Langenehm J.F., Ulrich R.L.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF496306; AAC06980.1; -; Genomic DNA.
DR GO; GO:0004370; F:glycylserine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Kinase; Transferase.
FT NON TER 17
SQ SEQUENCE 17 AA; 1878 MW; 424DDE87D29A0C64 CRC64;

Query Match 27.7%; Score 23; DB 2; Length 17;
Best Local Similarity 36.4%; Pred. No. 1.2e+04;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 5 VMDVLDSTASTT 15
Db :||:|:|:|
6 ILAIDEGTTST 16

Search completed: December 12, 2005, 22:14:25
Job time : 230 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 19:37:19 ; Search time 92.181 Seconds
(without alignments)
81.030 Million cell updates/sec

Title: US-10-758-165A-16
Perfect score: 83
Sequence: 1 EDGQVMDVLDLSTASTTQ 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*
9: Geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	17	ADRI0616	Human IGE
2	83	100.0	98	AAR85587	FC(epsilo
3	83	100.0	106	AAR85587	FC(epsilo
4	83	100.0	128	ABG74778	Human mod
5	83	100.0	236	ABG74780	Human mod
6	83	100.0	255	AAP50305	Fused ant
7	83	100.0	315	AAR85582	FC(epsilo
8	83	100.0	320	AAO19667	Human IGE
9	83	100.0	323	AAU80286	Human IGE
10	83	100.0	323	AAU80285	Human IGE
11	83	100.0	323	AAU80284	Human IGE
12	83	100.0	324	AAR83559	FC(epsilo
13	83	100.0	325	AAR75225	Human IGE
14	83	100.0	325	AAR77241	Human IGE
15	83	100.0	325	AAR83582	CH2 to CH
16	83	100.0	325	AAV79994	Human imm
17	83	100.0	327	ADY21849	Human IGE
18	83	100.0	330	AAU80289	Human IGE
19	83	100.0	331	AAAB0362	Human IGE
20	83	100.0	331	ADP25768	Binding d
21	83	100.0	331	ADY21799	Human IGE
22	83	100.0	331	ADY21722	Human IGE
23	83	100.0	336	AAU80288	Human IGE
24	83	100.0	346	ABG74781	Human IGE

25	83	100.0	346	6	ABG74785	Abg74785 Human CH2
26	83	100.0	347	6	ABG74784	Abg74784 Human CH2
27	83	100.0	347	6	ABG74783	Abg74783 Human CH2
28	83	100.0	348	6	ABG74782	Abg74782 Human CH2
29	83	100.0	367	1	AAP80291	Aap80291 Interleuk
30	83	100.0	425	6	AAE35114	AAe35114 Human imm
31	83	100.0	427	6	AAO19666	AAo19666 Human IGE
32	83	100.0	428	2	AA42950	AAa42950 Human IGE
33	83	100.0	428	5	AAU80283	AAu80283 Human IGE
34	83	100.0	428	5	AAU80283	AAu80283 Human IGE
35	83	100.0	428	5	AAU80283	AAu80283 Human IGE
36	83	100.0	428	6	AAE35113	AAe35113 Human imm
37	83	100.0	428	7	ADD48440	ADd48440 Human Pro
38	83	100.0	428	7	ADE97382	ADe97382 Human IGE
39	83	100.0	441	5	AAU80287	AAu80287 Human IGE
40	83	100.0	493	1	AAP40065	AAP40065 Sequence
41	83	100.0	497	9	ADW24784	ADw24784 Human var
42	83	100.0	497	9	ADW24742	ADw24742 Human var
43	83	100.0	497	9	ADZ08809	ADz08809 Mammalian
44	83	100.0	497	9	ADZ08940	ADz08940 Mammalian
45	83	100.0	497	9	ADZ44466	ADz44466 Human imm

ALIGNMENTS

RESULT 1
ADRI0616
ID ADRI0616 standard; peptide; 17 AA.

ADRI0616;

21-OCT-2004 (first entry)

Human IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 16.

Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;

anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;

human.

WO2004065936-A2.

05-AUG-2004.

15-JAN-2004; 2004WO-US003566.

16-JAN-2003; 2003US-0440472P.

(UNNC-) UNIV NORTH CAROLINA STATE.

Hammerberg B;

WPI; 2004-593545/57.

Novel antibody that specifically binds to mammalian IGE epitope, useful for testing an allergen reactivity of IGE sample, detecting mammalian IGE or treating asthma or anaphylactic shock.

Example 6; Page 9; 14pp; English.

The present invention relates to a novel monoclonal antibody (I) that specifically binds to a mammalian IGE epitope, where the epitope is between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE. (I) is useful for testing an allergen reactivity of an IGE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (I) is also useful for detecting mammalian IGE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine IGE corresponding to amino acid residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE. The present sequence is the
 CC human IgE 3.76 recognition site.

XX
 SQ Sequence 17 AA;

Query Match 100.0%; Score 83; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDLSTASTTQ 17
 DB 1 EDGQVMDVDLSTASTTQ 17

RESULT 2

AA85588 standard; peptide; 98 AA.

XX
 AC AAR85588;

DT 06-MAR-1996 (first entry)

DE Fc(epsilon) CH2'-CH4 amino acids 234-330.

XX Fc(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter;
 KM constant heavy region; E.coli; glycosylation; antigenic; immunogenic;
 KM histamine; anti-allergenic; vaccine; immune response.

XX Synthetic.

XX FR2715304-A1.

XX 28-JUL-1995.

XX 26-JAN-1994; 94FR-00000846.

XX 26-JAN-1994; 94FR-00000846.

PA (INMR) PASTEUR MERIEUX SERUMS & VACCINS.

PI Hurpin CM, Panero MJM;

DR WPI; 1995-265243/35.

XX Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain - has
 PT epitope(s) not present in native IgE, also derived antibodies for
 PT treating or preventing allergies, inflammatory immune disease, etc.

XX Claim 7; Page 32-33; 44pp; French.

CC Peptides AAR85582-9 are fragments of the Fc(epsilon) CH2'-CH4 fragment
 CC (AAR85589). This sequence covers amino acids 234-330 of the Fc(epsilon)
 CC constant heavy chain. The subfragments were derived from the sequence of
 CC the Fc(epsilon) CH2'-CH4 coding sequence (AAT01865) by recombinant
 CC methods from the plasmid pE2-4(7). When expressed in E.coli, the peptides
 CC produced are non-glycosylated Fc(epsilon) fragments. Altering the pattern
 CC of glycosylation unmasks new antigenic sites thus rendering the Fc
 CC fragment immunogenic and able to induce antibodies that recognise native
 CC IgE but do not form histamine-releasing complexes. The Fc fragments can
 CC be used in anti-allergic vaccines to modulate the intensity of immune
 CC responses mediated by IgE

XX
 SQ Sequence 98 AA;

Query Match 100.0%; Score 83; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDLSTASTTQ 17
 ||||||||||||||||

DB 38 EDGQVMDVDLSTASTTQ 54

RESULT 3

AA85587 standard; peptide; 106 AA.

XX
 AC AAR85587;

DT 06-MAR-1996 (first entry)

DE Fc(epsilon) CH2'-CH4 amino acids 226-330.

XX Fc(epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter;
 KM constant heavy region; E.coli; glycosylation; antigenic; immunogenic;
 KM histamine; anti-allergenic; vaccine; immune response.

XX Synthetic.

XX FR2715304-A1.

XX 28-JUL-1995.

XX 26-JAN-1994; 94FR-00000846.

XX 26-JAN-1994; 94FR-00000846.

PA (INMR) PASTEUR MERIEUX SERUMS & VACCINS.

PI Hurpin CM, Panero MJM;

DR WPI; 1995-265243/35.

XX Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain - has
 PT epitope(s) not present in native IgE, also derived antibodies for
 PT treating or preventing allergies, inflammatory immune disease, etc.

XX Claim 7; Page 32-33; 44pp; French.

CC Peptides AAR85582-9 are fragments of the Fc(epsilon) CH2'-CH4 fragment
 CC (AAR85589). This sequence covers amino acids 226-330 of the Fc(epsilon)
 CC constant heavy chain. The subfragments were derived from the sequence of
 CC the Fc(epsilon) CH2'-CH4 coding sequence (AAT01865) by recombinant
 CC methods from the plasmid pE2-4(7). When expressed in E.coli, the peptides
 CC produced are non-glycosylated Fc(epsilon) fragments. Altering the pattern
 CC of glycosylation unmasks new antigenic sites thus rendering the Fc
 CC fragment immunogenic and able to induce antibodies that recognise native
 CC IgE but do not form histamine-releasing complexes. The Fc fragments can
 CC be used in anti-allergic vaccines to modulate the intensity of immune
 CC responses mediated by IgE

XX
 SQ Sequence 106 AA;

Query Match 100.0%; Score 83; DB 2; Length 106;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDLSTASTTQ 17
 DB 46 EDGQVMDVDLSTASTTQ 62

RESULT 4

ABG74778 standard; protein; 128 AA.

XX
 AC ABG74778;

DT 05-JUN-2003 (first entry)

DE Human modified IgE CH2 domain.

XX CH3 domain; IgE; antigen; non-anaphylactic; anti-IgE; fusion protein;

OS	Homo sapiens.
OS	Synthetic.
NN	EPI262491-A2.
PD	04-DEC-2002.
PE	22-MAY-2002; 2002EP-00253606.
PR	22-MAY-2001; 2001US-0292638P.
PA	(PFIZ) PFIZER PROD INC.
PI	Brown TM, Morsey MA;
XX	WPI: 2003-122561/12.
DR	N-PSDB; ACA55176.
PT	Novel isolated antigenic peptide comprising amino acid residues of CH3 domain of IGE molecule from first species and a second unrelated species,
PT	induces non-anaphylactic anti-IGE immune response in animal.
PS	Claim 15; Page 32; 50pp; English.
XX	This invention describes a novel antigenic peptide comprising amino acid
CC	residues of an IGE CH3 domain from a first species (ADE1) and amino acid
CC	residues of an IGE CH3 domain of a second unrelated species (ADE2), where
CC	ADE1 is conserved in the IGE CH3 domain of the second species and ADE2 is
CC	not conserved in the IGE CH3 domain of the first species. The novel
CC	antigenic peptide induces a non-anaphylactic anti-IGE immune response in
CC	an animal. The invention also discloses the polynucleotide sequence
CC	encoding the antigenic peptide and an antigenic fusion protein comprising
CC	the antigenic peptide of the invention and a heterologous protein
CC	carrier, where the fusion protein induces an anti-IGE immune response
CC	that does not cause anaphylaxis when administered to an animal. The
CC	products of the invention have dermatological, antiinflammatory and
CC	ophthalmological activity. The antigenic peptide described is capable of
CC	preventing IGE from binding to high affinity receptors on mast cells and
CC	basophils. The products of the invention are useful in the manufacture of
CC	a medicament for treating or preventing IGE-mediated allergic disorders
CC	including asthma, allergic rhinitis, gastrointestinal allergies such as
CC	food allergies, eosinophilia, conjunctivitis, glomerular nephritis, flea
CC	allergies or atopic dermatitis, in an animal, e.g. human or dog. The
CC	polynucleotide products are useful for treating IGE-mediated allergic
CC	disorders, by gene therapy. Antigenic peptides comprising conserved amino
CC	acid residues of the CH3 domain of an IGE molecule from one species
CC	flanked by variable amino acid residues of the CH3 domain of an IGE
CC	molecule from a second unrelated species are capable of inducing a high
CC	titer of anti-IGE antibodies when administered to an animal without
CC	causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences
CC	used in designing the constructs described in the disclosure of the
CC	invention
XX	
SO	Sequence 128 AA:
Query Match	100.0%; Score 83; DB 6; Length 128;
Best Local Similarity	100.0%; Pred. No. 2.5e+06;
Matches	17; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 EDGQVMDVDLSTASTTQ 17
Db	70 EDGQVMDVDLSTASTTQ 86
RESULT 5	
ABG74780	
ID	ABG74780 etandard; protein; 236 AA.
XX	

AC ABG74780;
XX
DT 05-JUN-2003 (first entry)
XX
DE Human modified IGE CH2-CH4 carrier protein.
XX
KW CH3 domain; IGE; antigen; non-anaphylactic; anti-IGE; fusion protein;
KW dermatological; antinflammatory; ophthalmological; allergy; asthma;
KW allergic rhinitis; gastrointestinal allergy; food allergy; eosinophilia;
KW conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis;
KW gene therapy; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN EP1262491-A2.
XX
PD 04-DEC-2002.
XX
PF 22-MAY-2002; 2002EP-00253606.
XX
PR 22-MAY-2001; 2001US-0292638P.
XX
PA (PF1Z) PRIZER PROD INC.
XX
P1 Brown TM, Morsey MA;
XX
DR WPI; 2003-122561/12.
XX
DR N-PSDB; ACAA55178.
XX
PT Novel isolated antigenic peptide comprising amino acid residues of CH3
PT domain of IGE molecule from first species and a second unrelated species,
PT induces non-anaphylactic anti-IGE immune response in animal.
XX
PS Claim 15; Page 33-34; 50pp: English.
XX
XX This invention describes a novel antigenic peptide comprising amino acid
XX residues of an IGE CH3 domain from a first species (ADE1) and amino acid
XX residues of an IGE CH3 domain of a second unrelated species (ADE2), where
XX ADE1 is conserved in the IGE CH3 domain of the second species and ADE2 is
XX not conserved in the IGE CH3 domain of the first species. The novel
XX antigenic peptide induces a non-anaphylactic anti-IGE immune response in
XX an animal. The invention also discloses the polynucleotide sequence
XX encoding the antigenic peptide and an antigenic fusion protein comprising
XX the antigenic peptide of the invention and a heterologous protein
XX carrier, where the fusion protein induces an anti-IGE immune response
XX that does not cause anaphylaxis when administered to an animal. The
XX products of the invention have dermatological, antinflammatory and
XX ophthalmological activity. The antigenic peptide described is capable of
XX preventing IGE from binding to high affinity receptors on mast cells and
XX basophils. The products of the invention are useful in the manufacture of
XX a medicament for treating or preventing IGE-mediated allergic disorders
XX including asthma, allergic rhinitis, gastrointestinal allergies such as
XX food allergies, eosinophilia, conjunctivitis, glomerular nephritis, flea
XX allergies or atopic dermatitis, in an animal, e.g. human or dog. The
XX polynucleotide products are useful for treating IGE-mediated allergic
XX disorders, by gene therapy. Antigenic peptides comprising conserved amino
XX acid residues of the CH3 domain of an IGE molecule from one species
XX flanked by variable amino acid residues of the CH3 domain of an IGE
XX molecule from a second unrelated species are capable of inducing a high
XX titre of anti-IGE antibodies when administered to an animal without
XX causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences
XX used in designing the constructs described in the disclosure of the
XX invention
XX
XX Sequence 236 AA;
XX
XX Query Match 100.0%; Score 83; DB 6; Length 236;
XX Best Local Similarity 100.0%; Prod. No. 5,1e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 EDGQVMDVLSASTTQ 17

```

Db          70 EDGQVMDVDLSTASTQ 86

RESULT 6
AAP50305
ID AAP50305 standard; protein; 255 AA.
XX
AC AAP50305;
XX
XX 25-MAR-2003 (revised)
DT 15-JAN-1992 (first entry)
XX
DE Fused antibody recognition site and interleukin-2 fragment.
XX
XX IGB; hIL-2.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX Protein 3. .118
XX Protein /label= IGE Ab recognition site
XX Protein 123. .255
XX Protein /label= IL-2 structural protein
XX
XX W08504673-A.
XX
XX 24-OCT-1985.
XX
XX 10-APR-1984; 84WO-JP000181.
XX
XX 10-APR-1984; 84WO-JP000181.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Senoo M, Onda H, Igarashi K;
XX
XX WPI; 1985-276145/44.
XX
XX N-PSDB; AAN50356.
XX
XX Novel DNA contg. DNA with structural gene coding peptide - contg.
XX antibody recognition site and DNA contg. structural gene coding human
XX interleukin 2 peptide.
XX
XX Disclosure; Fig 2; 36pp; Japanese.
XX
XX The fused IGE-IL-2 product may be used in refining the human interleukin
XX -2 antibody. The product may be expressed by an E.coli host under the
XX control of the trp promoter in plasmid pGEL 1028. (Updated on 25-MAR-2003
XX to correct PA field.)
XX
XX Sequence 255 AA;
SQ

Query Match 100.0%; Score 83; DB 1; Length 255;
Best Local Similarity 100.0%; Pred. NO. 5.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDLSTASTQ 17
   |||||||
Db 56 EDGQVMDVDLSTASTQ 72

RESULT 7
AAR85582
ID AAR85582 standard; peptide; 315 AA.
XX
AC AAR85582;
XX
XX 06-MAR-1996 (first entry)
DT
XX
DE Fc(epsilon) CH2'-CH4 amino acids 234-547.
XX
XX Fc(epsilon); antibody; human; myeloma; probe; IGE; tryptophan promoter;
XX constant heavy region; E.coli; glycosylation; antigenic; immunogenic;
XX

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```

KW histamine; anti-allergenic; vaccine; immune response.
XX
XX Synthetic.
XX
XX FR2715304-A1.
XX
XX 28-JUL-1995.
XX
XX 26-JAN-1994; 94FR-00000846.
XX
XX 26-JAN-1994; 94FR-00000846.
XX
XX 26-JAN-1994; 94FR-00000846.
XX
XX (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
XX
XX Hurpin CM, Panero MJM;
XX
XX WPI; 1995-265243/35.
XX
XX Antiallergic vaccine contg. polypeptide fragment of IGE heavy chain - has
XX epitope(s) not present in native IGE, also derived antibodies for
XX treating or preventing allergies, inflammatory immune disease, etc.
XX
XX Claim 4; Page 32-33; 44pp; French.
XX
XX Peptides AAR85582-9 are fragments of the Fc(epsilon) CH2'-CH4 fragment
XX (AAR83559). This sequence covers amino acids 234-547 of the Fc(epsilon)
XX constant heavy chain. The subfragments were derived from the sequence of
XX the Fc(epsilon) CH2'-CH4 coding sequence (AAT01865) by recombinant
XX methods from the plasmid pE2-4(17). When expressed in E.coli, the peptides
XX produced are non-glycosylated Fc(epsilon) fragments. Altering the pattern
XX of glycosylation unmask new antigenic sites thus rendering the Fc
XX fragment immunogenic and able to induce antibodies that recognise native
XX IGE but do not form histamine-releasing complexes. The Fc fragments can
XX be used in anti-allergenic vaccines to modulate the intensity of immune
XX responses mediated by IGE
XX
XX Sequence 315 AA;
SQ

Query Match 100.0%; Score 83; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. NO. 7.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDLSTASTQ 17
   |||||||
Db 38 EDGQVMDVDLSTASTQ 54

RESULT 8
AAO19667
ID AAO19667 standard; protein; 320 AA.
XX
XX AAO19667;
XX
XX 28-MAR-2003 (first entry)
DT
XX
DE Human IGE heavy chain constant region CH2-CH3-CH4 portion.
XX
XX Human; IGE; immunoglobulin E; immunotherapy; immune disease;
XX Fc(epsilon) receptor; autoimmune disease; constant region; heavy chain;
XX antiaesthetic; anti-allergic; antiinflammatory; dermatological;
XX antidiabetic; antineurotic; antidiabetic; neuroprotective;
XX CH2-CH3-CH4 region.
XX
XX Homo sapiens.
XX
XX W0200288317-A2.
XX
XX 07-NOV-2002.
XX
XX 01-MAY-2002; 2002WO-US013527.
XX
XX 01-MAY-2001; 2001US-00847208.
XX
XX 24-OCT-2001; 2001US-00000439.
XX

```

XX (REGC) UNIV CALIFORNIA.
PA Saxon A, Zhang K, Zhu D;
PI WPI; 2003-103456/09.
XX
XX New fusion molecules comprising polypeptide sequences that bind to IgG
PT inhibitory receptor and native IGE receptor. useful for treating IGE-
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or
PT autoimmune diseases.
XX
XX Claim 21; Fig 6; 116pp; English.
XX
XX The present invention relates to a fusion molecule comprising a first
CC polypeptide sequence capable of specific binding to a native IGE
CC inhibitory receptor consisting of an immune receptor tyrosine-based
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,
CC functionally connected to a second polypeptide sequence capable of
CC specific binding directly or indirectly to a native IGE receptor
CC (FcεRI). Also provided are nucleotide sequences encoding such a
CC fusion protein. The fusion molecules and compositions are useful for
CC creating an IGE-mediated biological response, preferably an IGE-mediated
CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic
CC dermatitis, severe food allergies, chronic urticaria, angioedema or
CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,
CC type-1 diabetes mellitus, or multiple sclerosis, and for preventing of,
CC or symptoms resulting from, a type I hypersensitivity reaction in a
CC subject receiving immunotherapy. The present sequence is the human IGE
CC heavy chain constant region CH2-CH3-CH4 portion
XX
SQ Sequence 320 AA;
XX
XX Query Match 100.0%; Score 83; DB 6; Length 320;
Best Local Similarity 100.0%; Pred. No. 7.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 EDGQVMDVDLSTASTTQ 17
Db 43 EDGQVMDVDLSTASTTQ 59
XX
XX RESULT 9
AAU80286
ID AAU80286 standard; protein; 323 AA.
XX
XX AAU80286;
XX
XX 30-JUL-2002 (first entry)
XX
XX Human IGE C2-C3-C4 domains for E.Coli expression.
XX
XX IGE; allergy; human; antiallergic; immunosuppressive; anti-anaphylactic;
XX antiaesthetic; dermatological; anti-inflammatory; immunoglobulin E; IGE;
XX vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
XX heavy chain C domain.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200220038-A2.
XX
XX 14-MAR-2002.
XX
XX 06-SEP-2001; 2001WO-DK000579.
XX
XX 06-SEP-2000; 2000DK-00001326.
XX
XX 15-SEP-2000; 2000US-0232831P.
XX
XX (PHAR-) PHARMEXA AS.
XX
XX Klyener S, Von Hoegen P, Voldborg B, Gautam A;
XX

DR WPI; 2002-383033/41.
DR N-PSDB; ABK51134.
XX
XX Inducing immune response against autologous immunoglobulin E in an
PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte
PT epitope an/or B-cell epitope derived from the immunoglobulin.
XX
XX Disclosure; Page 112-113; 151pp; English.
XX
XX This invention relates to a novel method for inducing an immune response
CC against autologous immunoglobulin E (IGE) in an animal. The method
CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte
CC (CTL) epitope and/or B-cell epitope derived from IGE, and T helper cell
CC epitope (TH epitope) which is foreign to the animal, by antigen
CC presenting cells (APCs) of the animal's immune system. The epitopes of
CC the invention may be used as a vaccine against allergic diseases. The
CC method of the invention is useful for inducing an immune response against
CC autologous IGE in an animal, which is useful for downregulating
CC autologous IGE in the animal. This method is useful in the prevention and
CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,
CC asthma and atopic dermatitis. The present sequence represents the human
CC IGE heavy chain C2-C3-C4 domains optimised for expression in an E. Coli
CC system, this sequence was used to create the epitopes of the invention
XX
SQ Sequence 323 AA;
XX
XX Query Match 100.0%; Score 83; DB 5; Length 323;
Best Local Similarity 100.0%; Pred. No. 7.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 EDGQVMDVDLSTASTTQ 17
Db 46 EDGQVMDVDLSTASTTQ 62
XX
XX RESULT 10
AAU80285
ID AAU80285 standard; protein; 323 AA.
XX
XX AAU80285;
XX
XX 30-JUL-2002 (first entry)
XX
XX Human IGE C2-C3-C4 domains for mammalian expression.
XX
XX IGE; allergy; human; antiallergic; immunosuppressive; anti-anaphylactic;
XX antiaesthetic; dermatological; anti-inflammatory; immunoglobulin E; IGE;
XX vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;
XX heavy chain C domain.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200220038-A2.
XX
XX 14-MAR-2002.
XX
XX 06-SEP-2001; 2001WO-DK000579.
XX
XX 06-SEP-2000; 2000DK-00001326.
XX
XX 15-SEP-2000; 2000US-0232831P.
XX
XX (PHAR-) PHARMEXA AS.
XX
XX Klyener S, Von Hoegen P, Voldborg B, Gautam A;
XX
XX WPI; 2002-383033/41.
XX
XX N-PSDB; ABK51133.
XX
XX Inducing immune response against autologous immunoglobulin E in an
PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte
PT epitope an/or B-cell epitope derived from the immunoglobulin.
XX

PS Disclosure; Page 108-110; 151pp; English.

XX This invention relates to a novel method for inducing an immune response

CC against autologous immunoglobulin E (IgE) in an animal. The method

CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte

CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell

CC epitope (TH epitope) which is foreign to the animal, by antigen

CC presenting cells (APCs) of the animal's immune system. The epitopes of

CC the invention may be used as a vaccine against allergic diseases. The

CC method of the invention is useful for inducing an immune response against

CC autologous IgE in an animal, which is useful for downregulating

CC autologous IgE in the animal. This method is useful in the prevention and

CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,

CC asthma and atopic dermatitis. The present sequence represents the human

CC IgE heavy chain C2-C3-C4 domains optimised for expression in a mammalian

CC system, this sequence was used to create the epitopes of the invention

XX

SQ Sequence 323 AA;

Query Match 100.0%; Score 83; DB 5; Length 323;

Best Local Similarity 100.0%; Pred. No. 7.4e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDGQVMDVLDSTASTQ 17

Db 46 EDGQVMDVLDSTASTQ 62

RESULT 11

AAU80284

ID AAU80284 standard; protein; 323 AA.

XX

AC AAU80284;

XX

DT 30-JUL-2002 (first entry)

XX

DE Human IgE heavy chain C2-C3-C4 domains.

XX

KW IgE; allergy; human; anti-allergic; immunosuppressive; antianaphylactic;

KW antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE;

KW vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;

KW heavy chain C domain.

XX

OS Homo sapiens.

XX

PH Key

FT Location/Qualifiers

FT 8..103

FT Domain /note= "IgE heavy chain C2 domain"

FT 100..114

FT Region /note= "Epitope including C2C3 linker"

FT 104..111

FT Domain /note= "Linker between domains C2 and C3"

FT 112..211

FT /label= IgE heavy chain C3 domain

FT 139..145

FT Region /note= "Epitope in BC loop"

FT 167..175

FT Region /note= "Epitope in DB loop"

FT 196..206

FT Domain /note= "Epitope in FG loop"

FT 210..218

FT Region /note= "Epitope including C3C4 linker"

FT 212..215

FT Region /note= "Linker between domains C3 and C4"

FT 216..317

FT Domain /note= "IgE heavy chain C4 domain"

XX

W0200220038-A2.

XX

PD 14-MAR-2002.

XX

PF 06-SEP-2001; 2001WO-DK000579.

XX

PR 06-SEP-2000; 2000DK-00001326.

PR 15-SEP-2000; 2000US-0232831P.

XX

PA (PHAR-) PHARMEXA AS.

XX

PI Klysnar S, Von Hoegen P, Voldborg B, Gautam A;

XX

DR WPI: 2002-383033/41.

XX

XX Inducing immune response against autologous immunoglobulin E in an

PT animal, by effecting simultaneous presentation of cytotoxic T lymphocyte

PT epitope an/or B-cell epitope derived from the immunoglobulin.

XX

PS Disclosure; Page 105-106; 151pp; English.

XX

XX This invention relates to a novel method for inducing an immune response

CC against autologous immunoglobulin E (IgE) in an animal. The method

CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte

CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell

CC epitope (TH epitope) which is foreign to the animal, by antigen

CC presenting cells (APCs) of the animal's immune system. The epitopes of

CC the invention may be used as a vaccine against allergic diseases. The

CC method of the invention is useful for inducing an immune response against

CC autologous IgE in an animal, which is useful for downregulating

CC autologous IgE in the animal. This method is useful in the prevention and

CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis,

CC asthma and atopic dermatitis. The present sequence represents the human

CC IgE heavy chain C2-C3-C4 domains used to create the epitopes of the

CC invention

XX

SQ Sequence 323 AA;

Query Match 100.0%; Score 83; DB 5; Length 323;

Best Local Similarity 100.0%; Pred. No. 7.4e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDGQVMDVLDSTASTQ 17

Db 46 EDGQVMDVLDSTASTQ 62

RESULT 12

AAU83559

ID AAR83559 standard; protein; 324 AA.

XX

AC AAR83559;

XX

DT 06-MAR-1996 (first entry)

XX

DE Fc(epsilon) CH2'-CH4 protein sequence.

XX

KW Fc(epsilon); antibody; human; myeloma; probe; IgE; cryptophan promoter;

KW constant heavy region; E coli; glycosylation; antigenic; immunogenic;

KW histamine; anti-allergenic; vaccine; immune response.

XX

OS Synthetic.

XX

PN FR2715304-A1.

XX

PD 28-JUL-1995.

XX

PF 26-JAN-1994; 94FR-00000846.

XX

PR 26-JAN-1994; 94FR-00000846.

XX

XX (INMR) PASTEUR MERIEUX SERUMS & VACCINS.

XX

PI Hurpin CM, Panero MM;

XX

XX WPI: 1995-265243/35.

XX

DR N-PSDB; AAT01865.

XX

PT Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain - has

PT epitope(s) not present in native IGE, also derived antibodies for
 PT treating or preventing allergies, inflammatory immune disease, etc.

PS Claim 3; Page 32-33; 44pp; French.

XX The amino acid sequence of the Fc(epsilon) CH2'-CH4 fragment covering
 CC amino acids 226-547. The DNA sequence was isolated from a human myeloma
 CC 266BL CDNA library screened with a probe corresp. to the N-terminus of
 CC IGE. The region encoding amino acids 218-547 was cloned into the vector
 CC pMT211 under control of the tryptophan promoter. The resultant protein
 CC produced contains some non-Fc amino acids. These were removed by
 CC replacing their coding sequence with a bicistronic linker. The resultant
 CC construct encodes the Fc(epsilon) constant heavy region from amino acids
 CC 226-547. When it is expressed in E.coli, the protein produced is a non-
 CC glycosylated Fc(epsilon) fragment. Altering the pattern of glycosylation
 CC unmaskes new antigenic sites thus rendering the Fc fragment immunogenic
 CC and able to induce antibodies that recognise native IGE but do not form
 CC histamine-releasing complexes. The Fc fragments can be used in anti-
 CC allergic vaccines to modulate the intensity of immune responses
 CC mediated by IGE

XX Sequence 324 AA;

Query Match 100.0%; Score 83; DB 2; Length 324;
 Best Local Similarity 100.0%; Pred. No. 7.4e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDGQVMDVLDLSTASTTQ 17
 |||||
 Db 47 EDGQVMDVLDLSTASTTQ 63

RESULT 13

ID AAR75225 standard; protein; 325 AA.

XX AAR75225;

XX 25-MAR-2003 (revised)

DT 10-NOV-1995 (first entry)

XX Human IGE Fc chain (amino acids 224-547) mutant sequence.

KM IGE Fc fragment; antiallergic.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Misc-difference 1 /label= Val124

FT Misc-difference 2 /note= "any AA or deletion"

FT Misc-difference 3 /label= Cys225

FT Misc-difference 4 /note= "Ala, any other AA, or deletion"

FT Misc-difference 5 /label= Ser226

FT Misc-difference 6 /label= Arg227

FT Misc-difference 7 /note= "any AA or deletion"

FT Misc-difference 8 /label= Asp228

FT Misc-difference 9 /note= "any AA or deletion"

FT Misc-difference 10 /label= Asn371

FT Misc-difference 11 /note= "glycosylation site"

FT Misc-difference 12 /label= Asn394

FT /note= "glycosylation site"

XX W09514779-A1.

XX 01-JUN-1995.

XX 22-NOV-1994; 94WO-GB002561.
 PF
 XX 22-NOV-1993; 93GB-00024013.
 PR

XX (THRE-) 31 RES EXPL LTD.
 PA (CLLT) CELLTech THERAPEUTICS LTD.

PI Gould HU, Young RJ, Sutton BJ, Owens RJ;

XX WPI, 1995-206936/27.

DR N-PSDB; AAQ87474.

XX Mutated glycosylated polypeptide(s) contg. parts of human IGE-Fc - useful
 PT to study and treat allergy.

PS Disclosure; Page 6; 55pp; English.

XX The sequence represents a mutant sequence of a human IGE-Fc chain (amino
 CC acids 224-547) which is of sufficient length to bind Fc-epsilon RI and/or
 CC Fc-epsilon FII IGE receptor sites on human cells. The protein is useful
 CC in the study and treatment of allergy. (Updated on 25-MAR-2003 to correct
 CC PN field.)

XX Sequence 325 AA;

Query Match 100.0%; Score 83; DB 2; Length 325;
 Best Local Similarity 100.0%; Pred. No. 7.5e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDGQVMDVLDLSTASTTQ 17
 |||||
 Db 48 EDGQVMDVLDLSTASTTQ 64

RESULT 14

ID AAR77241 standard; protein; 325 AA.

XX AAR77241;

XX 25-MAR-2003 (revised)

DT 10-NOV-1995 (first entry)

XX Human IGE Fc chain (amino acids 224-547) wild-type sequence.

KM IGE Fc fragment; antiallergic.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Misc-difference 149 /label= Asn371

FT Misc-difference 172 /note= "glycosylation site"

FT Misc-difference 172 /label= Asn394

FT /note= "glycosylation site"

XX W09514779-A1.

XX 01-JUN-1995.

XX 22-NOV-1994; 94WO-GB002561.

XX 22-NOV-1993; 93GB-00024013.

XX (THRE-) 31 RES EXPL LTD.

PA (CLLT) CELLTech THERAPEUTICS LTD.

PI Gould HU, Young RJ, Sutton BJ, Owens RJ;

XX WPI, 1995-206936/27.

XX N-PSDB; AAQ91170.

XX Mutated glycosylated polypeptide(s) contg. parts of human IgE-Fc - useful
PT to study and treat allergy.
XX
XX
PS Disclosure; Page 35-36; 55pp; English.
XX
CC The sequence represents the wild-type sequence of a human IgE-Fc chain
CC (amino acids 224-547) which is of sufficient length to bind Fc-epsilon RI
CC and/or Fc-epsilon RI IgE receptor sites on human cells. The sequence is
CC preferably mutated (see AAR75225) to represent a protein encoding a
CC protein where Cys225 is mutated, optionally together with Val224, Ser226
CC and Arg227. The protein is useful in the study and treatment of allergy.
CC (Updated on 25-MAR-2003 to correct PW field.)
XX
SQ Sequence 325 AA;

Query Match 100.0%; Score 83; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 7.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDLSTASTTQ 17
|||
48 EDGQVMDVDLSTASTTQ 64
Db

SQ Sequence 325 AA;

Query Match 100.0%; Score 83; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 7.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDGQVMDVDLSTASTTQ 17
|||
Db 48 EDGQVMDVDLSTASTTQ 64

Search completed: December 12, 2005, 20:30:34
Job time : 94.181 secs

RESULT 15
AAR83582
ID AAR83582 standard; protein; 325 AA.
XX
AC AAR83582;
XX
DT 13-JUN-1996 (first entry)
XX
DE CH2 to CH4 of human IgE epsilon chain.
XX
XX
KM IGE; CH4: immunoglobulin; epsilon; immunogen; helper T cell; epitope;
KM vaccine; allergy; antibody; constant heavy chain.
XX
OS Homo sapiens.
XX
PN MO9526365-A1.
XX
PD 05-OCT-1995.
XX
PF 24-MAR-1995; 95WO-US003741.
XX
PR 28-MAR-1994; 94US-00218461.
PR 25-OCT-1994; 94US-00328912.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
PI
PI WPI; 1995-351297/45.
DR
XX
XX
PT Synthetic peptide-based immunogen contg. IgE CH4 peptide and helper T
PT cell epitope - useful for eliciting antibody prodn. for allergy
PT treatment.
XX
PS Disclosure; Page 55; 87pp; English.
XX
CC AAR83582 represents the human IgE epsilon chain from the CH2 to the CH4.
CC Human IgE CH4 region peptides can be derived from this sequence and used
CC in the preparation of a peptide immunogen that is useful in vaccines for
CC treating allergic reactions. In the immunogen the IgE CH4 peptide is
CC attached C-terminally to a series of amino acids including a helper T
CC cell epitope. The immunogen may also opt. contain a fatty acid or fatty
CC acid derivative, an invasin domain or alpha-NH2. The immunogen produces
CC high titres of antibodies to the effector site in human IgE heavy chain
CC (the CH4 domain peptide) which inhibit mast cell activation and reduce
CC allergen-induced IgE prodn. The immunogens may be used in either a
CC radially branching multimeric form or a linearly arranged monomeric form
XX

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OM protein - protein search, using bw model

Run on: December 12, 2005, 19:23:41 ; Search time 23.1552 Seconds
(without alignments)
60.699 Million cell updates/sec

Title: US-10-758-165A-16

Perfect score: 83
Sequence: 1 EDGQVMDVLDLSTASTTQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	83	100.0	325	2	US-09-701-623C-1
2	83	100.0	331	2	US-09-401-636-1
3	42	50.6	337	2	US-09-605-703B-136
4	42	50.6	404	2	US-09-605-703B-134
5	41	49.4	303	2	US-09-107-532A-6113
6	40	48.2	105	2	US-09-902-540-16521
7	40	48.2	160	1	US-08-441-629-7
8	40	48.2	160	1	US-08-776-207-7
9	40	48.2	160	2	US-09-507-773-7
10	40	48.2	160	2	US-10-016-447-7
11	40	48.2	160	4	PCT-US95-09172-7
12	40	48.2	211	2	US-09-252-991A-29508
13	40	48.2	531	2	US-08-687-590-29
14	39	47.0	176	2	US-09-605-703B-388
15	39	47.0	176	2	US-09-605-703B-390
16	39	47.0	268	2	US-09-543-681A-4704
17	39	47.0	361	1	US-08-483-926A-9
18	39	47.0	361	1	US-08-737-045-13
19	38.5	46.4	90	2	US-09-227-357-635
20	38.5	46.4	90	2	US-09-973-278-408
21	38.5	46.4	199	2	US-09-949-016-8343
22	38.5	46.4	232	1	US-08-773-910-1
23	38.5	46.4	232	2	US-09-199-892-1
24	38	45.8	119	2	US-10-104-047-2322
25	38	45.8	138	2	US-09-621-976-5032
26	38	45.8	197	2	US-09-248-796A-27136
27	38	45.8	255	2	US-09-902-540-12488

28	38	45.8	340	2	US-10-155-947-6	Sequence 6, Appl1
29	38	45.8	359	1	US-08-483-926A-8	Sequence 8, Appl1
30	38	45.8	359	1	US-08-737-045-11	Sequence 11, Appl1
31	38	45.8	359	2	US-08-932-871B-1	Sequence 1, Appl1
32	38	45.8	359	2	US-09-476-919-1	Sequence 1, Appl1
33	38	45.8	359	2	US-08-780-311A-1	Sequence 1, Appl1
34	38	45.8	364	1	US-08-483-926A-10	Sequence 10, Appl1
35	38	45.8	364	1	US-08-737-045-10	Sequence 10, Appl1
36	38	45.8	431	2	US-09-252-991A-32589	Sequence 32589, A
37	38	45.8	951	2	US-09-252-991A-23338	Sequence 23338, A
38	38	45.8	971	1	US-08-446-010B-19	Sequence 19, Appl1
39	38	45.8	971	1	US-08-805-445-19	Sequence 19, Appl1
40	38	45.8	971	1	US-08-064-067D-19	Sequence 19, Appl1
41	38	45.8	971	1	US-08-064-067D-19	Sequence 19, Appl1
42	38	45.8	971	1	US-09-066-208-19	Sequence 19, Appl1
43	37	44.6	84	2	US-09-248-796A-26360	Sequence 26360, A
44	37	44.6	170	2	US-09-107-532A-5092	Sequence 5092, Ap
45	37	44.6	207	2	US-09-270-767-32889	Sequence 32889, A

ALIGNMENTS

```
RESULT 1
US-09-701-623C-1
; Sequence 1, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 325
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; OTHER INFORMATION: CH2CH3 of human IgE
; PUBLICATION INFORMATION:
; AUTHORS: Dorrington,
; JOURNAL: Immunology
; VOLUME: 41
; PAGES: 3-25
; DATE: 1978
; US-09-701-623C-1

Query Match          100.0%  Score 83;  DB 2;  Length 325;
Best Local Similarity 100.0%;  Pred. No. 2.9e-06;
Matches 17;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1  EDGQVMDVLDLSTASTTQ 17
Db      48 EDGQVMDVLDLSTASTTQ 64

RESULT 2
US-09-401-636-1
; Sequence 1, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
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; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-1

Query Match      100.0%; Score 83; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVMDVLDLSTASTTQ 17
Db      54 EDGQVMDVLDLSTASTTQ 70

RESULT 3
US-09-605-703B-136
; Sequence 136, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Krieger, Burkhard
; APPLICANT: Schröder, Hartwig
; APPLICANT: Zeidler, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 136
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-605-703B-136

Query Match      50.6%; Score 42; DB 2; Length 337;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      2 DGOVMDVLDLSTASTTQ 17
Db      205 EGTLPVDLVQVAVSTR 220

RESULT 4
US-09-605-703B-134
; Sequence 134, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Krieger, Burkhard
; APPLICANT: Schröder, Hartwig
; APPLICANT: Zeidler, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
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; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 134
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-605-703B-134

Query Match      50.6%; Score 42; DB 2; Length 404;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      2 DGOVMDVLDLSTASTTQ 17
Db      205 EGTLPVDLVQVAVSTR 220

RESULT 5
US-09-107-532A-6113
; Sequence 613, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSER: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (B) LOCATION 1...303
; SEQUENCE DESCRIPTION: SEQ ID NO: 6113:
US-09-107-532A-6113

Query Match      49.4%; Score 41; DB 2; Length 303;
Best Local Similarity 56.2%; Pred. No. 42;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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QY 1 EDGQVMDVLDSTAST 16
:|||||:|:|
Db 209 KDGOVSDVITSTMAST 224

RESULT 6
US-09-902-540-16521

; Sequence 16521, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16521
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16521

Query Match 48.2%; Score 40; DB 2; Length 105;
Best Local Similarity 64.3%; Pred. No. 17;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GQWMDVLDSTAST 16
:|||||:|:|
Db 57 GRPHVDLSTADRT 70

RESULT 7

US-08-441-629-7
; Sequence 7, Application US/08441629
; Patent No. 5766923
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, No. 5766923iyuki
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,629
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/279,217
; FILING DATE: 22-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: HU95-01A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-629-7

Query Match 48.2%; Score 40; DB 1; Length 160;
Best Local Similarity 57.1%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 DGQWMDVLDSTAST 15
:|||||:|:|
Db 134 DGHVMDQDLKASRT 147

RESULT 8

US-08-776-207-7
; Sequence 7, Application US/08776207A
; Patent No. 6080718
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, No. 6080718iyuki
; TITLE OF INVENTION: Receptor-Ligand Assay
; FILE REFERENCE: HU95-01A2
; CURRENT APPLICATION NUMBER: US/08/776,207A
; CURRENT FILING DATE: 1997-06-23
; EARLIER APPLICATION NUMBER: PCT/US95/09172
; EARLIER FILING DATE: 1995-07-19
; EARLIER APPLICATION NUMBER: 08/441,629
; EARLIER FILING DATE: 1995-05-15
; EARLIER APPLICATION NUMBER: 08/279,217
; EARLIER FILING DATE: 1994-07-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-776-207-7

Query Match 48.2%; Score 40; DB 2; Length 160;
Best Local Similarity 57.1%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 DGQWMDVLDSTAST 15
:|||||:|:|
Db 134 DGHVMDQDLKASRT 147

RESULT 9

US-09-507-773-7
; Sequence 7, Application US/09507773
; Patent No. 6399386
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, No. 6399386iyuki
; TITLE OF INVENTION: Receptor-Ligand Assay
; FILE REFERENCE: HU95-01A2
; CURRENT APPLICATION NUMBER: US/09/507,773
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: 08/776,207
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/441,629
; PRIOR FILING DATE: 1995-05-15
; PRIOR APPLICATION NUMBER: 08/279,217
; PRIOR FILING DATE: 1994-07-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 160
; TYPE: PRT

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; ORGANISM: Mus musculus
; US-09-507-773-7
Query Match      48.2%; Score 40; DB 2; Length 160;
Best Local Similarity 57.1%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2 DGVMDVLDLSTAST 15
Db      134 DGHVMDLKLKASRT 147

RESULT 10
US-10-016-447-7
; Sequence 7, Application US/10016447
; Patent No. 6844193
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; TITLE OF INVENTION: Receptor-Ligand Assay
; FILE REFERENCE: HU95-01A2
; CURRENT APPLICATION NUMBER: US/10/016,447
; PRIORITY FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/08/776,207
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/441,629
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-05-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/279,217
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-07-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-016-447-7

Query Match      48.2%; Score 40; DB 2; Length 160;
Best Local Similarity 57.1%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2 DGVMDVLDLSTAST 15
Db      134 DGHVMDLKLKASRT 147

RESULT 11
PCT-US95-09172-7
; Sequence 7, Application PC/TUS9509172
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, Noriyuki
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09172
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/279,217
; FILING DATE: 22-JUL-1994
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,629
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: HU95-01A PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09172-7

Query Match      48.2%; Score 40; DB 4; Length 160;
Best Local Similarity 57.1%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2 DGVMDVLDLSTAST 15
Db      134 DGHVMDLKLKASRT 147

RESULT 12
US-09-252-991A-29508
; Sequence 29508, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIORITY FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29508
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29508

Query Match      48.2%; Score 40; DB 2; Length 211;
Best Local Similarity 57.1%; Pred. No. 40;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 EDGQVMDVLDLSTAS 14
Db      108 EDGQVLAHAEFLTVAS 121

RESULT 13
US-08-687-590-29
; Sequence 29, Application US/08687590
; Patent No. 6255070
; GENERAL INFORMATION:
; APPLICANT: Willison, Keith Robert
; APPLICANT: Kubota, Hiroyoshi
; APPLICANT: Ashworth, Alan
; TITLE OF INVENTION: Folding Proteins
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```

STATE: California
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,590
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00192
FILING DATE: 31-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9401791.0
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9418234.2
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 084619-000000US
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 531 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-687-590-29

Query Match 48.2%; Score 40; DB 2; Length 531;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQVMDVLDST 12
| | | | |
| | | | |
Db 472 ESGQLVGVLDST 483

RESULT 14
US-09-605-703B-388
Sequence 388, Application US/09605703B
Patent No. 6962389
GENERAL INFORMATION:
APPLICANT: Pompeius, Markus
APPLICANT: Krogger, Burkhard
APPLICANT: Schröder, Hartwig
APPLICANT: Zeidler, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: BGI-129CP
CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 388
LENGTH: 176
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-605-703B-388

Query Match 47.0%; Score 39; DB 2; Length 176;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQVMDVLDST 12

Db 30 ENGQVPEVDAST 41

RESULT 15
US-09-605-703B-390
Sequence 390, Application US/09605703B
Patent No. 6962389
GENERAL INFORMATION:
APPLICANT: Pompeius, Markus
APPLICANT: Krogger, Burkhard
APPLICANT: Schröder, Hartwig
APPLICANT: Zeidler, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: BGI-129CP
CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
SEQ ID NO 390
LENGTH: 176
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-605-703B-390

Query Match 47.0%; Score 39; DB 2; Length 176;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQVMDVLDST 12
| | | | |
| | | | |
Db 30 ENGQVPEVDAST 41

Search completed: December 12, 2005, 19:37:08
Job time : 24.1552 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:33:42 ; Search time 75.9138 Seconds
(without alignments)
93.568 Million cell updates/sec

Title: US-10-758-165A-16
Perfect score: 83
Sequence: 1 EDGQVMDVDSLSTASTTQ 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	17	US-10-758-165-16	Sequence 16, Appl
2	83	100.0	128	US-10-152-190-7	Sequence 7, Appl
3	83	100.0	236	US-10-152-190-9	Sequence 9, Appl
4	83	100.0	320	US-09-847-208-6	Sequence 6, Appl
5	83	100.0	320	US-10-000-439-6	Sequence 6, Appl
6	83	100.0	323	US-09-949-375A-2	Sequence 2, Appl
7	83	100.0	323	US-09-949-375A-4	Sequence 4, Appl
8	83	100.0	323	US-09-949-375A-6	Sequence 6, Appl
9	83	100.0	323	US-10-363-954A-2	Sequence 4, Appl
10	83	100.0	323	US-10-363-954A-4	Sequence 4, Appl
11	83	100.0	323	US-10-363-954A-6	Sequence 6, Appl
12	83	100.0	327	US-10-627-556-224	Sequence 224, App
13	83	100.0	330	US-09-949-375A-10	Sequence 10, Appl
14	83	100.0	330	US-10-363-954A-10	Sequence 10, Appl
15	83	100.0	331	US-09-401-636-1	Sequence 1, Appl
16	83	100.0	331	US-10-176-664-1	Sequence 1, Appl
17	83	100.0	331	US-10-207-655-329	Sequence 329, App
18	83	100.0	331	US-10-673-594-1	Sequence 1, Appl
19	83	100.0	331	US-10-627-556-97	Sequence 174, Appl
20	83	100.0	331	US-10-627-556-174	Sequence 8, Appl
21	83	100.0	336	US-09-949-375A-8	Sequence 8, Appl
22	83	100.0	336	US-10-363-954A-8	Sequence 10, Appl
23	83	100.0	346	US-10-152-190-10	Sequence 10, Appl
24	83	100.0	346	US-10-152-190-14	Sequence 14, Appl
25	83	100.0	347	US-10-152-190-12	Sequence 12, Appl
26	83	100.0	347	US-10-152-190-13	Sequence 13, Appl
27	83	100.0	348	US-10-152-190-11	Sequence 11, Appl

28	83	100.0	427	US-09-847-208-5	Sequence 5, Appl
29	83	100.0	427	US-10-000-439-5	Sequence 5, Appl
30	83	100.0	428	US-09-916-230-1	Sequence 1, Appl
31	83	100.0	428	US-09-949-375A-1	Sequence 1, Appl
32	83	100.0	428	US-10-047-542-60	Sequence 60, Appl
33	83	100.0	428	US-10-363-954A-1	Sequence 1, Appl
34	83	100.0	441	US-09-949-375A-7	Sequence 7, Appl
35	83	100.0	441	US-10-363-954A-7	Sequence 7, Appl
36	83	100.0	497	US-10-872-932A-35	Sequence 35, Appl
37	83	100.0	497	US-10-810-881A-34	Sequence 34, Appl
38	83	100.0	497	US-10-981-936-34	Sequence 34, Appl
39	83	100.0	569	US-09-847-208-7	Sequence 7, Appl
40	83	100.0	569	US-10-000-439-7	Sequence 7, Appl
41	83	100.0	574	US-10-047-542-45	Sequence 45, Appl
42	83	100.0	574	US-10-214-524-37	Sequence 37, Appl
43	83	100.0	574	US-10-050-902-176	Sequence 176, App
44	83	100.0	574	US-10-050-888-176	Sequence 176, App
45	83	100.0	586	US-10-627-556-384	Sequence 384, App

ALIGNMENTS

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RESULT 1
US-10-758-165-16
; Sequence 16, Application US/10758165
; Publication No. US20050196616A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-758-165-16

Query Match      100.0%; Score 83; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDGQVMDVDSLSTASTTQ 17
      |||||
DB      1 EDGQVMDVDSLSTASTTQ 17

RESULT 2
US-10-152-190-7
; Sequence 7, Application US/10152190
; Publication No. US20030096369A1
; GENERAL INFORMATION:
; APPLICANT: Moresey, Mohamad A.
; TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IgE vaccines
; FILE REFERENCE: PC11011A
; CURRENT APPLICATION NUMBER: US/10/152,190
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Modified Human CH2 domain
US-10-152-190-7

Query Match      100.0%; Score 83; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy      1 EDGQVMDVDSIASTTQ 17
      |||||
Db      70 EDGQVMDVDSIASTTQ 86

RESULT 3
US-10-152-190-9
; Sequence 9, Application US/10152190
; Publication No. US20030096369A1
; GENERAL INFORMATION:
; APPLICANT: Morse, Mohamed A.
; TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic Ige vaccines
; FILE REFERENCE: PC11011A
; CURRENT APPLICATION NUMBER: US/10/152.190
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Modified Human CH2-CH4 carrier protein
US-10-152-190-9

Query Match      100.0%; Score 83; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 EDGQVMDVDSIASTTQ 17
      |||||
Db      70 EDGQVMDVDSIASTTQ 86

RESULT 4
US-09-847-208-6
; Sequence 6, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847.208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-6

Query Match      100.0%; Score 83; DB 3; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 EDGQVMDVDSIASTTQ 17
      |||||
Db      43 EDGQVMDVDSIASTTQ 59

RESULT 5
US-10-000-439-6
; Sequence 6, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES
; FILE REFERENCE: UC067.004A
; CURRENT APPLICATION NUMBER: US/10/000.439
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; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847,208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-6

Query Match      100.0%; Score 83; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 EDGQVMDVDSIASTTQ 17
      |||||
Db      43 EDGQVMDVDSIASTTQ 59

RESULT 6
US-09-949-375A-2
; Sequence 2, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-011P
; CURRENT APPLICATION NUMBER: US/09/949.375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 323
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (8)..(103)
; OTHER INFORMATION: Human Ige heavy chain C2 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (112)..(211)
; OTHER INFORMATION: Human Ige heavy chain C3 domain
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (216)..(317)
; OTHER INFORMATION: Human Ige heavy chain C4 domain
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (104)..(111)
; OTHER INFORMATION: Linker between domains C2 and C3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (212)..(215)
; OTHER INFORMATION: Linker between domains C3 and C4
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (100)..(114)
; OTHER INFORMATION: Epitope including C2C3 linker
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (210)..(218)
; OTHER INFORMATION: Epitope including C3C4 linker
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (139)..(145)
; OTHER INFORMATION: Epitope in BC loop
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (167)..(175)
; OTHER INFORMATION: Epitope in DE loop
; FEATURE:
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```
NAME/KEY: MISC FEATURE
LOCATION: (196)..(206)
OTHER INFORMATION: Epitope in FG loop
US-09-949-375A-2
```

```
Query Match      100.0%; Score 83; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 EDGQVMDVDLSTASTTQ 17
      |||||
Db      46 EDGQVMDVDLSTASTTQ 62
```

```
RESULT 7
US-09-949-375A-4
Sequence 4, Application US/09949375A
Patent No. US20020172673A1
GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING ICE
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 323
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 3.
US-09-949-375A-4
```

```
Query Match      100.0%; Score 83; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 EDGQVMDVDLSTASTTQ 17
      |||||
Db      46 EDGQVMDVDLSTASTTQ 62
```

```
RESULT 8
US-09-949-375A-6
Sequence 6, Application US/09949375A
Patent No. US20020172673A1
GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING ICE
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 323
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 5.
US-09-949-375A-6
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Query Match      100.0%; Score 83; DB 3; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 EDGQVMDVDLSTASTTQ 17
      |||||
Db      46 EDGQVMDVDLSTASTTQ 62
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RESULT 9

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US-10-363-954A-2
Sequence 2, Application US/10363954A
Publication No. US20040156838A1
GENERAL INFORMATION:
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APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING ICE
FILE REFERENCE: 4614-0115P
CURRENT APPLICATION NUMBER: US/10/363,954A
CURRENT FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: US 60/232,831
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: DK PA 2000 01326
PRIOR FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 323
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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NAME/KEY: DOMAIN
LOCATION: (8)..(103)
OTHER INFORMATION: Human IGE heavy chain C2 domain
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (112)..(211)
OTHER INFORMATION: Human IGE heavy chain C3 domain
FEATURE:
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NAME/KEY: DOMAIN
LOCATION: (216)..(317)
OTHER INFORMATION: Human IGE heavy chain C4 domain
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (104)..(111)
OTHER INFORMATION: Linker between domains C2 and C3
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (212)..(215)
OTHER INFORMATION: Linker between domains C3 and C4
FEATURE:
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NAME/KEY: MISC FEATURE
LOCATION: (100)..(114)
OTHER INFORMATION: Epitope including C2C3 linker
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (210)..(218)
OTHER INFORMATION: Epitope including C3C4 linker
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (139)..(145)
OTHER INFORMATION: Epitope in BC loop
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (167)..(175)
OTHER INFORMATION: Epitope in DE loop
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (196)..(206)
OTHER INFORMATION: Epitope in FG loop
US-10-363-954A-2
```

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Query Match      100.0%; Score 83; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 EDGQVMDVDLSTASTTQ 17
      |||||
Db      46 EDGQVMDVDLSTASTTQ 62
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```
RESULT 10
US-10-363-954A-4
Sequence 4, Application US/10363954A
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; Publication No. US20040156838A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 4614-0115P
; CURRENT APPLICATION NUMBER: US/10/363,954A
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 60/232,831
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: DK PA 2000 01326
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial protein sequence optimized for expression in mammalian
; OTHER INFORMATION: cells of human IGE heavy chain fragment spanning C2, C3, and C4.
; NAME/KEY: DOMAIN
; LOCATION: (11)..(116)
; OTHER INFORMATION: Human IGE heavy chain C1 domain
US-10-363-954A-4
```

Query Match 100.0%; Score 83; DB 4; Length 323;

Best Local Similarity 100.0%; Pred. No. 1.2e-05; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 EDGQVMDVDLSTASTQ 17
Db 46 EDGQVMDVDLSTASTQ 62
```

```
RESULT 11
US-10-363-954A-6
; Sequence 6, Application US/10363954A
; Publication No. US20040156838A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 4614-0115P
; CURRENT APPLICATION NUMBER: US/10/363,954A
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 60/232,831
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: DK PA 2000 01326
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial protein sequence optimized for expression in
; OTHER INFORMATION: E. coli of human IGE heavy chain fragment spanning C2,
; OTHER INFORMATION: C3, and C4
US-10-363-954A-6
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Query Match 100.0%; Score 83; DB 4; Length 323;

Best Local Similarity 100.0%; Pred. No. 1.2e-05; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 EDGQVMDVDLSTASTQ 17
Db 46 EDGQVMDVDLSTASTQ 62
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```
RESULT 12
US-10-627-556-224
; Sequence 224, Application US/10627556
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; Publication No. US20050136049A1
; GENERAL INFORMATION:
; APPLICANT: LEDBETTER, JEFFREY A.
; APPLICANT: HAYDEN-LEDBETTER, MARTHA
; APPLICANT: THOMPSON, PETER A.
; TITLE OF INVENTION: BINDING CONSTRUCTS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 49076.000004.C1P2
; CURRENT APPLICATION NUMBER: US/10/627,556
; CURRENT FILING DATE: 2003-07-26
; PRIOR APPLICATION NUMBER: 10/053,530
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/367,358
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/765,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/385,691
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 699
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 224
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid sequence
US-10-627-556-224
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Query Match 100.0%; Score 83; DB 5; Length 327;

Best Local Similarity 100.0%; Pred. No. 1.3e-05; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EDGQVMDVDLSTASTQ 17
Db 50 EDGQVMDVDLSTASTQ 66
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```
RESULT 13
US-09-949-375A-10
; Sequence 10, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
; FILE REFERENCE: 3631-0111P
; CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 9.
US-09-949-375A-10
```

Query Match 100.0%; Score 83; DB 3; Length 330;

Best Local Similarity 100.0%; Pred. No. 1.3e-05; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 EDGQVMDVDLSTASTQ 17
Db 46 EDGQVMDVDLSTASTQ 62
```

```
RESULT 14
US-10-363-954A-10
; Sequence 10, Application US/10363954A
; Publication No. US20040156838A1
; GENERAL INFORMATION:
; APPLICANT: KLYSNER, Steen et al.
; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
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```

; FILE REFERENCE: 4614-0115P
; CURRENT APPLICATION NUMBER: US/10/363,954A
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 60/232,831
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: DK PA 2000 01326
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial protein sequence optimised for expression in
; OTHER INFORMATION: mammalian cells of human IGE fragment spanning C2, C3, C4
; US-10-363-954A-10

```

```

Query Match          100.0%; Score 83; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 EDGQVMDVLDLSTASTTQ 17
        |||||
Db      46 EDGQVMDVLDLSTASTTQ 62

```

```

RESULT 15
US-09-401-636-1
; Sequence 1, Application US/09401636
; Patent No. US2001003843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-1

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```

Query Match          100.0%; Score 83; DB 3; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 EDGQVMDVLDLSTASTTQ 17
        |||||
Db      54 EDGQVMDVLDLSTASTTQ 70

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Search completed: December 12, 2005, 20:19:26
Job time : 76.9136 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:34:33 ; Search time 2.78448 Seconds
(without alignments)
34.094 Million cell updates/sec

Title: US-10-758-165A-16

Perfect score: 83

Sequence: 1 EDGQVMDVLDSTASTTQ 17

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New:*
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_NEM_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEM_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	325	6	US-10-723-207-1
2	83	100.0	497	6	US-10-999-866-34
3	83	100.0	497	7	US-11-061-821-34
4	38	45.8	317	7	US-11-055-822-320
5	38	45.8	340	7	US-11-100-352-6
6	38	45.8	359	6	US-10-888-962-5
7	37	44.6	340	7	US-11-100-352-2
8	37	44.6	340	7	US-11-100-352-5
9	37	44.6	1049	7	US-11-137-462-42
10	36	43.4	772	6	US-10-658-986-2
11	36	43.4	772	6	US-10-658-986-4
12	35	42.2	112	6	US-10-467-657-6306
13	35	42.2	193	6	US-11-055-822-568
14	35	42.2	352	6	US-10-888-962-8
15	35	42.2	612	6	US-10-518-018-1
16	35	42.2	895	6	US-10-485-517-129
17	34	41.0	263	6	US-10-467-657-6102
18	34	41.0	319	6	US-10-878-556A-159
19	34	41.0	753	6	US-10-467-657-6852
20	34	41.0	2516	6	US-10-647-956A-2
21	34	41.0	2828	7	US-11-080-991-54
22	34	41.0	2828	7	US-11-186-284-49
23	33	39.8	226	6	US-10-467-657-6482
24	33	39.8	279	6	US-10-467-657-996
25	33	39.8	339	6	US-10-821-234-1507

26	33	39.8	382	7	US-11-055-822-302	Sequence 302, App
27	33	39.8	382	7	US-11-055-822-344	Sequence 344, App
28	33	39.8	710	7	US-11-045-802-22	Sequence 22, Appl
29	33	39.8	710	7	US-11-045-802-23	Sequence 23, Appl
30	33	39.8	3717	6	US-10-821-234-1076	Sequence 1076, Ap
31	32	38.6	169	7	US-11-110-082-22	Sequence 22, Appl
32	32	38.6	219	6	US-10-793-626-32	Sequence 32, Appl
33	32	38.6	250	6	US-10-821-234-1297	Sequence 1297, Ap
34	32	38.6	257	6	US-10-467-657-720	Sequence 720, App
35	32	38.6	293	6	US-10-821-234-1374	Sequence 1374, Ap
36	32	38.6	306	6	US-10-878-556A-56	Sequence 56, Appl
37	32	38.6	317	6	US-10-821-234-1529	Sequence 1529, Ap
38	32	38.6	333	7	US-11-074-176-32	Sequence 32, Appl
39	32	38.6	334	7	US-11-129-143-103	Sequence 103, App
40	32	38.6	367	6	US-10-888-962-6	Sequence 6, Appli
41	32	38.6	384	6	US-10-858-710-216	Sequence 216, App
42	32	38.6	393	7	US-11-055-822-356	Sequence 356, App
43	32	38.6	393	7	US-11-055-822-974	Sequence 974, App
44	32	38.6	493	6	US-10-878-556A-65	Sequence 65, Appl
45	32	38.6	581	6	US-10-793-626-28	Sequence 28, Appl

ALIGNMENTS

```
RESULT 1
US-10-723-207-1
Sequence 1, Application US/10723207
Publication No. US20050250934A1
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
FILE REFERENCE: 1151-4153US2
CURRENT FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: 09/701,623
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US99/13959
PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 09/100,287
PRIOR FILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 325
TYPE: PRT
ORGANISM: HUMAN
FEATURE:
OTHER INFORMATION: CH2CH3 of human Igt
PUBLICATION INFORMATION:
AUTHORS: Dorrington,
JOURNAL: Immunology
VOLUME: 41
PAGES: 3-25
DATE: 1978
US-10-723-207-1
Query Match 100.0%; Score 83; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EDGQVMDVLDSTASTTQ 17
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Db 48 EDGQVMDVLDSTASTTQ 64
RESULT 2
US-10-999-866-34
Sequence 34, Application US/10999866
Publication No. US20050266004A1
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```
; GENERAL INFORMATION:
; APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann
; TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AN
; FILE REFERENCE: CEN5042NP
; CURRENT APPLICATION NUMBER: US/10/999,866
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: 60/527,794
; PRIOR FILING DATE: 2003-12-08
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(497)
; OTHER INFORMATION: Ige heavy chain constant region
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (104)..(210)
; OTHER INFORMATION: CH1
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (104)..(210)
; OTHER INFORMATION: CH2
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (211)..(318)
; OTHER INFORMATION: CH3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (319)..(497)
; OTHER INFORMATION: CH4
; OTHER INFORMATION: CH4
US-10-999-866-34

Query Match      100.0%; Score 83; DB 6; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVMDVLDSTASTQ 17
Db      151 EDGQVMDVLDSTASTQ 167

RESULT 3
US-11-061-821-34
; Sequence 34, Application US/11061821
; Publication No. US2005026605A1
; GENERAL INFORMATION:
; APPLICANT: Heavner, George; Li, Li; Oneil, Karyn
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING IL-13 RELATED PATHOLOGIES
; FILE REFERENCE: CEN5048 NP
; CURRENT APPLICATION NUMBER: US/11/061,821
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/548,648
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver 3.3
; SEQ ID NO 34
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(497)
; OTHER INFORMATION: Ige heavy chain constant region
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(103)
; OTHER INFORMATION: CH1
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (104)..(210)
; OTHER INFORMATION: CH2
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (211)..(318)
; OTHER INFORMATION: CH3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (319)..(497)
; OTHER INFORMATION: CH4
; OTHER INFORMATION: CH4
US-11-061-821-34
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; LOCATION: (104)..(210)
; OTHER INFORMATION: CH2
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (211)..(318)
; OTHER INFORMATION: CH3
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (319)..(497)
; OTHER INFORMATION: CH4
; OTHER INFORMATION: CH4
US-11-061-821-34

Query Match      100.0%; Score 83; DB 7; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDGQVMDVLDSTASTQ 17
Db      151 EDGQVMDVLDSTASTQ 167

RESULT 4
US-11-055-822-320
; Sequence 320, Application US/11055822
; Publication No. US2005026707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burthard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habernauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-12ICPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 320
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-11-055-822-320

Query Match      45.8%; Score 38; DB 7; Length 317;
Best Local Similarity 42.9%; Pred. No. 6.8;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      1 EDGQVMDVLDSTAS 14
Db      185 EDGQVMDVLDSTAS 198
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; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-42
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```

Query Match          44.6%; Score 37; DB 7; Length 1049;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY      1 EDGQVMDVD 9
Db      119 EDGQVCEID 127
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RESULT 10
US-10-658-986-2
; Sequence 2, Application US/10/658986
; Publication No. US20050255476A1
; GENERAL INFORMATION:
; APPLICANT: Wordinger, Robert J.
; TITLE OF INVENTION: Methods for Diagnosing Glaucoma and Discovering Anti-Glaucoma Dru
; FILE REFERENCE: 1581 US F
; CURRENT APPLICATION NUMBER: US/10/658,986
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: PCT/US97/21054
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: USSN 60/033,227
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 742
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-658-986-2

Query Match          43.4%; Score 36; DB 6; Length 742;
Best Local Similarity 46.7%; Pred. No. 43;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
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QY      3 GQWVDVLTASTTQ 17
Db      329 GQWYHDMNTASLSQ 343
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RESULT 11
US-10-658-986-4
; Sequence 4, Application US/10/658986
; Publication No. US20050255476A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Abbot F.
; APPLICANT: Wordinger, Robert J.
; TITLE OF INVENTION: Methods for Diagnosing Glaucoma and Discovering Anti-Glaucoma Dru
; FILE REFERENCE: 1581 US F
; CURRENT APPLICATION NUMBER: US/10/658,986
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: PCT/US97/21054
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; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: USSN 60/033,227
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 777
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-658-986-4
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Query Match          43.4%; Score 36; DB 6; Length 777;
Best Local Similarity 46.7%; Pred. No. 45;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
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QY      3 GQWVDVLTASTTQ 17
Db      329 GQWYHDMNTASLSQ 343
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RESULT 12
US-10-467-657-6306
; Sequence 6306, Application US/10/467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqW1n9, version 1.04
; SEQ ID NO 6306
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6306
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Query Match          42.2%; Score 35; DB 6; Length 112;
Best Local Similarity 50.0%; Pred. No. 65;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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QY      1 EDGQVMDVLTAS 14
Db      4 EDGQVREVSAGAAA 17
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RESULT 13
US-11-055-822-568
; Sequence 568, Application US/11/055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BG1-121PCPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
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; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 568
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-568

Query Match          42.2%; Score 35; DB 7; Length 193;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy      3 GQVMDVDLSTASTT 16
        |||::|||::|
Db      77 GAVVDVDTGAAYT 90

RESULT 14
US-10-888-962-8
; Sequence 8, Application US/10888962
; Publication No. US20050266531A1
; GENERAL INFORMATION:
; APPLICANT: Saint Louis University
; APPLICANT: Ray, Ranjit
; APPLICANT: Yie-Hwa, Chang
; APPLICANT: Ray, Ratna
; APPLICANT: Baau, Arnab
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Liver Stellate Cell
; FILE REFERENCE: SLU 03-013 PCT
; CURRENT APPLICATION NUMBER: US/10/888,962
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/487,126
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-888-962-8

Query Match          42.2%; Score 35; DB 6; Length 352;
Best Local Similarity 42.9%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy      3 GQVMDVDLSTASTT 16
        |||::|||::|
Db      75 GQVVELDIDLETT 88

RESULT 15
US-10-518-018-1
; Sequence 1, Application US/10518018
; Publication No. US20050249715A1
; GENERAL INFORMATION:
; APPLICANT: Shiroki, Kimiyasu
; APPLICANT: Kurokawa, Masahiko
```

```

; APPLICANT: Tamura, Yoshitaka
; APPLICANT: Yamauchi, Koji
; APPLICANT: Wakabayashi, Hiroyuki
; APPLICANT: Shin, Kouichirou
; TITLE OF INVENTION: Inhibitor of Interleukin-6 Production
; FILE REFERENCE: TOYAI08.008APC
; CURRENT APPLICATION NUMBER: US/10/518,018
; PRIOR FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: PCT/JP2003/015009
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2003-45509
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-518-018-1

Query Match          42.2%; Score 35; DB 6; Length 612;
Best Local Similarity 46.7%; Pred. No. 51;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Oy      3 GQVMDVDLSTASTTQ 17
        |||::|||::|
Db      121 GQIVDHDIDFAPETE 135
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Search completed: December 12, 2005, 20:19:50
Job time : 3.78448 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:49 ; Search time 14.3621 Seconds
(without alignments)
113.889 Million cell updates/sec

Title: US-10-758-165A-16
Perfect score: 83
Sequence: 1 EDGQVMDVLDISTASTTQ 17

Scoring table: BLASTUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	83	100.0	428	1	EHNU
2	78	99.0	426	2	Ig epsilon-chain C
3	44	53.0	118	2	G84322
4	44	53.0	578	2	H65006
5	44	53.0	757	2	T05688
6	42	50.6	361	2	E86692
7	41	49.4	225	1	J03040
8	41	49.4	374	2	H91251
9	41	49.4	694	2	J02041
10	41	49.4	675	2	H69200
11	41	49.4	677	2	A69210
12	41	49.4	879	2	F85875
13	41	49.4	879	2	E91031
14	41	49.4	1155	2	B66761
15	40	48.2	146	2	H85545
16	40	48.2	171	2	I49612
17	40	48.2	531	2	S43063
18	39	47.0	112	2	F70954
19	39	47.0	150	2	T24956
20	39	47.0	257	2	A10935
21	39	47.0	362	2	S22395
22	39	47.0	445	2	B40590
23	39	47.0	1459	2	T30196
24	39	47.0	1847	2	T28969
25	38.5	46.4	219	2	T34523
26	38	45.8	111	2	T35386
27	38	45.8	120	1	R5H524
28	38	45.8	145	2	AH2102
29	38	45.8	203	2	C95882

30	38	45.8	205	2	T08272	probable thioredox
31	38	45.8	255	2	AB0986	conserved hypothet
32	38	45.8	347	2	H84270	geranylgeranyl ddp
33	38	45.8	359	2	A35714	feruin precursor -
34	38	45.8	364	2	S22394	feruin precursor -
35	38	45.8	537	1	Q08E30	BRP2 protein - hu
36	38	45.8	552	2	AB0496	probable membrane
37	38	45.8	568	2	T34522	hypothetical prote
38	38	45.8	720	2	F85572	probable outer mem
39	38	45.8	723	2	G90721	probable outer mem
40	38	45.8	730	2	B83592	hypothetical prote
41	38	45.8	818	1	E64807	outer membrane ush
42	38	45.8	1237	2	T37529	hypothetical prote
43	38	45.8	1502	2	T48309	hypothetical prote
44	38	45.8	1630	2	A53577	ascites siatoglyco
45	38	45.8	3856	2	T51174	ataxia-telangiecta

ALIGNMENTS

RESULT 1
EHNU
Ig epsilon chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1981 #sequence revision 13-Jun-1983 #text change 09-Jul-2004
C:Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46
R:Flanagan, J.G.; Rabbits, T.H.
EMBO J. 1, 655-660, 1982
A>Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gene
A:Reference number: A22771; MUID:84236029; PMID:6234164
A:Accession: A22771
A:Molecule type: DNA
A:Residues: 1-428 <FLA>
A:Cross-references: UNIPROT:P01854; UNIPARC:UPI000004BA848; GB:L00022; GB:J00227; GB:V005
R:Ueda, S.; Nakai, S.; Nishida, Y.; Hasejima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A>Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog
A:Reference number: A23195; MUID:84207910; PMID:6327276
A:Accession: A23195
A:Molecule type: DNA
A:Residues: 2-428 <UED>
A:Cross-references: UNIPARC:UPI0000173783; GB:J00222; NID:9184755
R:Zhang, K.; Saxon, A.; Max, E.E.
J. Exp. Med. 176, 233-243, 1992
A>Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
A:Reference number: PH1214; MUID:92308839; PMID:1613458
A:Accession: PH1214
A:Molecule type: DNA
A:Residues: 320-428 <ZHA>
A:Cross-references: UNIPARC:UPI000014452D; EMBL:X63693; GB:S36668; NID:932987
R:Seno, M.; Kurokawa, T.; Ono, Y.; Ono, H.; Saesada, R.; Izatsehl, K.; Kikuchi, M.; Sugi
Nucleic Acids Res. 11, 719-726, 1983
A>Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha
A:Reference number: A93491; MUID:83168897; PMID:6300763
A:Accession: A93491
A:Molecule type: mRNA
A:Residues: 1-428 <SEN>
A:Cross-references: UNIPARC:UPI000004BA48; GB:L00022; GB:J00227; GB:V00555; NID:9185035
R:Max, E.E.; Battey, J.; Ney, R.; Kirsch, I.R.; Leder, P.
Cell 29, 691-699, 1982
A>Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A:Reference number: A90824; MUID:83001945; PMID:6288268
A:Accession: A90824
A:Molecule type: DNA
A:Residues: 1-358, 'L', 360-428 <MAX>
A:Cross-references: UNIPARC:UPI0000173784; GB:J00222; NID:9184755
A>Note: This sequence difference may be due to polymorphism
R:Benich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
In Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
A:Reference number: A94418
A:Accession: A94418
A:Molecule type: protein

C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: H65006
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H65006
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-578 <BLAT>
A:Cross-references: UNIPARC:UPI000016ED73; GB:AE000322; GB:U00096; NID:G1788672; PIDN:AA
A:Experimental source: strain K-12, substrain MG1655

Query Match 53.0%; Score 44; DB 2; Length 578;
Best Local Similarity 57.1%; Pred. No. 18;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGQVMDVLDLSTAS 14
Db 346 QNGQVQEVYDISTAS 359

RESULT 5

hypothetical protein F20M13.160 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T05688

R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, February 1999

A:Reference number: Z15420

A:Accession: T05688

A:Molecule type: DNA

A:Residues: 1-757 <BEV>

A:Cross-references: UNIPROT:Q9S2N9; UNIPARC:UPI000004AFAC; EMBL:AL035540

A:Experimental source: cultivar Columbia; BAC clone F20M13

C:Genetics:

A:Map position: 4

A:Introns: 6/2; 235/1; 496/3; 571/3; 606/3; 633/3; 663/1; 696/3; 736/3

A:Note: F20M13.160

Query Match 53.0%; Score 44; DB 2; Length 757;
Best Local Similarity 61.5%; Pred. No. 24;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDGQVMDVLDLSTA 13
Db 476 QDGRLDVPLSTA 488

RESULT 6

E86622 N-acetylglutamate-L-alanine amidase (EC 3.5.1.28) [imported] - Lactococcus lactis subsp.
N:Alternate names: N-acetylglutamate

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C:Accession: E86622

R:Botolin, A.; Winkler, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: E86622

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-361 <STO>

A:Cross-references: UNIPROT:Q9C125; UNIPARC:UPI000006859; GB:AE005176; PID:G12723426; F

C:Genetics:

A:Gene: acMD

C:Keywords: hydrolase

Query Match 50.6%; Score 42; DB 2; Length 361;
Best Local Similarity 57.1%; Pred. No. 23;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 GQVMDVLDLSTASTT 16
Db 297 GQVMDVLDLSTASTT 310

RESULT 7

nonstructural protein V - simian paramyxovirus SV41

C:Species: simian paramyxovirus SV41

C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

C:Accession: J02040

R:Kawano, M.; Teurndone, M.; Ok, N.; Nishio, M.; Komada, H.; Matsunura, H.; Kusagawa, S.

U:Gen. Virol. 74, 911-916, 1993

A:Title: Sequence determination of the P gene of simian virus 41: presence of irregular

A:Reference number: J02040; MUID:93260408; PMID:8492098

A:Accession: J02040

A:Molecule type: genomic RNA

A:Residues: 1-225 <KAW>

A:Cross-references: UNIPROT:P36315; UNIPARC:UPI0000138296; GB:S60811; NID:G385516; PIDN:

C:Genetics:

A:Gene: V

C:Superfamily: simian paramyxovirus nonstructural protein V; V/P protein homology

C:Keywords: alternative splicing; nonstructural protein

F.1-163/Domain: V/P protein homology <VPN>

Query Match 49.4%; Score 41; DB 1; Length 225;
Best Local Similarity 46.7%; Pred. No. 20;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 GQVMDVLDLSTASTQ 17
Db 109 GRMTDLDLATGTVTQ 123

RESULT 8

H91251 Probable tail protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C:Accession: H91251

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gsawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hatori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A:Reference number: A96229; MUID:21156231; PMID:11258796

A:Accession: H91251

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-374 <HAY>

A:Cross-references: UNIPROT:O8X2Y0; UNIPARC:UPI000002A42; GB:BA000007; PIDN:BA038407.1;

A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:

A:Gene: EC64984

C:Superfamily: phage Mu gene P protein

Query Match 49.4%; Score 41; DB 2; Length 374;
Best Local Similarity 53.3%; Pred. No. 35;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGQVMDVLDLSTAST 15
Db 287 ENGQVMDVLDLSTAST 301

RESULT 9

J02041 polymerase-associated nucleocapsid phosphoprotein - simian paramyxovirus SV41

N:Alternate names: P protein

C:Species: simian paramyxovirus SV41

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C/Accession: JQ2041
R/Kawano, M.; Tsurudome, M.; Oki, N.; Nishio, M.; Komada, H.; Matsumura, H.; Kusagawa, S.
J. Gen. Virol. 74, 911-916, 1993
A/Title: Sequence determination of the P gene of simian virus 41: presence of irregular
A/Reference number: JQ2040; MUID:93260408; PMID:8492098
A/Accession: JQ2041
A/Molecule type: mRNA
A/Residues: 1-394 <KAW>
A/Cross-references: UNIPROT:Q86606; UNIPARC:UPI0000178672
C/Genetics:
A/Genes: P
C/Superfamily: simian paramyxovirus P protein; V/P protein homology
C/Keywords: nucleocapsid; phosphoprotein; RNA editing
F:1-163/Domain: V/P protein homology <VPN>

Query Match 49.4%; Score 41; DB 2; Length 394;
Best Local Similarity 46.7%; Pred. No. 37;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 GQVMDVLDLSTASTQ 17
:::|::|::|
Db 109 GRMTDLDLATGTVTQ 123

RESULT 10
H69200
heavy-metal transporting CPX-type ATPase - Methanobacterium thermoautotrophicum (strain
C/Species: Methanobacterium thermoautotrophicum
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: H69200
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaltre, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A/Reference number: A69000; MUID:98037514; PMID:9371463
A/Accession: H69200
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Residues: 1-675 <MTH>
A/Molecule type: DNA
A/Cross-references: UNIPROT:Q26849; UNIPARC:UPI0000066732; GB:AE000854; GB:AE000666; NID
C/Genetics:
A/Experimental source: strain Delta H
C/Genetics:
A/Genes: MTH755
C/Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding d
F:76-413/Domain: ATPase transduction domain homology <ATT>
F:484-626/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 49.4%; Score 41; DB 2; Length 675;
Best Local Similarity 72.7%; Pred. No. 68;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGOVMDVDLST 12
|::|::|::|
Db 176 DGKVEDVDVST 186

RESULT 11
A69210
sensory transduction histidine kinase - Methanobacterium thermoautotrophicum (strain Del
C/Species: Methanobacterium thermoautotrophicum
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: A69210
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaltre, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A/Reference number: A69000; MUID:98037514; PMID:9371463
A/Accession: A69210
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA

A/Residues: 1-677 <MTH>
A/Cross-references: UNIPROT:Q26913; UNIPARC:UPI0000066738; GB:AE000859; GB:AE000666; NID
A/Experimental source: strain Delta H
C/Genetics:
A/Genes: MTH823
A/Start codon: TTG

Query Match 49.4%; Score 41; DB 2; Length 677;
Best Local Similarity 46.7%; Pred. No. 68;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGOVMDVDLSTAST 15
|::|::|::|
Db 395 EDGRILDVNSTLAGT 409

RESULT 12
F85875
probable fimbrial usher Z3600 [imported] - Escherichia coli (strain O157:H7, substrain E
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: F85875
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: F85875
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-879 <STO>
A/Cross-references: UNIPROT:Q8XCP4; UNIPARC:UPI000016589B; GB:AE005174; NID:q12516702; P
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Genes: Z3600
C/Superfamily: outer membrane usher protein fimb

Query Match 49.4%; Score 41; DB 2; Length 879;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGOVMDVDLSTAS 14
:::|::|::|
Db 345 QNGQVDEYDINTAS 358

RESULT 13
E91031
probable outer membrane protein Ecs3221 [imported] - Escherichia coli (strain O157:H7, su
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C/Accession: E91031
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yaeunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: E91031
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-879 <HAY>
A/Cross-references: UNIPROT:Q8XCP4; UNIPARC:UPI000000D0453; GB:BA000007; PIDN:BA036644.1;
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Genes: Ecs3221
C/Superfamily: outer membrane usher protein fimb

Query Match 49.4%; Score 41; DB 2; Length 879;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDGOVMDVDLSTAS 14
:::|::|::|

Db 345 QNGOVQEXYDINTAS 358

RESULT 14

B96761 Probable protein kinase T9L24.36 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C/Accession: B96761

R/Theologian: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A6141; MUID:21016719; PMID:11130712

A/Accession: B96761

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-1155 <STO>

A/Cross-references: UNIPROT:Q9FX38; UNIPARC:UPI000009FSD2; GB:AE005173; NID:g11120796; F

C/Genetics:

A/Gene: T9L24.36

A/Map position: 1

Query Match 49.4%; Score 41; DB 2; Length 1155;

Best Local Similarity 50.0%; Pred. No. 1.3e+02;

Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 DGGVMDVLDLSTAQ 17
 DB 520 DGGVMDVLDLSTAQ 535

RESULT 15

H83545 Hypothetical protein PA0803 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C/Accession: H83545

R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bz

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: H83545

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-146 <STO>

A/Cross-references: UNIPROT:Q91SD5; UNIPARC:UPI00000C5160; GB:AE004515; GB:AE004091; NID

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA0803

Query Match 48.2%; Score 40; DB 2; Length 146;

Best Local Similarity 57.1%; Pred. No. 18;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDGQMDVLDLSTAS 14
 DB 43 EDGQMDVLDLSTAS 56

Search completed: December 12, 2005, 20:42:55
 Job time : 16.3621 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:41 ; Search time 92.3276 Seconds
(without alignments)
129.907 Million cell updates/sec

Title: US-10-758-165A-16
Perfect score: 83
Sequence: 1 EDGQVMDVDLSTASTQ 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprotc:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	83	100.0	1 IGHE_HUMAN	P01854 homo sapien
2	47	56.6	2 Q9PUV3_PTELE	Q9PUV3 habus tetr
3	46	55.4	2 Q5LX57_STILO	Q5LX57 silicibacte
4	46	55.4	2 P91775_PACLE	P91775 pacifistacu
5	45	54.2	2 Q4S4N1_TETNG	Q4S4N1 tetracodon
6	45	54.2	2 Q7VHC8_HELHP	Q7VHC8 helicobacte
7	45	54.2	2 Q4KMD7_BRARE	Q4KMD7 brachydant
8	44	53.0	1 RL24_HALSA	09hpc3 halobacteri
9	44	53.0	2 Q72PFB_LEPIC	Q72PFB leptospira
10	44	53.0	2 Q8F6B9_LEPIN	Q8F6B9 leptospira
11	44	53.0	2 Q8G7N6_BIFLO	Q8G7N6 blifidobacte
12	44	53.0	2 Q9SZN9_ARATH	Q9SZN9 arabidopsi
13	44	53.0	2 Q7NGR5_GLOVI	Q7NGR5 gloeobacter
14	44	53.0	2 Q5V826_HALMA	Q5V826 halocarcula
15	44	53.0	1 YFCU_ECOLI	P77196 escherichia
16	44	53.0	2 Q6WWM4_ARATH	Q6WWM4 arabidopsi
17	43	51.8	2 Q69XUS_ORYSA	Q69XUS oryza sativ
18	43	51.8	2 Q873P6_RHOTO	Q873P6 rhodospo
19	43	51.8	2 Q7S2C7_NEUCR	Q7S2C7 neurospora
20	43	51.8	2 Q52F86_MAGGR	Q52F86 magnaporthe
21	43	51.8	2 Q7PTM4_ANOGA	Q7PTM4 anopheles g
22	43	51.8	2 Q9N595_CABEL	Q9N595 caenorhabdi
23	42	50.6	2 Q711B1_LACDL	Q711B1 lactobacilli
24	42	50.6	2 Q4UPGJ_XANCP	Q4UPGJ xanthomonas
25	42	50.6	2 Q8R3Y3_XANCP	Q8R3Y3 xanthomonas
26	42	50.6	2 Q6TE28_9PERC	Q6TE28 trachinus d
27	42	50.6	2 Q6TE27_9PERC	Q6TE27 noctentia
28	42	50.6	2 Q9PUV5_9PERC	Q9PUV5 colissa lali
29	42	50.6	2 Q9C125_LACTA	Q9C125 lactococcus
30	42	50.6	2 Q6B383_PSEFL	Q6B383 pseudomonas
31	42	50.6	2 Q8NP11_CORGL	Q8NP11 corynobacte

32	42	50.6	820	2	Q6CRE9_KLUUA	Q6cre9 kluyveromyc
33	42	50.6	885	2	Q57T59_SALCH	Q57t59 salmone
34	42	50.6	885	2	Q87658_SALRY	Q87658 salmone
35	42	50.6	1420	2	Q4PH85_USDMA	Q4ph85 usiliago ma
36	42	50.6	3004	2	Q54C20_DICDI	Q54c20 dictyosteli
37	41.5	50.0	291	2	Q7M2H1_PHOIL	Q7m2h1 photobactu
38	41	49.4	96	2	Q98F99_RHILIO	Q98f99 rhizobium i
39	41	49.4	171	2	Q7T006_MOUSE	Q7tq06 mus musculu
40	41	49.4	214	2	Q67E22_9SMEG	Q67e22 syngnathus
41	41	49.4	225	1	VY_SVALI	P36315 simian viru
42	41	49.4	225	2	Q67E20_9PERC	Q67e20 pampus arge
43	41	49.4	238	2	Q67E16_PTELE	Q67e16 hoplostetich
44	41	49.4	248	2	Q64AB8_9ARCH	Q64ab8 uncultured
45	41	49.4	273	2	Q9PUV6_9PERC	Q9puv6 stromateus

ALIGNMENTS

RESULT 1
ID IGHE_HUMAN STANDARD; PRT; 428 AA.
AC P01854;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig epsilon chain C region.
GN Name=IGHE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBT_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=8316897; PubMed=630763;
RA Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,
RA Kikuchi M., Sugino Y., Nishida Y., Honjo T.;
RT "Molecular cloning and nucleotide sequencing of human immunoglobulin
epsilon chain cDNA.";
RL Nucleic Acids Res. 11:719-726(1983).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND VARIANT LEU-35.
RX MEDLINE=83001945; PubMed=6288268; DOI=10.1016/0092-8674(82)90185-4;
RA Max E.E., Battey J., Ney R., Kirsch I.R., Leder P.;
RT "Duplication and deletion in the human immunoglobulin epsilon genes.";
RL Cell 29:691-699(1982).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84236029; PubMed=6234164;
RA Planagan J.G., Rabbitts T.H.;
RT "The sequence of a human immunoglobulin epsilon heavy chain constant
region gene, and evidence for three non-allelic genes.";
RL EMBO J. 1:655-660(1982).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=84207910; PubMed=6327276;
RA Ueda S., Nakai S., Nishida Y., Hisajima H., Honjo T.;
RT "Long terminal repeat-like elements flank a human immunoglobulin
epsilon pseudogene that lacks introns.";
RL EMBO J. 1:1539-1544(1982).
RN [5]
RP PRELIMINARY PROTEIN SEQUENCE (MYELOMA PROTEIN ND).
RA Benich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RT Immediate hypersensitivity: modern concepts and developments, pp.1-36,
Marcel Dekker, New York (1978).
RN [6]
RP NUCLEOTIDE SEQUENCE OF 1-40; 68-114 AND 427-428.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Moogaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human

RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [7]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=87089848; PubMed=3796618; DOI=10.1016/0161-5890(86)90005-2;
RA Padlan E.A., Davies D.R.;
RT "A model of the Fc of immunoglobulin E.";
RL Mol. Immunol. 23:1063-1075(1986).
CC -1- SIMILARITY: Contains 4 Ig-like (immunoglobulin-like) domains.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; I00022; AAB59424.1; ALT_INIT; Genomic_DNA.
DR PIR; A22771; EHHU.
DR PDB; 1F6A; X-ray; B/D=211-428.
DR PDB; 1FP5; X-ray; A=211-428.
DR PDB; 1G84; NMR; A=106-208.
DR PDB; 1IGE; Model; A/B=107-428.
DR PDB; 100V; X-ray; A/B=106-427.
DR Ensemble; ENSG0000017154; Homo sapiens.
DR HGN; HGN:5522; IGHE.
DR MIM; 147180; -.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; Pf07654; C1-set; 3.
DR Pfam; Pf00047; Ig; 1.
DR SMART; SM00407; IGc1; 4.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KM 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain; Repeat.
FT DOMAIN 6 103
FT DOMAIN 112 210
FT DOMAIN 214 318
FT DOMAIN 324 423
FT CARBOHYD 21 21
FT CARBOHYD 49 49
FT CARBOHYD 99 99
FT CARBOHYD 146 146
FT CARBOHYD 252 252
FT CARBOHYD 275 275
FT DISULFID 14 14
FT DISULFID 15 105
FT DISULFID 29 85
FT DISULFID 121 121
FT DISULFID 135 193
FT DISULFID 209 209
FT DISULFID 239 299
FT DISULFID 345 405
FT VARIANT 359 359
FT NON_TER 1 1
FT STRAND 113 119
FT STRAND 130 138
FT STRAND 148 151
FT TURN 152 153
FT STRAND 154 156
FT STRAND 158 160
FT HELIX 163 165
FT STRAND 173 181
FT STRAND 182 186
FT TURN 187 188
FT STRAND 191 196
FT STRAND 201 206
FT STRAND 218 221
FT HELIX 226 230

W -> L (possible polymorphism).
/Frid=VAR_003885.

FT TURN 231 232
FT STRAND 236 244
FT STRAND 252 257
FT TURN 258 259
FT STRAND 267 272
FT TURN 274 275
FT STRAND 278 285
FT HELIX 288 292
FT TURN 293 294
FT STRAND 297 302
FT TURN 304 305
FT STRAND 310 314
FT STRAND 322 322
FT STRAND 325 330
FT STRAND 334 334
FT TURN 335 336
FT TURN 337 337
FT STRAND 340 351
FT STRAND 356 361
FT TURN 362 363
FT STRAND 364 365
FT HELIX 368 370
FT STRAND 371 373
FT STRAND 377 378
FT STRAND 384 393
FT STRAND 394 399
FT HELIX 403 408
FT TURN 410 411
FT TURN 413 415
FT STRAND 417 422
SQ SEQUENCE 428 AA; 47019 MW; 25C4CA072AA558A0 CRC64;

Query Match 100.0%; Score 83; DB 1; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EDGQWMDVISTASTQ 17
Db 151 EDGQWMDVISTASTQ 167

RESULT 2
O9PUY3_9TELE PRELIMINARY; PRT; 247 AA.
AC O9PUY3;
DT 01-MAY-2000 (TEMBREL. 13, Created)
DT 01-MAY-2000 (TEMBREL. 13, Last sequence update)
DT 01-DEC-2001 (TEMBREL. 19, Last annotation update)
DE Mixed lineage leukemia-like protein (Fragment).
GN Name=M11;
OS Barbus tetrazona.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Barbus.
OX NCBI_TaxID=94221;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=9938697; PubMed=10468597; DOI=10.1073/pnas.96.18.10267;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF137224; AAD53447.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 247 247
SQ SEQUENCE 247 AA; 26620 MW; B9160D133798C71F CRC64;

Query Match 56.6%; Score 47; DB 2; Length 247;
Best Local Similarity 56.2%; Pred. No. 15;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 1 EDGQWMDVISTASTT 16
: ||| ||: ||: |||


```

Db          145 DDGSESDVSI8TSTT 160

RESULT 3
OSLX57_SILPO PRELIMINARY; PRT; 203 AA.
ID OSLX57_SILPO
AC OSLX57;
DT 01-FEB-2005 (TRENBLrel. 29, Created)
DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE Glutathione S-transferase family protein.
GN OrderedLocustNames=SP00270;
OS Silicibacter pomeroyi.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Silicibacter.
OX NCBI_TaxId=89184;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DSS-3 / ATCC 70808 / DSM 15171;
RX PubMed=15602564; DOI=10.1038/nature03170;
RA Moran M.A., Buchan A., Gonzalez J.M., Heidelberg J.F., Whitman W.B.,
RA Kiene R.P., Henriksen J.R., King G.M., Belas R., Fugua C.,
RA Brinkac L.M., Lewis M., Johri S., Weaver B., Pai G., Eichen J.A.,
RA Kane E., Sheldon W.M., Ye W., Miller T.R., Carlton J., Raeko D.A.,
RA Paulsen I.T., Ren Q., Daugherty S.C., DeBoy R.T., Dodson R.J.,
RA Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Rosovitz M.J.,
RA Haft D.H., Selengut J., Ward N.;
RT "Genome sequence of Silicibacter pomeroyi reveals adaptations to the
RT marine environment."
RL Nature 433:910-913(2004).
CC -I- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; CP000031; AAV93590.1; -; Genomic DNA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR004045; GST_Nterm.
DR InterPro; IPR012335; Thioredoxin-like.
DR InterPro; IPR012335; Thioredoxin_fold.
DR Pfam; PF02798; GST_N; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 203 AA; 22285 MW; 5D33E1A87C546E06 CRC64;

Query Match          55.4%; Score 46; DB 2; Length 203;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy          1 EDGQVMDVLDLSTASTT 16
Db          21 ESGQLDVLDLDTAGGT 36

RESULT 4
P91775_PACLE PRELIMINARY; PRT; 977 AA.
ID P91775_PACLE
AC P91775;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Pacificatin heavy chain precursor.
OS Pacificatinus lenusculus (Signal crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Plecycemata; Astacidae;
OC Astacodea; Astacidae; Pacificastacus.
OX NCBI_TaxId=6720;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP MEDLINE=97338078; PubMed=9192625; DOI=10.1073/pnas.94.13.6682;
RA Liang Z., Sottrup-Jensen L., Asapan A., Hall M., Soderhall K.;
RT "Pacificatin, a novel 155-kDa heterodimeric proteinase inhibitor
RT containing a unique transferrin chain."
RL Proc. Natl. Acad. Sci. U.S.A. 94:6682-6687(1997).
DR EMBL; U81824; AAC64660.1; -; mRNA.
DR HSP; P56410; IAOV.
DR GO; GO:0005576; C:extracellular region; IEA.

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DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006825; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR SMART; PR00422; TRANSFERRIN.
DR SMART; SMO0094; TR_FER; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
KW Signal.
FT SIGNAL.
FT CHAIN
SQ SEQUENCE 977 AA; 106866 MW; SEF1706133350E99 CRC64;

Query Match          55.4%; Score 46; DB 2; Length 977;
Best Local Similarity 57.1%; Pred. No. 97;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy          1 EDGQVMDVLDLSTAS 14
Db          935 EDGHTVDDSSNVS 948

RESULT 5
O4S4N1_TETNG PRELIMINARY; PRT; 475 AA.
ID O4S4N1_TETNG
AC O4S4N1_TETNG
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Chromosome 2 SCAP14738, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00024108001;
OS Tetradodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphi; Tetradontiformes;
OC Tetradontoidae; Tetradontidae; Tetradon.
OX NCBI_TaxId=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Maucel E., Bounau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Da Silva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Ubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Catolico L., Poulain J., De Bernardis V.,
RA Cruaud C., Duprat S., Broctier P., Coutanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Croillius H.;
RT "Genome duplication in the teleost fish Tetradodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
CC -I- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAEB01014738; CAG04401.1; -; Genomic DNA.
DR FT NON_TER
FT NON_TER
SQ SEQUENCE 475 AA; 53728 MW; FFB80CB714EF095 CRC64;

Query Match          54.2%; Score 45; DB 2; Length 475;
Best Local Similarity 47.1%; Pred. No. 67;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Oy          1 EDGQVMDVLDLSTASTTQ 17

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KW Complete proteome; Ribonucleoprotein; Ribosomal protein; RNA-binding;
 KW rRNA-binding.
 SQ SEQUENCE 118 AA; 13369 MW; 90C2F1C4577190A8 CRC64;

Query Match 53.0%; Score 44; DB 1; Length 118;
 Best Local Similarity 69.2%; Pred. No. 23;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 EDGQVMDVLDSTA 13
 |||:|||||
 DB 59 DGEVVDVLDLRA 71

RESULT 9
 072PM8_LEPIC PRELIMINARY; PRT; 574 AA.

AC 072PM8; 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=LIC12349;
 OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
 OS Copenhagen).
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=44275;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Fiocruz L1-130;
 RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
 RA Nascimben A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
 RA Ho P.L., Haake D.A., Verjovsky-Almeida S., Hartke R.A.,
 RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carier H.,
 RA Coutinho L.L., Degraive W.M., Dellagostin O.A., El-Dorry H.,
 RA Ferro E.S., Ferro M.I.T., Furian L.R., Gamberini M., Gigliotti E.A.,
 RA Goes-Melo A., Goldman G.H., Goldman M.H.S., Harakava R.,
 RA Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T.,
 RA Kurama E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
 RA de Oliveira R.C., Pereira G.G., Reis M.S., Schrieffer A.,
 RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
 RA Camargo L.E.A., Kitajima J.P., Secubal J.C., Van Sluys M.A.;
 RT "Comparative genomics of two Leptospira interrogans serovars reveals
 novel insights into physiology and pathogenesis.";
 RL J. Bacteriol. 186:2164-2172(2004).
 DR EMBL; AE017296; AAS70918.1; -; Genomic_DNA.
 DR InterPro; IPR000585; Hemopexin.
 DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 574 AA; 65826 MW; 1F5E2B1C8183306C CRC64;

Query Match 53.0%; Score 44; DB 2; Length 574;
 Best Local Similarity 69.2%; Pred. No. 1.2e+02;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 DGQVMDVLDSTAS 14
 |||:|||||
 DB 497 DGEVVDVLDLRA 509

RESULT 10
 08F6B9_LEPIN PRELIMINARY; PRT; 574 AA.

AC 08F6B9; 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DE Hypothetical protein.
 GN OrderedLocustNames=IA1389;
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=173;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar Iai;
 RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
 RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
 RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
 RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
 RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
 RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
 RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
 RA Xu J.-G., Zhao G.-P.;
 RT "Unique physiological and pathogenic features of Leptospira
 RT interrogans revealed by whole-genome sequencing.";
 RL Nature 422:888-893(2003).
 DR EMBL; AE011318; AAN48588.1; -; Genomic_DNA.
 DR InterPro; IPR000585; Hemopexin.
 DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 574 AA; 65826 MW; 1F5E2B1C8183306C CRC64;

Query Match 53.0%; Score 44; DB 2; Length 574;
 Best Local Similarity 69.2%; Pred. No. 1.2e+02;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 DGQVMDVLDSTAS 14
 |||:|||||
 DB 497 DGEVVDVLDLRA 509

RESULT 11
 08G7N6_BIFLO PRELIMINARY; PRT; 632 AA.

AC 08G7N6; 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DE Hypothetical protein.
 GN OrderedLocustNames=BL0213;
 OS Bifidobacterium longum.
 OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
 OC Bifidobacteriaceae; Bifidobacterium.
 OX NCBI_TaxID=216816;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=NCC 2705;
 RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
 RA Schell M.A., Karmaliantzou M., Snel B., Vilanova D., Berger B.,
 RA Peesli G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,
 RA Fridmore R.D., Atgion F.;
 RT "The genome sequence of Bifidobacterium longum reflects its adaptation
 RT to the human gastrointestinal tract.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
 DR EMBL; AE014295; AAN24065.1; -; Genomic_DNA.
 DR InterPro; IPR001173; Glyco_trans_2.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 632 AA; 72156 MW; 31F5A3ADCCF3A7D CRC64;

Query Match 53.0%; Score 44; DB 2; Length 632;
 Best Local Similarity 46.7%; Pred. No. 1.3e+02;
 Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 2 DGQVMDVLDSTASTT 16
 |||:|||||
 DB 150 DGEULDIPLSLSTTT 164

RESULT 12
 09S2N9_ARATH PRELIMINARY; PRT; 757 AA.

AC 09S2N9; 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE Hypothetical protein F20M13.160 (Hypothetical protein ATg38600).
 GN Name=F20M13.160; Synonyms=ATg38600;

```

OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Weiler H., Kutzner M., Wambutt R., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Schueller C.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Weiler H., Kutzner M., Wambutt R., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL035540; CAB37516.1; -; Genomic DNA.
DR EMBL: AL161593; CAB80524.1; -; Genomic DNA.
DR PIR: T05688; T05688.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0006512; F:ubiquitin cycle; IEA.
DR InterPro: IPR000569; HECT.
DR Pfam: PF00637; HECT.1.
DR SMART: SM00119; HECTc; 1.
DR PROSITE: PS50237; HECT.1.
DR Hypothetical protein.
SQ SEQUENCE 757 AA; 82683 MW; 9F7E225EC65C0656 CRC64;

Query Match 53.0%; Score 44; DB 2; Length 757;
Best Local Similarity 61.5%; Pred. No. 1.6e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Cy 1 EDGQVMDVLDSTA 13
Db 476 EDGRLLDVPJLSTA 488

RESULT 13
ID Q7NGR5_GLOVI PRELIMINARY; PRT; 773 AA.
AC Q7NGR5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G113103 protein.
GN OrderedLocustNames=G113103;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteriales; Gloeobacter.
OX NCBI_TaxId=33072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:137-145 (2003).
DR EMBL: BA000045; BAC91044.1; -; Genomic DNA.
DR HSSP; P06129; IJW.
DR GO: GO:0019867; C:outer membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.

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DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000531; TonB_receptor.
DR Pfam: PF00593; TonB_dep_Rec; 1.
KW Complete proteome; Membrane; Outer membrane; TonB box.
SQ SEQUENCE 773 AA; 83958 MW; F129A553B6DA848 CRC64;

Query Match 53.0%; Score 44; DB 2; Length 773;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Cy 1 EDGQVMDVLDSTA 14
Db 347 EDGRLLMADNYTAS 360

RESULT 14
ID Q5V826_HALMA PRELIMINARY; PRT; 812 AA.
AC Q5V826;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE ATP-dependant helicase.
GN Name=yrcJ1; OrderedLocustNames=pNG2034;
OS Haloarcula marismortui (Halobacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxId=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RX PubMed=15520287; DOI=10.1101/gr.2700304;
RA Baliga N.S., Bonneau R., Facciolo M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
RT "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
the Dead Sea.";
RL Genome Res. 14:2221-2234 (2004).
DR EMBL: AY596291; AAY44326.1; -; Genomic DNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR011545; DEAD/DEAH_N.
DR InterPro: IPR001650; Helicase_C.
DR Pfam: PF00270; DEAD.1.
DR Pfam: PF00271; Helicase_C.1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELICc; 1.
KW ATP-binding; Complete proteome; DNA-binding; Helicase; Hydrolase;
KW Plasmid.
SQ SEQUENCE 812 AA; 89620 MW; B1BDA603A8216CF CRC64;

Query Match 53.0%; Score 44; DB 2; Length 812;
Best Local Similarity 58.8%; Pred. No. 1.8e+02;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Cy 1 EDGQVMDVLDSTA 17
Db 276 EDDSTADVDEDTASTQ 292

RESULT 15
ID YFCU_ECOCI STANDARD; PRT; 881 AA.
AC P77196; P77532;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical outer membrane usher protein yfcU precursor.
GN Name=yfcU; OrderedLocustNames=b23337/b2338;

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OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden W.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Alba H., Baba T., Hayaishi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubraman S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiiuchi T.;
RT "Construction of a contiguous 874-Kb sequence of the Escherichia coli-
RT K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
CC -1- FUNCTION: Involved in the export and assembly of a fimbrial
CC subunit across the outer membrane (By similarity).
CC -1- INTERACTION:
CC P60240:YAP; NBExp-1; InAct=EBI-551635; EBI-551542;
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC (by similarity).
CC -1- SIMILARITY: Belongs to the fimbrial export usher family.
CC -1- CAUTION: This is a conceptual translation.
CC -1- CAUTION: Ref.1 and Ref.2 sequences differ from that shown due to a
CC stop codon in position 579.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U00096; AAC75398.1; ALT_SEQ; Genomic DNA.
DR EMBL; U00096; AAC75397.1; ALT_INIT; Genomic DNA.
DR EMBL; D90864; BAA16191.1; ALT_INIT; Genomic DNA.
DR EMBL; D90864; BAA16192.1; ALT_SEQ; Genomic DNA.
DR InAct; P77196; -.
DR EcoBASE; EB3876; -.
DR EcoGene; EG14124; yfcU.
DR InterPro; IPR000015; Fimb_usher.
DR Pfam; PF00577; Usher; 1.
DR PROSITE; PS01151; FIMBRIAL_USHER; 1.
KM Complete proteome: Fimbrial Hypothetical protein; Membrane;
KW Outer membrane; Signal; Transmembrane; Transport.
FT SIGNAL 1 29 Potential.
FT CHAIN 1 881 Hypothetical outer membrane usher protein
FT yfcU.
SQ SEQUENCE 881 AA; 97439 MW; 23DE53B67541E041 CRC64;

Query Match 53.0%; Score 44; DB 1; Length 881;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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Oy 1 EDGQVMDVLDSTAS 14
 ::|||:|:|:|
 Db 346 ONGQVQVEYDISTS 359

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 12, 2005, 19:37:19 ; Search time 81.3362 Seconds
(without alignments)
81.030 Million cell updates/sec

Title: US-10-758-165A-1
Perfect score: 81
Sequence: 1 RNDSP1QTDYTTTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

1:	Geneseqp1980s:*
2:	Geneseqp1990s:*
3:	Geneseqp2000s:*
4:	Geneseqp2001s:*
5:	Geneseqp2002s:*
6:	Geneseqp2003as:*
7:	Geneseqp2003bs:*
8:	Geneseqp2004s:*
9:	Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	ADRI0601	Dog IGE e
2	81	100.0	312	AAV79995	Dog immun
3	81	100.0	417	AAW23067	Canine Ig
4	81	100.0	426	AAV7753	Canine Ig
5	81	100.0	426	ABP96583	Dog IGE h
6	53	65.4	15	ADRI0607	Pig IGE e
7	53	65.4	567	ABP96588	Pig IGE h
8	48	59.3	15	ADRI0602	Cat IGE e
9	48	59.3	431	ADG73237	Cat immun
10	48	59.3	496	ABP96580	Cat IGE h
11	48	59.3	496	ABU09338	Feline Ig
12	48	59.3	496	ABU09336	Feline Ig
13	48	59.3	496	ADG73251	Cat parti
14	48	59.3	496	ADG73252	Cat parti
15	43	53.1	1633	ABU42513	Protein e
16	42	51.9	1067	ABP91309	Herbicida
17	41	50.6	15	ADRI0603	Horse IGE
18	41	50.6	151	AAU57418	Propionib
19	41	50.6	424	ABM53937	Propionib
20	41	50.6	424	AAU50103	Equine Ig
21	41	50.6	424	AAU50104	Equine Ig
22	41	50.6	533	ABP39208	Staphyloc
23	41	50.6	533	ADSO5754	Staphyloc
24	41	50.6	569	ABP96585	Horse IGE

25	40	49.4	356	4	ABB64299	Abb64299 Drosophila
26	40	49.4	488	8	ADY09532	Plant full
27	40	49.4	555	8	ADA24243	Pseudomon
28	40	49.4	632	7	ABM90457	Rice abio
29	40	49.4	632	7	ABM85909	Rice abio
30	40	49.4	667	6	ADA33007	Actinobac
31	40	49.4	1180	3	AAU01845	Haemophil
32	40	49.4	1188	3	AAU01844	Haemophil
33	40	49.4	2349	6	AAO16359	Human tra
34	40	49.4	2400	4	ABG20278	Novel hum
35	40	49.4	2415	4	ABG20279	Novel hum
36	39	48.1	226	8	ADRI4996	SrSNG3 an
37	39	48.1	276	3	AAU08697	Arabidops
38	39	48.1	276	3	AAU42639	Arabidops
39	39	48.1	281	8	AD128921	Sarcocyst
40	39	48.1	281	8	ADRI4989	Sarcocyst
41	39	48.1	294	3	AAU08696	Arabidops
42	39	48.1	294	3	AAU42638	Arabidops
43	39	48.1	294	8	ADU061841	Transcrip
44	39	48.1	295	3	AAU42637	Arabidops
45	39	48.1	295	3	AAU08695	Arabidops

ALIGNMENTS

RESULT 1
ADRI0601 standard; peptide, 15 AA.

ADRI0601;
21-OCT-2004 (first entry)

Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.

Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; aetna;
anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.

Canis familiaris.
WO2004065936-A2.
05-AUG-2004.
15-JAN-2004; 2004WO-US003566.
16-JAN-2003; 2003US-0440472P.
(UNNC-) UNIV NORTH CAROLINA STATE.
Hammerberg B;
WPI, 2004-593545/57.

Novel antibody that specifically binds to mammalian IGE epitope, useful
for testing an allergen reactivity of IGE sample, detecting mammalian IGE
or treating asthma or anaphylactic shock.

Example 6; Page 9; 14pp; English.

The present invention relates to a novel monoclonal antibody (I) that
specifically binds to a mammalian IGE epitope, where the epitope is
between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
(I) is useful for testing an allergen reactivity of an IGE sample. The
allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
and corn allergens. The sample is a biological sample collected from a
dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
antibodies recognise epitopes on canine IGE corresponding to amino acid
residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and

CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IgE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IgE.
XX
XX

SO Sequence 15 AA;

Query Match 100.0%; Score 81; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSP1QTDQYTTTG 15
1 RNDSP1QTDQYTTTG 15
Db 1 RNDSP1QTDQYTTTG 15

RESULT 2
AAV79995
ID AAV79995 standard; protein; 312 AA.

AC AAV79995;
XX
DT 15-MAY-2000 (first entry)
XX

DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KM immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KM antibody; allergy; allergic disease; immunisation; anti-allergic;
XX anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

OS Canis sp.

PN WO967293-A1.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US013959.

PR 20-JUN-1998; 98US-00100287.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy.

XX Example 1; Page 66-68; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
CC a target effector site on the epsilon-heavy chain of IgE, and so
CC preventing triggering and activation of mast cells and basophils and
CC downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe (non-
CC anaphylactogenic) antibodies. AAV79994 to AAV80084 represent amino acid
CC sequences used in the exemplification of the present invention
XX

SO Sequence 312 AA;

Query Match 100.0%; Score 81; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RNDSP1QTDQYTTTG 15
1 RNDSP1QTDQYTTTG 15
Db 255 RNDSP1QTDQYTTTG 269

RESULT 3
AAW23067
ID AAW23067 standard; protein; 417 AA.

AC AAW23067;
XX
DT 30-JUN-2005 (revised)
DT 16-JUN-2005 (revised)
DT 19-FEB-1998 (first entry)
XX

DE Canine IgE heavy chain constant region (exon 1-4 product).

XX IgE; immunoglobulin; antibody; heavy chain constant region; allergy;
KM hypersensitivity; therapy; dog; antisense; immunomodulation.

OS Canis familiaris.

XX Key Location/Qualifiers

FT Misc-difference 55 /note= "encoded by ACC"

FT Misc-difference 56 /note= "encoded by TAC"

FT Misc-difference 67 /note= "encoded by GCC"

FT Misc-difference 83 /note= "encoded by NNT"

FT Misc-difference 174 /note= "encoded by GGN"

FT Misc-difference 175 /note= "encoded by NNG"

FT Misc-difference 176 /note= "encoded by TGN"

FT Misc-difference 203 /note= "encoded by TCC"

FT Misc-difference 204 /note= "encoded by GAC"

XX WO9730156-A2.

PD 21-AUG-1997.

PF 14-FEB-1997; 97WO-US002322.

PR 14-FEB-1996; 96US-00601197.

PA (IDEX-) IDEXX LAB INC.

PI Mermer B, Harris RA, Siefiring AE;

XX WPI; 1997-425031/39.

DR N-PSDB; AAT79278.

PT Isolated canine IgE heavy chain constant region DNA - useful to develop
PT products for treatment of canine allergies and for immunomodulation in
PT dogs.

PS Disclosure; Page 35-39; 59pp; English.

XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE
CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,
CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant
CC peptides encoded by exons 1-6 can be produced in eukaryotic or
CC prokaryotic cells. Such peptides, and antibodies raised against them, are
CC used in methods to treat the manifestation of allergy in dogs, e.g. to
CC treat Type I immediate hypersensitivity, and for immunomodulation

CC Revised record issued on 30-JUN-2005 : Typo in comments
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 81; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNDSP1QTDQYTTTG 15
|||
Db 352 RNDSP1QTDQYTTTG 366

RESULT 4

AAR97753
ID AAR97753 standard; protein; 426 AA.

AC AAR97753;

DT 28-AUG-1996 (first entry)

XX Canine IGE.

XX IGE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.

XX Canis familiaris.

XX WO961467-A1.

XX 23-MAY-1996.

XX 03-NOV-1995; 95WO-US013795.

XX 09-NOV-1994; 94US-00336583.

XX 09-NOV-1994; 94US-00336891.

XX (MERI) MERCK & CO INC.

XX Hollis GF, Patel MD;

XX WPI; 1996-277321/28.

XX N-PSDB; AAT29824.

XX New DNA encoding canine IGE and IGA - useful in vaccines, anti-sense

XX therapy, assays, drug screening, etc.

XX Claim 11; Page 29-30; 49pp; English.

XX The canine IGE amino acid sequence (AAR97753) was deduced from an

XX isolated gene (AAT29824) obtcd. from a canine liver DNA library. The

XX cloning of the IGE gene allows prodn. of large quantities of recombinant

XX IGE using bacterial, yeast, mammalian, insect or viral systems. The IGE

XX development and anti-IGE antibody generation). Fragments of IGE can be

XX used in vaccines or to prevent IGE-mediated hypersensitivity. The new

XX sequence information permits targeted modulation of IGE-mediated immune

XX responses

XX Sequence 426 AA;

Query Match 100.0%; Score 81; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNDSP1QTDQYTTTG 15
|||
Db 357 RNDSP1QTDQYTTTG 371

AC ABP96583;
XX
DT 28-MAY-2003 (first entry)

XX Dog IGE heavy chain amino acid sequence SEQ ID NO:28.

XX Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;

XX immune response; major histocompatibility complex; MHC; immunogenic;

XX antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;

XX dermatological; antiinflammatory; IGE-mediated condition; food allergy;

XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;

XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;

XX urticaria hives.

XX Canis familiaris.

XX WO2003015716-A2.

XX 27-FEB-2003.

XX 08-AUG-2002; 2002WO-US026986.

XX 13-AUG-2001; 2001US-0312120P.

XX (IGRT-) IGB THERAPEUTICS INC.

XX Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX WPI; 2003-268242/26.

XX Example 7; Page 152-154; 187pp; English.

XX The present invention describes a method (M1) for identifying peptides

XX that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin

XX E (IGE), comprising providing a test peptide (T) response suspected of being able

XX to bind to major histocompatibility complex (MHC) class I molecule, and

XX evaluating (T) for ability to elicit in a mammal a CTL response to

XX naturally processed and presented IGE peptides, where a peptide that

XX induces such a response is identified. Also described are compositions;

XX (C1) comprising at least one immunogenic peptide (I) identified by (M1);

XX (C2) comprising at least one isolated polynucleotide encoding (I); and

XX (C3) comprising antigen-presenting cells that recognise at least one (I).

XX Where C1-3 are able to bind to at least one MHC class I molecule and to

XX elicit in a mammal a CTL response to naturally processed and presented

XX IGE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,

XX vasotropic, dermatological, antiinflammatory and cytostatic activities,

XX and can be used as inducers of a CTL response against IGE, and in

XX vaccines. C1-3 can be used for modulating an IGE-mediated condition in a

XX mammal. C1-3 are useful for modulating an IGE-mediated condition such as

XX IGE-mediated atopic hypersensitivity condition. IGE-mediated non-atopic

XX hypersensitivity condition. IGE myeloma in a mammal. Preferably, C1-3 are

XX useful for treating atopic hypersensitivity conditions (such as allergic

XX rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-

XX atopic hypersensitivity conditions (such as anaphylaxis, and urticaria

XX hives). The present sequence represents an IGE heavy chain amino acid

XX sequence, which is given in an example from the present invention

XX Sequence 426 AA;

Query Match 100.0%; Score 81; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNDSP1QTDQYTTTG 15
|||
Db 357 RNDSP1QTDQYTTTG 371

```

RESULT 6
ADRI0607
ID ADRI0607 standard; peptide; 15 AA.
XX
XX
AC ADRI0607;
XX
XX
DT 21-OCT-2004 (first entry)
XX
XX
DE Pig IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.
XX
XX
KM Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KM pig.
XX
XX
OS Sus scrofa.
XX
XX
PN WO2004065936-A2.
XX
XX
PD 05-AUG-2004.
XX
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
XX
PR 16-JAN-2003; 2003US-0440472P.
XX
XX
PA (UNCL-) UNIV NORTH CAROLINA STATE.
XX
XX
PI Hammerberg B;
XX
XX
DR WPI; 2004-593545/57.
XX
XX
PT Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
XX
PS Example 6; Page 9; 14pp; English.
XX
XX
CC The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC (I) is useful for testing an allergen reactivity of an IGE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IGE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IGE. The present sequence is the
CC pig IGE 5.91 recognition site.
XX
XX
SQ Sequence 15 AA;
XX
XX
Query Match 65.4%; Score 53; DB 8; Length 15;
Best Local Similarity 57.1%; Pred. No. 0.042;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
XX
XX
OY 1 RNDSPITQDYTTT 14
DB 1 RNDAPVQADRHSTT 14
XX
XX
RESULT 7
ABP96588
ID ABP96588 standard; protein; 567 AA.
XX
XX
AC ABP96588;
XX
XX
XX
DT 28-MAY-2003 (first entry)
XX
XX
DE Pig IGE heavy chain amino acid sequence SEQ ID NO:33.

```

```

XX
XX
KM Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
KM immune response; major histocompatibility complex; MHC; immunogenic;
KM antiallergic; antiaesthetic; immunosuppressive; vasotropic; cytostatic;
KM dermatological; antiinflammatory; IGE-mediated condition; food allergy;
KM atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KM atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
KM urticaria hives.
XX
XX
OS Sus scrofa.
XX
XX
PN WO2003015716-A2.
XX
XX
PD 27-FEB-2003.
XX
XX
PF 08-AUG-2002; 2002WO-US026986.
XX
XX
PR 13-AUG-2001; 2001US-0312120P.
XX
XX
PA (IGET-) IGE THERAPEUTICS INC.
XX
XX
PI Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX
XX
DR WPI; 2003-268242/26.
XX
XX
PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
PT against IGE, by identifying peptide eliciting CTL response to IGE
PT peptides naturally presented by major histocompatibility complex class I
PT protein.
XX
XX
PS Example 7; Page 164-167; 187pp; English.
XX
XX
CC The present invention describes a method (M1) for identifying peptides
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
CC B (IGE), comprising providing a test peptide (T) suspected of being able
CC to bind to major histocompatibility complex (MHC) class I molecule, and
CC evaluating (T) for ability to elicit in a mammal a CTL response to
CC naturally processed and presented IGE peptides, where a peptide that
CC induces such a response is identified. Also described are compositions:
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
CC (C2) comprising at least one isolated polynucleotide encoding (I); and
CC (C3) comprising antigen-presenting cells that recognise at least one (I).
CC where C1-3 are able to bind to at least one MHC class I molecule and to
CC elicit in a mammal a CTL response to naturally processed and presented
CC IGE peptides. C1-3 have antiallergic, antiaesthetic, immunosuppressive,
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
CC and can be used as inducers of a CTL response against IGE, and in
CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as
CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
CC useful for treating atopic hypersensitivity conditions (such as allergic
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
CC hives). The present sequence represents an IGE heavy chain amino acid
CC sequence, which is given in an example from the present invention
XX
XX
SQ Sequence 567 AA;
XX
XX
Query Match 65.4%; Score 53; DB 6; Length 567;
Best Local Similarity 57.1%; Pred. No. 2.1;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
XX
XX
OY 1 RNDSPITQDYTTT 14
DB 499 RNDAPVQADRHSTT 512
XX
XX
RESULT 8
ADRI0602
ID ADRI0602 standard; peptide; 15 AA.
XX
XX
AC ADRI0602;
XX
XX
XX

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XX 21-OCT-2004 (first entry)
XX
XX Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.
DE
XX Antiaesthatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX cat.
XX
XX Felis catus.
XX
XX WO2004065936-A2.
XX
XX 05-AUG-2004.
XX
XX 15-JAN-2004; 2004WO-US003566.
XX
XX 16-JAN-2003; 2003US-0440472P.
XX
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hammerberg B;
XX
XX WPI; 2004-593545/57.
XX
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
XX for testing an allergen reactivity of IGE sample, detecting mammalian IGE
XX or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (I) that
XX specifically binds to a mammalian IGE epitope, where the epitope is
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX (I) is useful for testing an allergen reactivity of an IGE sample. The
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX and corn allergens. The sample is a biological sample collected from a
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX antibodies recognise epitopes on canine IGE corresponding to amino acid
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
XX cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
XX 3.76 were observed to have good cross-reactivity with the epsilon-chain
XX of IGE from cat and horse, but did not exhibit cross-reactivity with
XX either pig or human epsilon-chains of IGE. The present sequence is the
XX cat IGE 5.91 recognition site.
XX
XX Sequence 15 AA;
XX
XX Query Match 59.3%; Score 48; DB 8; Length 15;
XX Best Local Similarity 61.5%; Pred. No. 0.31;
XX Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Oy 2 NDSPIQTDQYTTT 14
Db 2 NDSPIQTDQYTTT 14

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XX US2003216565-A1.
XX
XX 20-NOV-2003.
XX
XX 07-APR-2003; 2003US-00409772.
XX
XX 07-JAN-1999; 99US-0115033P.
XX
XX 07-JAN-2000; 2000US-00479614.
XX
XX (MCCA/) MCCALL C.
XX
XX (WEBER/) WEBER E.
XX
XX McCall C, Weber E;
XX
XX WPI; 2004-010802/01.
XX
XX N-PSDB; ADG73236.
XX
XX New isolated nucleic acid molecule encoding a portion of a feline IGE
XX heavy chain protein, useful for treating and/or eliciting feline immune
XX responses for IGE-mediated responses, such as allergies.
XX
XX Claim 12; SEQ ID NO 14; 44pp; English.
XX
XX The invention describes an isolated nucleic acid molecule (I) encoding a
XX portion of a feline IGE heavy chain protein. The methods and compositions
XX of the present invention are useful for eliciting feline immune responses
XX for and/or treating IGE-mediated responses, such as allergies. This is
XX the amino acid sequence of a cat immunoglobulin E (IGE) constant region.
XX
XX Sequence 431 AA;
XX
XX Query Match 59.3%; Score 48; DB 8; Length 431;
XX Best Local Similarity 61.5%; Pred. No. 11;
XX Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Oy 2 NDSPIQTDQYTTT 14
Db 363 NDSPIQTDQYTTT 375

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RESULT 9
ADG73237
ID ADG73237 standard; protein; 431 AA.
XX
XX ADG73237;
XX
XX 11-MAR-2004 (first entry)
XX
XX Cat immunoglobulin E (IGE) constant region.
XX
XX antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;
XX immune response; IGE-mediated response; allergy; cat; constant region.
XX
XX Felis catus.
XX

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```

RESULT 10
ABP96580
ID ABP96580 standard; protein; 496 AA.
XX
XX ABP96580;
XX
XX 28-MAY-2003 (first entry)
XX
XX Cat IGE heavy chain amino acid sequence SEQ ID NO:25.
XX
XX Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
XX immune response; major histocompatibility complex; MHC; immunogenic;
XX antiallergic; antiaesthatic; immunosuppressive; vasotropic; cytostatic;
XX dermatological; antiinflammatory; IGE-mediated condition; food allergy;
XX atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
XX atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
XX urticaria hives.
XX
XX Felis catus.
XX
XX WO2003015716-A2.
XX
XX 27-FEB-2003.
XX
XX 08-AUG-2002; 2002WO-US026386.
XX
XX 13-AUG-2001; 2001US-0312120P.
XX
XX (IGET-) IGE THERAPEUTICS INC.
XX
XX Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX

```

DR WPI; 2003-268242/26.
 XX
 XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
 PT against IGE, by identifying peptide eliciting CTL response to IGE
 PT peptides naturally presented by major histocompatibility complex class I
 PT protein.
 XX
 XX
 PS Example 7, Page 145-147; 187pp; English.
 XX
 CC The present invention describes a method (M1) for identifying peptides
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
 CC E (IGE), comprising providing a test peptide (T) suspected of being able
 CC to bind to major histocompatibility complex (MHC) class I molecule, and
 CC evaluating (T) for ability to elicit in a mammal a CTL response to
 CC naturally processed and presented IGE peptides, where a peptide that
 CC induces such a response is identified. Also described are compositions:
 CC (1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (2) comprising at least one isolated polynucleotide encoding (I); and
 CC (3) comprising antigen-presenting cells that recognise at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC IGE peptides, C1-3 have anti-allergic, anti-asthmatic, immunosuppressive,
 CC vasotropic, dermatological, anti-inflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against IGE, and in
 CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
 CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as
 CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
 CC atopic hypersensitivity conditions (such as anaphylaxis), and urticaria
 CC hives). The present sequence represents an IGE heavy chain amino acid
 CC sequence, which is given in an example from the present invention
 XX
 XX
 SQ Sequence 496 AA;
 XX
 Query Match 59.3%; Score 48; DB 6; Length 496;
 Best Local Similarity 61.5%; Pred. No. 13;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 2 NDSPIOTDYYTTT 14
 |||||:|:|
 Db 428 NDSPVRTQQATT 440
 XX
 RESULT 11
 ABU09338
 ID ABU09338 standard; protein; 496 AA.
 XX
 AC ABU09338;
 XX
 XX 27-JUN-2003 (first entry)
 DT
 DE Feline IGE epsilon heavy chain #2.
 XX
 XX Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;
 KM IGE-mediated immune response; allergy; neoplasia; vaccine technology;
 KM antibody technology; anti-allergic; antiparasitic; cyostatic.
 XX
 OS Felis catus.
 XX
 PN US2003013183-A1.
 PD 16-JAN-2003.
 XX
 PF 07-JAN-2000; 2000US-00479614.
 XX
 PR 07-JAN-1999; 99US-0115033P.
 XX
 PA (MCCA/) MCCA.LL C.
 PA (WEBE/) WEBER E.
 XX
 PI Mccall C, Weber E;

XX
 DR WPI; 2003-391997/37.
 DR N-PSDB; ABX95715.
 XX
 XX New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or
 PT light chain protein, useful for treating feline IGE-mediated responses
 PT e.g. allergies, parasitic infections or neoplasia.
 FT
 XX
 XX Claim 1; Page 37-39; 45pp; English.
 PS
 XX
 CC The present invention relates to the isolation of feline immunoglobulin E
 CC (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the
 CC polynucleotide sequences encoding them. The sequences of the invention
 CC are useful for treating feline IGE-mediated immune responses (e.g.
 CC allergies, parasitic infections or neoplasia), in vaccine technology,
 CC small molecule/antibody technology, molecular biology, and various
 CC immunological techniques related to feline IGE and its functions. The
 CC present sequence represents feline IGE epsilon heavy chain #2
 XX
 XX
 SQ Sequence 496 AA;
 XX
 Query Match 59.3%; Score 48; DB 6; Length 496;
 Best Local Similarity 61.5%; Pred. No. 13;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 2 NDSPIOTDYYTTT 14
 |||||:|:|
 Db 428 NDSPVRTQQATT 440
 XX
 RESULT 12
 ABU09336
 ID ABU09336 standard; protein; 496 AA.
 XX
 AC ABU09336;
 XX
 XX 27-JUN-2003 (first entry)
 DT
 DE Feline IGE epsilon heavy chain #1.
 XX
 XX Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;
 KM IGE-mediated immune response; allergy; neoplasia; vaccine technology;
 KM antibody technology; anti-allergic; antiparasitic; cyostatic.
 XX
 OS Felis catus.
 XX
 FH Key
 FT Region
 FT Location/Qualifiers
 66..496
 /note="This sequence is given as SEQ ID No:14 and is
 specifically claimed in Claim 12"
 FT 284..309
 /note="This sequence is given as SEQ ID No:11 and is
 specifically claimed in Claim 9"
 FT 288..305
 /note="This sequence is given as SEQ ID No:8 and is
 specifically claimed in Claim 10"
 FT 291..302
 /note="This sequence is given as SEQ ID No:5 and is
 specifically claimed in Claim 11"
 FT
 XX
 PN US2003013183-A1.
 PD 16-JAN-2003.
 XX
 PF 07-JAN-2000; 2000US-00479614.
 XX
 PR 07-JAN-1999; 99US-0115033P.
 XX
 PA (MCCA/) MCCA.LL C.
 PA (WEBE/) WEBER E.
 XX
 PI Mccall C, Weber E;

DR WPI; 2003-39197/37.
DR N-PSDB; ABX95713.
PT New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or
PT light chain protein, useful for treating feline IGE-mediated responses
PT e.g. allergies, parasitic infections or neoplasia.
XX
XX Claim 1; Page 24-25; 45pp; English.
CC The present invention relates to the isolation of feline immunoglobulin E
CC (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the
CC polynucleotide sequences encoding them. The sequences of the invention
CC are useful for treating feline IGE-mediated immune responses (e.g.
CC allergies, parasitic infections or neoplasia), in vaccine technology,
CC small molecule/antibody technology, molecular biology, and various
CC immunological techniques related to feline IGE and its functions. The
CC present sequence represents feline IGE epsilon heavy chain #1
XX
SQ Sequence 496 AA;
Query Match 59.3%; Score 48; DB 6; Length 496;
Best Local Similarity 61.5%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 NDSPIQTDQYTTT 14
Db 428 NDSPIVTEQOATT 440
RESULT 13
ADG73251
ID ADG73251 standard; protein; 496 AA.
XX
XX ADG73251;
XX
XX 11-MAR-2004 (first entry)
XX
XX Cat partial immunoglobulin E (IGE) heavy chain #2.
XX
XX anti-allergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;
XX immune response; IGE-mediated response; allergy; cat; heavy chain.
XX
XX Felis catus.
XX
XX US2003216565-A1.
XX
XX 20-NOV-2003.
XX
XX 07-APR-2003; 2003US-00409772.
XX
XX 07-JAN-1999; 99US-0115033P.
XX 07-JAN-2000; 2000US-00479614.
XX
XX (MCCA/) MCCALL C.
XX (WEBE/) WEBER E.
XX
XX McCall C, Weber E;
XX
XX WPI; 2004-010802/01.
XX N-PSDB; ADG73250.
DR
XX
XX New isolated nucleic acid molecule encoding a portion of a feline IGE
XX heavy chain protein, useful for treating and/or eliciting feline immune
XX responses for IGE-mediated responses, such as allergies.
XX
XX Claim 8; SEQ ID NO 29; 44pp; English.
XX
XX
XX The invention describes an isolated nucleic acid molecule (I) encoding a
XX portion of a feline IGE heavy chain protein. The methods and compositions
XX of the present invention are useful for eliciting feline immune responses
XX for and/or treating IGE-mediated responses, such as allergies. This is
XX the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy
XX chain.

XX
SQ Sequence 496 AA;
Query Match 59.3%; Score 48; DB 8; Length 496;
Best Local Similarity 61.5%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 NDSPIQTDQYTTT 14
Db 428 NDSPIVTEQOATT 440
RESULT 14
ADG73225
ID ADG73225 standard; protein; 496 AA.
XX
XX ADG73225;
XX
XX 11-MAR-2004 (first entry)
XX
XX Cat partial immunoglobulin E (IGE) heavy chain #1.
XX
XX anti-allergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;
XX immune response; IGE-mediated response; allergy; cat; heavy chain.
XX
XX Felis catus.
XX
XX US2003216565-A1.
XX
XX 20-NOV-2003.
XX
XX 07-APR-2003; 2003US-00409772.
XX
XX 07-JAN-1999; 99US-0115033P.
XX 07-JAN-2000; 2000US-00479614.
XX
XX (MCCA/) MCCALL C.
XX (WEBE/) WEBER E.
XX
XX McCall C, Weber E;
XX
XX WPI; 2004-010802/01.
XX N-PSDB; ADG73224.
XX
XX New isolated nucleic acid molecule encoding a portion of a feline IGE
XX heavy chain protein, useful for treating and/or eliciting feline immune
XX responses for IGE-mediated responses, such as allergies.
XX
XX Claim 8; SEQ ID NO 2; 44pp; English.
XX
XX
XX The invention describes an isolated nucleic acid molecule (I) encoding a
XX portion of a feline IGE heavy chain protein. The methods and compositions
XX of the present invention are useful for eliciting feline immune responses
XX for and/or treating IGE-mediated responses, such as allergies. This is
XX the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy
XX chain.
XX
XX Sequence 496 AA;
Query Match 59.3%; Score 48; DB 8; Length 496;
Best Local Similarity 61.5%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 NDSPIQTDQYTTT 14
Db 428 NDSPIVTEQOATT 440
RESULT 15
ABU42513
ID ABU42513 standard; protein; 1633 AA.
XX
XX ABU42513;

XX 19-JUN-2003 (first entry)
XX Protein encoded by Prokaryotic essential gene #28040.
DE
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
KM
XX Staphylococcus epidermidis.
OS
XX W0200277183-A2.
PN
XX 03-OCT-2002.
PD
XX 21-MAR-2002; 2002WO-US009107.
PF
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR N-PSDB; ACA46383.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 70437; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1633 AA:
SQ

QY 2 NDSPIDTDQYTTT 14
|||
Db 242 NDEPTQDVEYTTT 254
|||

Search completed: December 12, 2005, 20:30:25
Job time : 84.3362 secs

Query March 53.1%; Score 43; DB 6; Length 1633;
Best Local Similarity 61.5%; Pred. No. 3.6e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:23:41 ; Search time 20.431 seconds

(without alignments)
60.699 Million cell updates/sec

Title: US-10-758-165a-1

Perfect score: 81

Sequence: 1 RNDSPICQDYTTTG 15

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*
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6: /cgn2_6/ptodata/1/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	108	US-09-281-760E-37	Sequence 37, Appl
2	81	100.0	312	US-09-701-623C-2	Sequence 2, Appl
3	81	100.0	426	US-08-336-583-2	Sequence 2, Appl
4	81	100.0	426	US-09-13795-2	Sequence 2, Appl
5	48	59.3	431	US-09-479-614-14	Sequence 14, Appl
6	48	59.3	496	US-09-479-614-2	Sequence 2, Appl
7	48	59.3	496	US-09-479-614-29	Sequence 29, Appl
8	41	50.6	533	US-09-134-001C-4053	Sequence 4053, Ap
9	40	49.4	163	US-09-270-767-43446	Sequence 43446, A
10	40	49.4	667	US-09-328-352-4294	Sequence 4294, Ap
11	40	49.4	1180	US-09-206-942-65	Sequence 65, Appl
12	40	49.4	1180	US-10-193-764-61	Sequence 61, Appl
13	40	49.4	1188	US-09-206-942-63	Sequence 63, Appl
14	40	49.4	1188	US-10-193-764-59	Sequence 59, Appl
15	40	49.4	2186	US-09-949-016-10828	Sequence 10828, A
16	40	49.4	2349	US-09-538-092-914	Sequence 914, App
17	38.5	47.5	625	US-08-532-547-7	Sequence 7, Appl
18	38.5	47.5	625	US-08-532-547-9	Sequence 9, Appl
19	38.5	47.5	625	US-09-019-809-7	Sequence 7, Appl
20	38.5	47.5	625	US-09-019-809-9	Sequence 9, Appl
21	38.5	47.5	625	US-09-471-177-7	Sequence 7, Appl
22	38.5	47.5	625	US-09-471-177-9	Sequence 9, Appl
23	38.5	47.5	1156	US-09-002-285-72	Sequence 72, Appl
24	38.5	47.5	1156	US-09-589-477-72	Sequence 72, Appl
25	38.5	47.5	1156	US-09-661-322A-28	Sequence 28, Appl
26	38.5	47.5	1156	US-10-099-285A-72	Sequence 72, Appl
27	38.5	47.5	1157	US-08-532-547-5	Sequence 5, Appl

28	38.5	47.5	1157	1	US-08-379-656B-5	Sequence 5, Appl
29	38.5	47.5	1157	2	US-08-455-838-5	Sequence 5, Appl
30	38.5	47.5	1157	2	US-09-019-809-5	Sequence 5, Appl
31	38.5	47.5	1157	2	US-09-471-177-5	Sequence 5, Appl
32	38.5	47.5	1157	2	US-09-220-806-5	Sequence 5, Appl
33	38	46.9	48	2	US-09-270-767-38395	Sequence 38395, A
34	38	46.9	48	2	US-09-270-767-53612	Sequence 53612, A
35	38	46.9	131	2	US-09-949-016-9319	Sequence 9319, Ap
36	38	46.9	334	2	US-09-248-796A-19132	Sequence 19132, A
37	38	46.9	485	2	US-09-489-039A-8129	Sequence 8129, Ap
38	38	46.9	503	2	US-09-248-796A-15409	Sequence 15409, A
39	38	46.9	769	2	US-10-191-436A-5	Sequence 5, Appl
40	38	46.9	1155	2	US-09-710-279-1780	Sequence 1780, Ap
41	38	46.9	1742	2	US-09-386-962C-4	Sequence 4, Appl
42	38	46.9	1742	2	US-09-386-959-4	Sequence 4, Appl
43	37	45.7	139	2	US-09-634-238-335	Sequence 335, App
44	37	45.7	386	2	US-09-248-796A-21802	Sequence 21802, A
45	37	45.7	420	2	US-09-844-006A-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-09-281-760E-37
; Sequence 37, Application US/09281760E
; Patent No. 6734287
;
GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Wermer, Brian
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (413)..(414)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (451)..(451)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (460)..(462)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (500)..(500)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (530)..(530)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (568)..(568)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (847)..(849)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (853)..(853)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1382)..(1382)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1832)..(1832)
; OTHER INFORMATION: "n" stands for any nucleic acid
US-09-281-760E-37

Query Match          100.0%; Score 81; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RNDSP1QTDQYTTTG 15
        |||||
Db      43 RNDSP1QTDQYTTTG 57

RESULT 2
US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Pn.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701.623C
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog Ige
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-09-701-623C-2

Query Match          100.0%; Score 81; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RNDSP1QTDQYTTTG 15
        |||||
Db      255 RNDSP1QTDQYTTTG 269

RESULT 3
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
```

```
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-336-583-2

Query Match          100.0%; Score 81; DB 1; Length 426;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RNDSP1QTDQYTTTG 15
        |||||
Db      357 RNDSP1QTDQYTTTG 371

RESULT 4
PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
```


TELEPAX: (908) 594-4720
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 426 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-13795-2

Query Match 100.0%; Score 81; DB 4; Length 426;
 Best Local Similarity 100.0%; Pred. No. 5.3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NDSPLOTDOYTTG 15
 Db 357 NDSPLOTDOYTTTG 371

RESULT 5
 US-09-479-614-14
 Sequence 14, Application US/09479614
 Patent No. 6573372
 GENERAL INFORMATION:
 APPLICANT: McCall, Catherine
 APPLICANT: Weber, Eric
 TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
 FILE REFERENCE: P-1047
 CURRENT APPLICATION NUMBER: US/09/479,614
 CURRENT FILING DATE: 2000-01-07
 EARLIER APPLICATION NUMBER: 60/115,033
 EARLIER FILING DATE: 1999-01-07
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 14
 LENGTH: 431
 TYPE: PRT
 ORGANISM: Felis catus
 US-09-479-614-14

Query Match 59.3%; Score 48; DB 2; Length 431;
 Best Local Similarity 61.5%; Pred. No. 2.8;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPLOTDOYTTT 14
 Db 363 NDSPRTEQOAT 375

RESULT 6
 US-09-479-614-2
 Sequence 2, Application US/09479614
 Patent No. 6573372
 GENERAL INFORMATION:
 APPLICANT: McCall, Catherine
 APPLICANT: Weber, Eric
 TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
 FILE REFERENCE: P-1047
 CURRENT APPLICATION NUMBER: US/09/479,614
 CURRENT FILING DATE: 2000-01-07
 EARLIER APPLICATION NUMBER: 60/115,033
 EARLIER FILING DATE: 1999-01-07
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 2
 LENGTH: 496
 TYPE: PRT
 ORGANISM: Felis catus
 US-09-479-614-2

Query Match 59.3%; Score 48; DB 2; Length 496;
 Best Local Similarity 61.5%; Pred. No. 3.3;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPLOTDOYTTT 14
 Db 428 NDSPRTEQOAT 440

RESULT 7
 US-09-479-614-29
 Sequence 29, Application US/09479614
 Patent No. 6573372
 GENERAL INFORMATION:
 APPLICANT: McCall, Catherine
 APPLICANT: Weber, Eric
 TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
 FILE REFERENCE: P-1047
 CURRENT APPLICATION NUMBER: US/09/479,614
 CURRENT FILING DATE: 2000-01-07
 EARLIER APPLICATION NUMBER: 60/115,033
 EARLIER FILING DATE: 1999-01-07
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 29
 LENGTH: 496
 TYPE: PRT
 ORGANISM: Felis catus
 US-09-479-614-29

Query Match 59.3%; Score 48; DB 2; Length 496;
 Best Local Similarity 61.5%; Pred. No. 3.3;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPLOTDOYTTT 14
 Db 428 NDSPRTEQOAT 440

RESULT 8
 US-09-134-001C-4053
 Sequence 4053, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 4053
 LENGTH: 533
 TYPE: PRT
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-4053

Query Match 50.6%; Score 41; DB 2; Length 533;
 Best Local Similarity 58.3%; Pred. No. 59;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPLOTDOYTTT 13
 Db 466 NDAPQSDQIYT 477

RESULT 9
 US-09-270-767-43446
 Sequence 43446, Application US/09270767
 Patent No. 6703491
 GENERAL INFORMATION:
 APPLICANT: Homburger et al.

;; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;; FILE REFERENCE: File Reference: 7326-094
;; CURRENT APPLICATION NUMBER: US/09/270,767
;; NUMBER OF SEQ ID NOS: 1999-03-17
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 43446
;; LENGTH: 163
;; TYPE: PRT
;; ORGANISM: Drosophila melanogaster
;; FEATURE:
;; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43446

Query Match 49.4%; Score 40; DB 2; Length 163;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RNDSPLOTDOYTTT 14
||:|:|:|:|:|
Db 85 RNNEPLIADNYIT 98

RESULT 10
US-09-328-352-4294
; Sequence 4294, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Bretton et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4294
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4294

Query Match 49.4%; Score 40; DB 2; Length 667;
Best Local Similarity 70.0%; Pred. No. 1,1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PIOTDOYTTT 14
||:|:|:|:|:|
Db 614 PLEADOTTT 623

RESULT 11
US-09-206-942-65
; Sequence 65, Application US/09206942
; Patent No. 6432669
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
; FILE REFERENCE: 1038-861 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/206,942
; CURRENT FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: 09/167,568
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 65
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-206-942-65

Query Match 49.4%; Score 40; DB 2; Length 1180;
Best Local Similarity 40.0%; Pred. No. 2,1e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNDSPLOTDOYTTG 15
||:|:|:|:|:|
Db 13 RSDTNLENEYTG 27

RESULT 12
US-10-193-764-61
; Sequence 61, Application US/10193764
; Patent No. 6849447
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
; FILE REFERENCE: 1038-1239MIS
; CURRENT APPLICATION NUMBER: US/10/193,764
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 09/167,568
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 61
; LENGTH: 1180
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-193-764-61

Query Match 49.4%; Score 40; DB 2; Length 1180;
Best Local Similarity 40.0%; Pred. No. 2,1e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNDSPLOTDOYTTG 15
||:|:|:|:|:|
Db 13 RSDTNLENEYTG 27

RESULT 13
US-09-206-942-63
; Sequence 63, Application US/09206942
; Patent No. 6432669
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
; FILE REFERENCE: 1038-861 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/206,942
; CURRENT FILING DATE: 1998-12-08
; EARLIER APPLICATION NUMBER: 09/167,568
; EARLIER FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 63
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-206-942-63

Query Match 49.4%; Score 40; DB 2; Length 1188;
Best Local Similarity 40.0%; Pred. No. 2,2e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNDSPLOTDOYTTG 15
||:|:|:|:|:|
Db 21 RSDTNLENEYTG 35

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RESULT 14
US-10-193-764-59
; Sequence 59, Application US/10193764
; Patent No. 6849447
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena M.
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: PROTECTIVE RECOMBINANT HAEMOPHILUS INFLUENZAE HIGH
; FILE REFERENCE: 1038-1239WIS
; CURRENT APPLICATION NUMBER: US/10/193,764
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 09/167,568
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 59
; LENGTH: 1188
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-193-764-59

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Query Match      49.4%; Score 40; DB 2; Length 1188;
Best Local Similarity 40.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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OY      1 RNDSPLOTDOYTTG 15
Db      21 RSDTNLENEYTG 35

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RESULT 15
US-09-949-016-10828
; Sequence 10828, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10828
; LENGTH: 2186
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10828

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Query Match      49.4%; Score 40; DB 2; Length 2186;
Best Local Similarity 70.0%; Pred. No. 4.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY      5 PLOTDOYTTT 14
Db      1759 PLOSDOYTTT 1768

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Search completed: December 12, 2005, 19:37:03
Job time : 21.431 secs

RIGHT PAGE BLANK (OPTO)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:33:42 ; Search time 66.9828 Seconds
(without alignments)
93.568 Million cell updates/sec

Title: US-10-758-165A-1
Perfect score: 81
Sequence: 1 RNDSPIDQDYTTTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10_PUBSCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	US-10-758-165-1	Sequence 1, Appl1
2	81	100.0	426	US-10-214-524-28	Sequence 28, Appl1
3	53	65.4	15	US-10-758-165-7	Sequence 7, Appl1
4	53	65.4	567	US-10-214-524-33	Sequence 33, Appl1
5	48	59.3	15	US-10-758-165-2	Sequence 2, Appl1
6	48	59.3	431	US-09-479-614-14	Sequence 14, Appl1
7	48	59.3	431	US-10-409-772-14	Sequence 14, Appl1
8	48	59.3	496	US-09-479-614-2	Sequence 2, Appl1
9	48	59.3	496	US-09-479-614-29	Sequence 29, Appl1
10	48	59.3	496	US-10-214-524-25	Sequence 25, Appl1
11	48	59.3	496	US-10-409-772-2	Sequence 2, Appl1
12	48	59.3	496	US-10-409-772-29	Sequence 29, Appl1
13	43	53.1	68	US-10-424-559-250413	Sequence 250413, A
14	43	53.1	1633	US-10-282-122A-70437	Sequence 70437, A
15	42	51.9	123	US-10-437-963-169489	Sequence 169489, A
16	42	51.9	161	US-10-425-115-238239	Sequence 238239, A
17	41	50.6	15	US-10-758-165-3	Sequence 3, Appl1
18	41	50.6	68	US-10-424-559-211575	Sequence 211575, A
19	41	50.6	191	US-10-767-701-39191	Sequence 39191, A
20	41	50.6	424	US-10-451-078-2	Sequence 2, Appl1
21	41	50.6	424	US-10-451-078-4	Sequence 4, Appl1
22	41	50.6	514	US-10-424-559-177658	Sequence 177658, A
23	41	50.6	533	US-10-724-972A-5049	Sequence 5049, A
24	40	49.4	569	US-10-214-524-30	Sequence 30, Appl1
25	40	49.4	356	US-11-097-143-19689	Sequence 19689, A
26	40	49.4	374	US-10-732-923-17586	Sequence 17586, A
27	40	49.4	374	US-10-732-923-17624	Sequence 17624, A

28	40	49.4	433	4	US-10-425-115-355337	Sequence 355337, A
29	40	49.4	488	4	US-10-425-114-65347	Sequence 65347, A
30	40	49.4	539	4	US-10-437-963-135296	Sequence 135296, A
31	40	49.4	555	4	US-10-355-956-4	Sequence 4, Appl1
32	40	49.4	555	5	US-10-504-048-4	Sequence 4, Appl1
33	40	49.4	596	4	US-10-767-701-44580	Sequence 44580, A
34	40	49.4	1180	4	US-10-193-764-61	Sequence 61, Appl1
35	40	49.4	1188	4	US-10-193-764-59	Sequence 59, Appl1
36	40	49.4	2400	5	US-10-450-763-50637	Sequence 50637, A
37	40	49.4	2415	5	US-10-450-763-50638	Sequence 50638, A
38	39	48.1	51	4	US-10-425-115-26056	Sequence 26056, A
39	39	48.1	170	4	US-10-424-559-148645	Sequence 148645, A
40	39	48.1	281	4	US-10-369-430A-26	Sequence 26, Appl1
41	39	48.1	446	5	US-10-450-763-56495	Sequence 56495, A
42	39	48.1	523	4	US-10-437-963-117513	Sequence 117513, A
43	39	48.1	584	4	US-10-437-963-145953	Sequence 145953, A
44	39	48.1	598	4	US-10-424-559-241468	Sequence 241468, A
45	39	48.1	1589	4	US-10-425-115-303919	Sequence 303919, A

ALIGNMENTS

RESULT 1
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196616A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758.165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1

Query Match 100.0%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNDSPIDQDYTTTG 15
|||||
Db 1 RNDSPIDQDYTTTG 15

RESULT 2
US-10-214-524-28
; Sequence 28, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGB-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214.524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Dog (Canis familiaris)

US-10-214-524-28

Query Match 100.0%; Score 81; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNDSP1QTDQYTTT 15
|||||:|:|:|:|:|:|
DB 357 RNDSP1QTDQYTTT 371

RESULT 3

US-10-758-165-7
; Sequence 7, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammetberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-7

Query Match 65.4%; Score 53; DB 5; Length 15;
Best Local Similarity 57.1%; Pred. No. 0.035;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNDSP1QTDQYTTT 14
|||:|:|:|:|:|
DB 1 RNDAPVQADRHSTT 14

RESULT 4

US-10-214-524-33
; Sequence 33, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Swei-Shen Alex
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Pig (Sus scrofa)
US-10-214-524-33

Query Match 65.4%; Score 53; DB 4; Length 567;
Best Local Similarity 57.1%; Pred. No. 1.9;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNDSP1QTDQYTTT 14
|||:|:|:|:|:|
DB 499 RNDAPVQADRHSTT 512

RESULT 5

US-10-758-165-2

; Sequence 2, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammetberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-2

Query Match 59.3%; Score 48; DB 5; Length 15;
Best Local Similarity 61.5%; Pred. No. 0.26;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14
|||:|:|:|:|:|
DB 2 NDSPVRTQOATT 14

RESULT 6

US-09-479-614-14
; Sequence 14, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match 59.3%; Score 48; DB 3; Length 431;
Best Local Similarity 61.5%; Pred. No. 10;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14
|||:|:|:|:|:|
DB 363 NDSPVRTQOATT 375

RESULT 7

US-10-409-772-14
; Sequence 14, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 14
LENGTH: 431
TYPE: PRT
ORGANISM: Felis catus
US-10-409-772-14

Query Match 59.3% Score 48; DB 4; Length 431;
Best Local Similarity 61.5% Pred. No. 10;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14
Db 363 NDSPVRTQOATT 375

RESULT 8
US-09-479-614-2
Sequence 2, Application US/09479614
Publication No. US20030013183A1
GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 496
TYPE: PRT
ORGANISM: Felis catus
US-09-479-614-2

Query Match 59.3% Score 48; DB 3; Length 496;
Best Local Similarity 61.5% Pred. No. 12;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14
Db 428 NDSPVRTQOATT 440

RESULT 9
US-09-479-614-29
Sequence 29, Application US/09479614
Publication No. US20030013183A1
GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 29
LENGTH: 496
TYPE: PRT
ORGANISM: Felis catus
US-09-479-614-29

Query Match 59.3% Score 48; DB 3; Length 496;
Best Local Similarity 61.5% Pred. No. 12;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14
Db 428 NDSPVRTQOATT 440

RESULT 10
US-10-214-524-25
Sequence 25, Application US/10214524
Publication No. US20030073142A1
GENERAL INFORMATION:
APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Yang, Yong-Min
APPLICANT: Barankiewicz, Theresa J.
APPLICANT: Chen, Zhong
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
FILE REFERENCE: IGE-00101.P.1.1
CURRENT APPLICATION NUMBER: US/10/214,524
CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: 60/312,120
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patent In version 3.1
SEQ ID NO 25
LENGTH: 496
TYPE: PRT
ORGANISM: Cat (Felis catus)
US-10-214-524-25

Query Match 59.3% Score 48; DB 4; Length 496;
Best Local Similarity 61.5% Pred. No. 12;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14
Db 428 NDSPVRTQOATT 440

RESULT 11
US-10-409-772-2
Sequence 2, Application US/10409772
Publication No. US20030216565A1
GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/10/409,772
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US/09/479,614
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 496
TYPE: PRT
ORGANISM: Felis catus
US-10-409-772-2

Query Match 59.3% Score 48; DB 4; Length 496;
Best Local Similarity 61.5% Pred. No. 12;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14
Db 428 NDSPVRTQOATT 440

RESULT 12
US-10-409-772-29
Sequence 29, Application US/10409772
Publication No. US20030216565A1
GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047

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; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-29

Query Match      59.3%, Score 48; DB 4; Length 496;
Best Local Similarity 61.5%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 NDSPIQTDQYTTT 14
DB      428 NDSPVTEQOATT 440

RESULT 13
US-10-424-599-250413
; Sequence 250413, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 250413
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(68)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_68150C.1.pep
US-10-424-599-250413

Query Match      53.1%, Score 43; DB 4; Length 68;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      4 SPIQTDQYTTTG 15
DB      21 TPRTDQYTTTG 32

RESULT 14
US-10-282-122A-70437
; Sequence 70437, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
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; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 70437
; LENGTH: 1633
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-70437

Query Match      53.1%, Score 43; DB 4; Length 1633;
Best Local Similarity 61.5%; Pred. No. 3.3e+02;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 NDSPIQTDQYTTT 14
DB      242 NDEPTQDVEYTTT 254

RESULT 15
US-10-437-963-169489
; Sequence 169489, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 169489
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67905C.1.pep
US-10-437-963-169489

Query Match      51.9%, Score 42; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	27	RNDSPIC	34

Search completed: December 12, 2005, 20:19:23
Job time : 67.9828 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:34:33 ; Search time 2.4569 seconds
(without alignments)
34.094 Million cell updates/sec

Title: US-10-758-165A-1
Perfect score: 81
Sequence: 1 RNDSPICQDQYTTTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA New:*
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3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCCT_NEW_PUB pep:*
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7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	312	6	US-10-723-207-2
2	38	46.9	1155	6	US-10-793-626-1780
3	36	44.4	543	6	US-10-689-742-78
4	35	43.2	128	6	US-10-467-657-5476
5	35	43.2	185	7	US-11-098-662-136
6	34	42.0	310	6	US-10-131-826A-538
7	34	42.0	310	7	US-11-025-834A-13
8	34	42.0	310	7	US-11-025-834A-15
9	34	42.0	354	6	US-10-467-657-5634
10	34	42.0	362	6	US-10-821-234-1148
11	34	42.0	428	6	US-10-821-234-997
12	34	42.0	790	6	US-10-763-712A-75
13	34	42.0	840	7	US-11-108-172-1102
14	33	40.7	180	7	US-11-098-662-114
15	33	40.7	181	7	US-11-098-662-32
16	33	40.7	181	7	US-11-098-662-42
17	33	40.7	181	7	US-11-098-662-46
18	33	40.7	181	7	US-11-098-662-50
19	33	40.7	181	7	US-11-098-662-70
20	33	40.7	181	7	US-11-098-662-74
21	33	40.7	181	7	US-11-098-662-78
22	33	40.7	181	7	US-11-098-662-82
23	33	40.7	181	7	US-11-098-662-110
24	33	40.7	182	7	US-11-098-662-34
25	33	40.7	182	7	US-11-098-662-38

26	33	40.7	182	7	US-11-098-662-44	Sequence 44, Appl
27	33	40.7	182	7	US-11-098-662-48	Sequence 48, Appl
28	33	40.7	182	7	US-11-098-662-52	Sequence 52, Appl
29	33	40.7	182	7	US-11-098-662-72	Sequence 72, Appl
30	33	40.7	182	7	US-11-098-662-76	Sequence 76, Appl
31	33	40.7	182	7	US-11-098-662-80	Sequence 80, Appl
32	33	40.7	182	7	US-11-098-662-84	Sequence 84, Appl
33	33	40.7	182	7	US-11-098-662-112	Sequence 112, Appl
34	33	40.7	182	7	US-11-098-662-128	Sequence 128, Appl
35	33	40.7	182	7	US-11-098-662-132	Sequence 132, Appl
36	33	40.7	183	7	US-11-098-662-136	Sequence 136, Appl
37	33	40.7	183	7	US-11-098-662-130	Sequence 130, Appl
38	33	40.7	200	7	US-11-098-662-4	Sequence 4, Appl
39	33	40.7	200	7	US-11-098-662-20	Sequence 20, Appl
40	33	40.7	310	6	US-10-793-626-120	Sequence 120, Appl
41	33	40.7	310	6	US-10-793-626-1270	Sequence 1270, Appl
42	33	40.7	322	7	US-11-055-822-66	Sequence 66, Appl
43	33	40.7	505	6	US-10-467-657-6228	Sequence 6228, Appl
44	33	40.7	735	7	US-11-184-380-24	Sequence 24, Appl
45	33	40.7	737	7	US-11-128-420-9	Sequence 9, Appl

ALIGNMENTS

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RESULT 1
US-10-723-207-2
; Sequence 2, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 1151-4153US2
; CURRENT FILING DATE: 2003-11-24
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IGE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2

Query Match      100.0%; Score 81; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. NO. 4.1e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RNDSPICQDQYTTTG 15
Db      255 RNDSPICQDQYTTTG 269

RESULT 2
US-10-793-626-1780
; Sequence 1780, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
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; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793.626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1780
; LENGTH: 1155
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1780

Query Match          46.9%; Score 38; DB 6; Length 1155;
Best Local Similarity 53.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2  RNDSPIQDQYTTT 14
Db      242  NDEPTQDVEHTTT 254

RESULT 3
US-10-689-742-78
; Sequence 78, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: lavalie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-78

Query Match          44.4%; Score 36; DB 6; Length 543;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy      1  RNDSPIQDQYTTTG 15
Db      69  RNPTLVDDQYENHG 83

RESULT 4
US-10-467-657-5476
; Sequence 5476, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
```

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; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5476
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5476

Query Match          43.2%; Score 35; DB 6; Length 128;
Best Local Similarity 35.7%; Pred. No. 4.9;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy      1  RNDSPIQDQYTTT 14
Db      24  RNSATVMADKYTS 37

RESULT 5
US-11-098-662-136
; Sequence 136, Application US/11098662
; Publication No. US2005024423A1
; GENERAL INFORMATION:
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Sivakumar, Pallavur V.
; APPLICANT: Henderson, Katherine E.
; TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION
; TITLE OF INVENTION: USING IL-28 AND IL-29 CYSTEINE MUTANTS
; FILE REFERENCE: 04-05
; CURRENT APPLICATION NUMBER: US/11/098,662
; CURRENT FILING DATE: 2005-04-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-29 Glu, Ala, and Glu inserted after N-terminal
; OTHER INFORMATION: Met, C175X
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (175)...(175)
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn
US-11-098-662-136

Query Match          43.2%; Score 35; DB 7; Length 185;
Best Local Similarity 46.2%; Pred. No. 7.4;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      3  DSPIQDQYTTTG 15
Db      4  BGPVPTSKPTTGG 16

RESULT 6
US-10-131-826A-538
; Sequence 538, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
```

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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 538
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-538

Query Match          42.0%; Score 34; DB 6; Length 310;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RNDSP1QTD 9
Db      175 RNDVPLPTD 183

RESULT 7
US-11-025-834A-13
; Sequence 13, Application US/11025834A
; Publication No. US20050266426A1
; GENERAL INFORMATION:
; APPLICANT: IMHOFF, BEAT ALBERT
; APPLICANT: AURRAND-LIONS, MICHEL
; TITLE OF INVENTION: CONFLUENCE REGULATED ADHESION MOLECULES USEFUL IN MODULATING VASC
; FILE REFERENCE: 011422-0314432
; CURRENT APPLICATION NUMBER: US/11/025,834A
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 09/524,531
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: EP 99,200746.8
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 310
; TYPE: PRT
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; ORGANISM: Mus musculus
US-11-025-834A-13

Query Match          42.0%; Score 34; DB 7; Length 310;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RNDSP1QTD 9
Db      175 RNDVPLPTD 183

RESULT 8
US-11-025-834A-15
; Sequence 15, Application US/11025834A
; Publication No. US20050266426A1
; GENERAL INFORMATION:
; APPLICANT: IMHOFF, BEAT ALBERT
; APPLICANT: AURRAND-LIONS, MICHEL
; TITLE OF INVENTION: CONFLUENCE REGULATED ADHESION MOLECULES USEFUL IN MODULATING VASC
; FILE REFERENCE: 011422-0314432
; CURRENT APPLICATION NUMBER: US/11/025,834A
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 09/524,531
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: EP 99,200746.8
; PRIOR FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-025-834A-15

Query Match          42.0%; Score 34; DB 7; Length 310;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 RNDSP1QTD 9
Db      175 RNDVPLPTD 183

RESULT 9
US-10-467-657-5634
; Sequence 5634, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 5634
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5634

Query Match          42.0%; Score 34; DB 6; Length 354;
Best Local Similarity 45.5%; Pred. No. 23;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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OY      2  NDSPIQTDQYTT 12
Db      178 SDQPIGESEYTT 188

RESULT 10
US-10-821-234-1148
; Sequence 1148, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Scache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1148
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1148

Query Match      42.0%; Score 34; DB 6; Length 362;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      1  RNDSPIQTD 9
Db      227 RNDVPLPTD 235

RESULT 11
US-10-821-234-997
; Sequence 997, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Scache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 997
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-997

Query Match      42.0%; Score 34; DB 6; Length 428;
Best Local Similarity 46.2%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 790
; TYPE: PRT
; ORGANISM: Geobacter metallireducens
US-10-763-712A-75

Query Match      42.0%; Score 34; DB 6; Length 790;
Best Local Similarity 53.8%; Pred. No. 57;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY      1  RNDSPIQTDQYTT 13
Db      517 RNDKPLVTNCTT 529

RESULT 13
US-11-108-172-1102
; Sequence 1102, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Scolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skelky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
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; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1102
; LENGTH: 840
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-662-1102

Query Match          42.0%; Score 34; DB 7; Length 840;
Best Local Similarity 55.6%; Pred. No. 61;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 NDSPIQTDQ 10
        |::|||
Db       506 NEEPMETDQ 514

RESULT 14
US-11-098-662-114
; Sequence 114, Application US/11098662
; Publication No. US20050244423A1
; GENERAL INFORMATION:
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Sivakumar, Pallavar V.
; APPLICANT: Henderson, Katherine E.
; TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION
; FILE REFERENCE: 04-05
; CURRENT APPLICATION NUMBER: US/11/098,662
; CURRENT FILING DATE: 2005-04-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-29 C170X, truncated after N-terminal Methionine
; OTHER INFORMATION: and Glycine
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (170)...(170)
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn
US-11-098-662-114

Query Match          40.7%; Score 33; DB 7; Length 180;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      5 PIQTDQYTTTG 15
        |::|||
Db       1 PVPISKPTTIG 11

RESULT 15
US-11-098-662-32
; Sequence 32, Application US/11098662
; Publication No. US20050244423A1
; GENERAL INFORMATION:
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Sivakumar, Pallavar V.
; APPLICANT: Henderson, Katherine E.
; TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION
; FILE REFERENCE: 04-05
; CURRENT APPLICATION NUMBER: US/11/098,662
```

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; CURRENT FILING DATE: 2005-04-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-29 mutant C171S
US-11-098-662-32

Query Match          40.7%; Score 33; DB 7; Length 181;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      5 PIQTDQYTTTG 15
        |::|||
Db       2 PVPISKPTTIG 12
```

Search completed: December 12, 2005, 20:19:48
Job time : 3.4569 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:49 ; Search time 12.6724 Seconds
(without alignments)
113.889 Million cell updates/sec

Title: US-10-758-165A-1

Perfect score: 81

Sequence: 1 RNDSPQTDQYTTTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	53.1	664	T20420	hypothetical prote
2	42	51.9	1008	T32986	hypothetical prote
3	42	51.9	1067	D96545	probable DNA polym
4	41	50.6	1117	S63399	probable membrane
5	40	49.4	234	T49737	hypothetical prote
6	40	49.4	1157	F97255	fusion of alpha-gl
7	40	49.4	2094	S3124	tptr protein - huma
8	39	48.1	187	UC4806	core protein G - p
9	39	48.1	187	S22331	gene G protein - p
10	39	48.1	294	T08408	transcription fact
11	39	48.1	514	S72443	DNA-binding protei
12	39	48.1	564	HMTVDA	hemagglutinin prec
13	39	48.1	587	F85084	probable athla-11
14	39	48.1	940	T01834	hypothetical prote
15	39	48.1	2161	A45389	genome polypeptid
16	39	48.1	138344	I38344	ctin, cardiac mus
17	38.5	47.5	1157	S49247	paraspinal crystal
18	38	46.9	173	S5150	hypothetical prote
19	38	46.9	201	T31492	hypothetical prote
20	38	46.9	205	T31489	hypothetical prote
21	38	46.9	254	F81265	cyto protein homol
22	38	46.9	281	AD2052	hypothetical prote
23	38	46.9	321	B32801	fibrial adhesin p
24	38	46.9	335	JF0115	zinc-finger protei
25	38	46.9	429	B84410	GTP-binding protei
26	38	46.9	450	A10345	probable heat shoc
27	38	46.9	468	T08139	shaggy-like protei
28	38	46.9	612	C90374	hypothetical prote
29	38	46.9	996	S76194	hypothetical prote

30	38	46.9	1158	2	AF1852	hypothetical prote
31	38	46.9	1450	2	A44027	165K myofibrillar
32	38	46.9	1465	2	S43529	165K protein, skel
33	38	46.9	1562	2	T07323	DNA-directed RNA p
34	38	46.9	1969	2	T38495	hypothetical prote
35	37.5	46.3	272	2	B69688	glutamate racemase
36	37.5	46.3	590	2	S63193	hypothetical prote
37	37	45.7	136	2	F84234	hypothetical prote
38	37	45.7	219	2	B71841	hypothetical prote
39	37	45.7	245	2	T33844	hypothetical prote
40	37	45.7	268	2	A71966	hypothetical prote
41	37	45.7	298	2	A70238	hypothetical prote
42	37	45.7	429	2	T06296	extensin-like prot
43	37	45.7	502	2	E71963	probable cardioli
44	37	45.7	521	2	A48650	agrocinope utili
45	37	45.7	521	2	A13244	hypothetical prote

ALIGNMENTS

RESULT 1
T20420
hypothetical protein E02H4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20420
R:Barlow, K.
submitted to the EMBL Data Library, November 1995
A:Reference number: Z19273
A:Accession: T20420
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-664 <WILL>
A:Cross-references: UNIPROT:Q19038; UNIPARC:UPI0000129186; EMBL:Z68003; PIDN:CAA91975.1;
C:Genetics:
A:Gene: CESP:E02H4.1
A:Map position: X
A:Intons: 57/3; 102/3; 135/3; 166/1; 191/1; 221/2; 254/3; 314/2; 355/2; 386/1; 472/3; 5
C:Superfamily: human amloride-sensitive sodium channel protein; fibronectin type I repe

Query Match
Best Local Similarity 80.0%; Score 43; DB 2; Length 664;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PQTDDQYTTT 14
| | | | |
| | | | |
Db 536 PQQDDQYTTT 545

RESULT 2
T32986
hypothetical protein C05D2.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32986
R:Du, Z.
submitted to the EMBL Data Library, February 1998
A:Description: The sequence of C. elegans cosmid C05D2.
A:Reference number: Z31260
A:Accession: T32986
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1008 <DUZ>
A:Cross-references: UNIPARC:UPI0000178734; EMBL:AF047651; PIDN:AA02723.1; GSPDB:GN00021
A:Experimental source: strain Bristol N2; clone C05D2
C:Genetics:
A:Gene: CESP:C05D2.6
A:Map position: 3
A:Intons: 23/1; 53/3; 141/1; 231/3; 307/3; 325/2; 420/1; 466/3; 499/3; 522/2; 594/1; 75

Query Match 51.9%; Score 42; DB 2; Length 1008;

Best Local Similarity 58.3%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPQTQDYTT 12
| | | | |
| | | | |
Db 41 REDPVTQYTT 52

RESULT 3

Probable DNA polymerase A family protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: D96545

R:Theologias, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hultzar, L.

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzalli,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D96545

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1067 <STO>

A:Cross-references: UNIPROT:Q9C6J5; UNIPARC:UPI0000048370; GB:AE005173; NID:g11094700; F

C:Genetics:

A:Gene: P8A12.8

A:Map position: 1

Query Match 51.9%; Score 42; DB 2; Length 1067;

Best Local Similarity 42.9%; Pred. No. 41;

Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTQDYTTG 15
| | | | |
| | | | |
Db 625 SDSPLSTENFTTASG 638

RESULT 4
S63399
probable membrane protein YNR067C - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein N3547

C:Species: Saccharomyces cerevisiae

C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004

C:Accession: S63399

R:Ducrestioeft, A.; Floeth, M.; Filtz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S62944

A:Accession: S63399

A:Molecule type: DNA

A:Residues: 1-1117 <DUE>

A:Cross-references: UNIPROT:P53753; UNIPARC:UPI000013BACB; EMBL:Z71682; NID:g1302597; P1

A:Experimental source: strain S288C

C:Genetics:

A:Gene: MIPS:YNR067C

A:Cross-references: SGD:S0005350

A:Map position: 14R

C:Keywords: transmembrane protein

F:6-22/Domain: transmembrane #status predicted <TMM>

Query Match 50.6%; Score 41; DB 2; Length 1117;

Best Local Similarity 58.3%; Pred. No. 65;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 5

T49737

hypothetical protein B24B19.90 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C:Accession: T49737

R:Schulte, U.; Aign, V.; Heisele, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25022

A:Accession: T49737

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-234 <SCH>

A:Cross-references: UNIPARC:UPI0000179DBA; EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.90

A:Experimental source: BAC clone B24B19; strain OR74A

C:Genetics:

A:Gene: NCSP:B24B19.90

A:Map position: 6

A:Insertions: 132/2

C:Superfamily: Neurospora crassa hypothetical protein B24B19.90

Query Match 49.4%; Score 40; DB 2; Length 234;

Best Local Similarity 70.0%; Pred. No. 17;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PIQTQDYTT 14
| | | | |
| | | | |
Db 65 PVPTQYTTT 74

RESULT 6
P97255
fusion of alpha-glucosidase (family 31 glycosyl hydrolase) and glycosidase (Trea/Mals fan

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C:Accession: P97255

R:Noiling, J.; Breton, G.; Omelchenko, M.V.; Markova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clof

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: P97255

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1157 <KUR>

A:Cross-references: UNIPROT:Q97F62; UNIPARC:UPI00000D755C; GB:AE001437; PIDN:AAK80833.1;

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC2891

Query Match 49.4%; Score 40; DB 2; Length 1157;

Best Local Similarity 58.3%; Pred. No. 1e+02;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTQDYTT 13
| | | | |
| | | | |
Db 889 NESDVFTQYTT 900

RESULT 7
S33124
tpr protein - human

N:Alternate names: kinase-related transforming protein (tpr-met); protein with promoter 1

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004

C:Accession: S33124; S23740; S00928; G01185

R:Michell, P.J.; Cooper, C.S.

Oncogene 7, 2329-2333, 1992

A:Title: The human tpr gene encodes a protein of 2094 amino acids that has extensive coil

A:Reference number: S33124; MUID:93064711; PMID:1437155

A:Accession: S33124

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA
A:Residues: 1-2094 <MIT>
A:Cross-references: UNIPROT:O15624; UNIPROT:O9UE33; UNIPARC:UPI000017CBF3; EMBL:X66397;
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
R:Mitcheil, P.J.; Cooper, C.S.
Oncogene 7, 383-388, 1992
A:Title: Nucleotide sequence analysis of human tpr cDNA clones.
A:Reference number: S23740; MUID:92195670; PMID:1549355
A:Accession: S23740
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-725, 'L' <MI2>
A:Cross-references: UNIPARC:UPI000062253; EMBL:X63105; NID:g37257; PIDN:CAA44819.1; PID
R:King, H.W.S.; Tempest, P.R.; Merrifield, K.R.; Rance, A.J.
Oncogene 2, 617-619, 1988
A:Title: Tpr homologues activate met and raf.
A:Reference number: S00928; MUID:88262257; PMID:3387099
A:Accession: S00928
A:Molecule type: mRNA
A:Residues: 1-31, 'R', '33-142 <KIN>
A:Cross-references: UNIPARC:UPI000016B112; EMBL:X06672; NID:g37255; PIDN:CAA68681.1; PID
R:Greco, A.
submitted to the EMBL Data Library, December 1995
A:Reference number: H00592
A:Accession: G01185
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 144-228 <GRE>
A:Cross-references: UNIPARC:UPI00000711D7; EMBL:X94208; NID:g1296797; PIDN:CAA63904.1; F
C:Genetics:
A:Gene: GDB:TPR
A:Cross-references: GDB:128821; OMIM:189940
A:Map position: 1q25-1q25
A:introns: 177/3

Query Match 49.4%; Score 40; DB 2; Length 2094;
Best Local Similarity 70.0%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLOTDQYTTT 14
DB 1922 PLOSDQYTTT 1931

RESULT 8
core protein G - phage phi-K
C:Species: phage phi-K
C:Date: 15-Aug-1996 #sequence revision 15-Oct-1996 #text_change 09-Jul-2004
C:Accession: JC4806; B04253; A04253
R:Kodaira, K.; Oki, M.; Kakikawa, M.; Kimoto, H.; Takeko, A.
J. Biochem. 119, 1062-1069, 1996
A:Title: The virion proteins encoded by bacteriophage phi-K and its host-range mutant ph
A:Reference number: JC4804; MUID:96424987; PMID:8827438
A:Accession: JC4806
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-187 <KOD>
A:Cross-references: UNIPROT:Q38042; UNIPARC:UPI0000138658; EMBL:X60333; NID:g1478118; PI
R:Sims, J.; Capon, D.; Dressler, D.
J. Biol. Chem. 254, 12615-12628, 1979
A:Title: dnag (primase)-dependent origins of DNA replication. Nucleotide sequences of th
A:Reference number: A92247; MUID:80049950; PMID:387790
A:Accession: B04253
A:Molecule type: DNA
A:Residues: 165-187 <SIM>
A:Cross-references: UNIPARC:UPI000009C0FB
C:Comment: This protein is one of the structural components of the bacteriophage capsid.
C:Genetics:
A:Gene: G
C:Superfamily: phage phi-X174 gene G protein
C:Keywords: capsid protein

Query Match 48.1%; Score 39; DB 2; Length 187;
Best Local Similarity 40.0%; Pred. No. 19;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPLOTDQYTTTG 15
DB 8 KHDTRLOTRSPSVTG 22

RESULT 9
gene G protein - phage alpha-3
C:Species: phage alpha-3
C:Date: 10-Mar-1994 #sequence revision 10-Mar-1994 #text_change 09-Jul-2004
C:Accession: S22331; A04253
R:Kodaira, K.I.; Nakano, K.; Okada, S.; Takeko, A.
Biochim. Biophys. Acta 1130, 277-288, 1992
A:Title: Nucleotide sequence of the genome of the bacteriophage alpha3: interrelationship
A:Reference number: S22324; MUID:92223109; PMID:1532908
A:Accession: S22331
A:Molecule type: DNA
A:Residues: 1-187 <KOD>
A:Cross-references: UNIPROT:P31281; UNIPARC:UPI0000113352; EMBL:X60322; NID:g14775; PIDN
R:Sims, J.; Capon, D.; Dressler, D.
J. Biol. Chem. 254, 12615-12628, 1979
A:Title: dnag (primase)-dependent origins of DNA replication. Nucleotide sequences of th
A:Reference number: A92247; MUID:80049950; PMID:387790
A:Accession: C04253
A:Molecule type: DNA
A:Residues: 165-187 <SIM>
A:Cross-references: UNIPARC:UPI000000389; GB:J02444; GB:M10725; NID:g16103; PIDN:AAA32
C:Comment: This protein is one of the structural components of the bacteriophage capsid.
C:Genetics:
A:Gene: G
C:Superfamily: phage phi-X174 gene G protein
C:Keywords: capsid protein

Query Match 48.1%; Score 39; DB 2; Length 187;
Best Local Similarity 40.0%; Pred. No. 19;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPLOTDQYTTTG 15
DB 8 KHDTRLOTRSPSVTG 22

RESULT 10
transcription factor homolog F18B3.150 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08408
R:Queller, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salancub
submitted to the Protein Sequence Database, May 1999
A:Reference number: T08409
A:Accession: T08408
A:Molecule type: DNA
A:Residues: 1-294 <QUR>
A:Cross-references: UNIPROT:Q9SVL2; UNIPARC:UPI00000A322F; EMBL:AL049862; GSPDB:GND0061;
A:Experimental source: cultivar Columbia; BAC clone F18B3
C:Genetics:
A:Gene: ATSP:F18B3.150
A:Map position: 3
A:introns: 172/3

Query Match 48.1%; Score 39; DB 2; Length 294;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 SPLOTDQY 11
DB 201 APVOTDQY 208

RESULT 11

S72443

DNA-binding protein WRKY1 - parsley

C/Species: Petroselinum crispum (parsley)

C/Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 31-Dec-2004

C/Accession: S72443

R/Rushon, P.J.; Tovar Torres, J.; Parniske, M.; Wernert, P.; Hahlbrock, K.; Somesich, I.

EMBO J. 15, 5690-5700, 1996

A/Title: Interaction of elicitor-induced DNA-binding proteins with elicitor response ele

A/Reference number: S72443; MUID:97051827; PMID:8896462

A/Accession: S72443

A/Molecule type: mRNA

A/Residues: 1-514 <RUS>

A/Cross-references: UNIPROT:Q40827; UNIPARC:UPI00000A1FF5; EMBL:U48831; NID:G1431871; P

C/Superfamily: DNA-binding protein WRKY1

C/Keywords: DNA binding

Query Match 48.1%; Score 39; DB 2; Length 514;
 Best Local Similarity 70.0%; Pred. No. 61;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 DSPIQDQYTT 12
 Db 53 DSPIQNNNT 62

RESULT 12

HMIYDA

hemagglutinin precursor - influenza A virus

N/Contains: hemagglutinin HA1; hemagglutinin HA2

C/Species: Influenza A virus

C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 16-Jun-2000

C/Accession: B39987; A04057; F3157

R/Nobusawa, E.; Aoyama, T.; Kato, H.; Suzuki, Y.; Tateo, Y.; Nakajima, K.

Virology 182, 475-485, 1991

A/Title: Comparison of complete amino acid sequences and receptor-binding properties amc

A/Reference number: A39987; MUID:91220697; PMID:2024485

A/Accession: B39987

A/Molecule type: genomic RNA

A/Residues: 1-564 <NOB>

A/Cross-references: UNIPARC:UPI000012C4DB; GB:D90307; NID:G221309; PIDN:BAH1437.1; PID:

A/Experimental source: strain A/duck/Alberta/60/76 [H1N5]

R/Air, G.M.

Proc. Natl. Acad. Sci. U.S.A. 78, 7639-7643, 1981

A/Title: Sequence relationships among the hemagglutinin genes of 12 subtypes of influen

A/Reference number: A93902; MUID:82150925; PMID:6174976

A/Accession: A04057

A/Molecule type: genomic RNA

A/Residues: 1-38, 'L', '40-51', 'G', '53-101 <AIR>

A/Cross-references: UNIPARC:UPI0000170F31; GB:J02104; NID:G324135; PIDN:AAA43180.1; PID:

A/Experimental source: strain A/duck/Alberta/60/76 [H12]

A/Note: the signal sequence and the amino end of the HA1 chain comprise residues 1-17 an

C/Genetics:

A/Map position: segment 4

C/Superfamily: Influenza virus hemagglutinin

C/Keywords: glycoprotein; hemagglutinin; homotrimer; transmembrane protein

F/1-17/Domain: signal sequence #status predicted <SIG>

F/18-342/Product: hemagglutinin HA2 #status predicted <HA1>

F/343-564/Product: hemagglutinin HA2 #status predicted <HA2>

F/535-551/Domain: transmembrane #status predicted <TM1>

F/27,28,140,151,152,222,302,309,496,523/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 48.1%; Score 39; DB 1; Length 564;
 Best Local Similarity 60.0%; Pred. No. 68;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PIQTDQYTTT 14
 Db 174 PVQTDYKNT 183

, RESULT 13

F85084
 Probable athlia-like protein [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C/Accession: F85084

R/Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A/Reference number: A85001; MUID:20083488; PMID:10617198

A/Accession: F85084

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-587 <STO>

A/Cross-references: UNIPROT:Q9W072; UNIPARC:UPI000009E989; GB:NC_001266; NID:G7267490; PJ

C/Genetics:

A/Gene: AT4g08490

A/Map position: 4

Query Match 48.1%; Score 39; DB 2; Length 587;
 Best Local Similarity 66.7%; Pred. No. 71;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 DSPIQDQYTTT 14
 Db 401 DRPQDQNPPT 412

RESULT 14

T01834

hypothetical protein T15F16.4 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004

C/Accession: T01834

R/Antonov, B.; Le, T.

submitted to the EMBL Data Library, August 1998

A/Description: The sequence of A. thaliana T15F16.

A/Reference number: Z14443

A/Accession: T01834

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-940 <ANT>

A/Cross-references: UNIPROT:O81471; UNIPARC:UPI000009DA3B; EMBL:AF076275; NID:G3293582; I

A/Experimental source: cultivar Columbia

C/Genetics:

A/Map position: 4

A/Introns: 108/1; 340/1

A/Note: T15F16.4

Query Match 48.1%; Score 39; DB 2; Length 940;
 Best Local Similarity 66.7%; Pred. No. 1.2e+02;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 DSPIQDQYTTT 14
 Db 754 DRPQDQNPPT 765

RESULT 15

A45389

genome polyprotein - canine distemper virus (strain Onderstepoort)

N/Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase

C/Species: canine distemper virus

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: A45389

R/Stidnu, M.S.; Menonna, J.P.; Cook, S.D.; Dowling, P.C.; Udem, S.A.

Virology 193, 50-65, 1993

A/Title: Canine distemper virus L gene: sequence and comparison with related viruses.

A/Reference number: A45389; MUID:93174968; PMID:8438585

A/Accession: A45389

A/Molecule type: genomic RNA

A/Residues: 1-2161 <SID>

A/Cross-references: UNIPROT:P24658; UNIPARC:UPI0000172721; GB:L13195; NID:G289531; PID:G

C;Genetics:

A;Gene: L

C;Superfamily: paraifluenza virus RNA-directed RNA polymerase
C;Keywords: ATP; nucleotidyltransferase; RNA biosynthesis; RNA replication

Query March 48.1%; Score 39; DB 1; Length 2161;
Best Local Similarity 63.6%; Pred. No. 3.1e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 NDSPIQTDQYT 12
||| |||
||| |||

Db 1656 NDKPILIDYS 1666

Search completed: December 12, 2005, 20:42:45
Job time : 14.6724 secs

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Q4SKB2.TETNG
ID Q4SKB2.TETNG PRELIMINARY; PRT; 340 AA.
AC Q4SKB2;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Chromosome 13 SCAP14566, whole genome shotgun sequence.
GN ORFNames-GSTENG0016807001;
OS Tetradon nigriviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthonard V., Ubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Bernardis V.,
RA Crenaud C., Duprat S., Brottier P., Contancan J.P., Gouy J.,
RA Perra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volt J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CAPE01014566; CAF98920.1; -!- Genomic DNA.
CC EMBL; CAPE01014566; CAF98920.1; -!- Genomic DNA.
SQ SEQUENCE 340 AA; 36745 MW; 1E282568C07674E5 CRC64;

Query Match 53.1%; Score 43; DB 2; Length 340;
Best Local Similarity 53.3%; Pred. No. 50;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 RNDSPIDQDTTGG 15
Db 322 RLDAPLADONATTTG 336

RESULT 3
OSHROS.STAEQ PRELIMINARY; PRT; 511 AA.
AC OSHROS;
DT 10-MAY-2005 (TREMBlrel. 30, Created)
DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
DE 5'-nucleotidase family protein.
GN OrderedLocustNames-SERP2288;
OS Staphylococcus epidermidis (strain ATCC 35984 / RP62A).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=176279;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15774886; DOI=10.1126/DB.187.7.2426-2438.2005.
RA Gill S.R., Fouts D.B., Archer G.U., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Uitterlbeck T.R., Lee C.,
RA Dmitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Frazer C.M.;
RT "Insights on evolution of virulence and resistance from the complete
genome analysis of an early methicillin-resistant Staphylococcus

RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain.";
RL J. Bacteriol. 187:2426-2438(2005).
AC EMBL; CP000029; AAW53170.1; -!- Genomic DNA.
DR TIGR; SERP2288; -!-
DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
DR GO; GO:0009166; P:nucleotide catabolism; IEA.
DR InterPro; IPR008334; 5'-Nucleotidase_C.
DR InterPro; IPR006146; 5'-Nucleotidase_N.
DR InterPro; IPR006179; 5'-Nucleotidase.
DR Pfam; PF02872; 5_nucleotid_C_1.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PRO1607; APYRASEFAMLY.
DR PROSITE; PS00786; 5_NUCLEOTIDASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 511 AA; 57847 MW; F160793204D4149C CRC64;

Query Match 53.1%; Score 43; DB 2; Length 511;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 NDSPIQDTQYTT 13
Db 444 NDAPIDSDQIYT 455

RESULT 4
OSHROS.STAEQ PRELIMINARY; PRT; 511 AA.
AC OSHROS;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Lactococcal phosphatase-like protein.
GN OrderedLocustNames-SERP2258;
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 12228;
RX PubMed=12950922; DOI=10.1046/j.1365-2958.2003.03671.x;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qin Z.-Q., Mao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228).";
RL Mol. Microbiol. 49:1577-1593(2003).
DR EMBL; AEO16751; AAC05900.1; -!- Genomic DNA.
DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
DR GO; GO:0009166; P:nucleotide catabolism; IEA.
DR InterPro; IPR008334; 5'-Nucleotidase_C.
DR InterPro; IPR006146; 5'-Nucleotidase_N.
DR InterPro; IPR006179; 5'-Nucleotidase.
DR Pfam; PF02872; 5_nucleotid_C_1.
DR Pfam; PF00149; Metallophos; 1.
DR PRINTS; PRO1607; APYRASEFAMLY.
DR PROSITE; PS00786; 5_NUCLEOTIDASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 511 AA; 57798 MW; 47487BE2096ADEC6 CRC64;

Query Match 53.1%; Score 43; DB 2; Length 511;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 NDSPIQDTQYTT 13
Db 444 NDAPIDSDQIYT 455

RESULT 5


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07RHP3 PLAYO
ID 07RHP3_PLAYO PRELIMINARY; PRT; 516 AA.
AC 07RHP3;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE GAR domain protein.
GN Name=PY03941;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=72239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=23368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiolini S.V., Suh B.B., Koof T.W., Pertia M.,
RA Silva J.C., Emolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.B., Riedmiller S.B., Feldlyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoatli A., Cummings L.M.,
RA Florens L., Yates J.R. II, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.",
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
DR EMBL; AAB01001174; EAA15729.1; -; Genomic_DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
SQ
SEQUENCE 516 AA; 62120 MW; 8CBA858FA3C373FC CRC64;

Query Match 53.1%; Score 43; DB 2; Length 516;
Best Local Similarity 54.5%; Pred. No. 80;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNDSPICDTQY 11
DB 53 KNDSPVSTDRY 63

RESULT 6
DELT_CAEEL STANDARD; PRT; 664 AA.
ID DELT_CAEEL
AC Q19038;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Degenerin del-1.
GN Name=del-1; ORFNames=E02H4.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Bristol N2;
RX Taverariakis N., Shreffler W., Wang S.L., Driscoll M.;
RL Submitted (OCT-1996) to the EMBL/genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.",
RL Science 282:2012-2018(1998).
CC -1- FUNCTION: Probable sodium channel subunit.

```

```

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the amiloride-sensitive sodium channel
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U76403; AAB39735.1; -; mRNA.
DR EMBL; Z68003; CA91975.1; -; Genomic_DNA.
DR PIR; T20420; T20420.
DR Ensemble; E02H4.1; Caenorhabditis elegans.
DR WormBase; WBGen0000952; del-1.
DR WormPep; E02H4.1; CE05547.
DR InterPro; IPR004726; Deg-1.
DR InterPro; IPR01873; Na+channel_ASC.
DR PANTHER; PTHR11690; Na+channel_ASC; 1.
DR Pfam; PF00858; ASC; 1.
DR PRINTS; PR01078; AMINACHANNEL.
DR TIGRFAMs; TIGR00867; deg-1; 1.
DR PROSITE; PS01206; ASC; 1.
DR Complete proteome; Glycoprotein; Ion transport; Ionic channel; Sodium;
KW Sodium channel; Sodium transport; Transmembrane; Transport.
FT TOPO_DOM 1 67
FT TRANSMEM 68 88
FT TOPO_DOM 89 607
FT TRANSMEM 608 628
FT TOPO_DOM 629 664
FT CARBOHYD 241 241
FT CARBOHYD 300 300
FT CARBOHYD 394 394
FT CARBOHYD 508 508
FT CARBOHYD 562 562
SQ SEQUENCE 664 AA; 75474 MW; 0D19C8EF79688F8D CRC64;

Query Match 53.1%; Score 43; DB 1; Length 664;
Best Local Similarity 80.0%; Pred. No. 1;le+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PIGTDQYTTT 14
DB 536 PQQDQYTTT 545

RESULT 7
Q819P8_9BIVA PRELIMINARY; PRT; 699 AA.
ID Q819P8_9BIVA
AC Q819P8;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN Name=Amy;
OS Corbicula fluminea.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Corbiculoidea; Corbiculidae; Corbicula.
OX NCBI_TaxID=45949;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Da Lage J.-L., Van Wormhoudt A., Carion M.-L.;
RT "Diversity and evolution of the alpha-amylase genes in Animals.";
RL Biologia 57:181-189(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14704857; DOI=10.1007/s00018-003-3334-Y;
RA Da Lage J.-L., Feller G., Janecsek S.;
RT "Horizontal gene transfer from Eukarya to bacteria and domain
RT shuffling: the alpha-amylase model.",
RL Cell. Mol. Life Sci. 61:97-109(2004).
RN [3]
RP NUCLEOTIDE SEQUENCE.

```

RA Da Lage J.-L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF468016; AA017927.2; -; Genomic_DNA.
DR HSSP; P04745; ISMD.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006048; Alpha-amyl_C.
DR InterPro; IPR006047; Alpha-amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_I3.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF02806; Alpha-amylase_C; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy; C.1.
SQ SEQUENCE 699 AA; 76544 MW; 25D57008165B04CB CRC64;

Query Match 53.1%; Score 43; DB 2; Length 699;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNDSPICQDQYTTTG 15
DB 241 QSNPEIKTSQYTSIG 255

RESULT 8

QAN289_THEPA PRELIMINARY; PRT; 809 AA.
AC QAN289;

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=rp04_0468;

OS Theileria parva.

OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;

OC Theileria.

OX NCBI_Taxid=5675;

RN [1]

NUCLEOTIDE SEQUENCE.

RC STRAIN=Muguga;

RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
Jiang L., Lynn J., Weaver B., Shoabi A., Wasawo D., Crabtree J.,
Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
Silva J.C., Utecherback T.R., Feldblum T.V., Perlea M., Allen J.,
Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
Venter J.C., Fraser C.M., Nene V.;

RA "genome sequence of Theileria parva, a bovine pathogen that transforms
lymphocytes.";

RT Science 309:134-137(2005).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=Muguga;

RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiao L.,
Lynn J., Weaver B., Shoabi A., Wasawo D., Crabtree J., Wortman J.R.,
Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
Utecherback T., Feldblum T., Perlea M., Allen J., Taracha E.L.,
Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
Fraser C.M., Nene V.;

RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.

CC EMBL; AAGK01000004; EAN31820.1; -; Genomic_DNA.

KM Hypothetical protein.

SQ SEQUENCE 809 AA; 92620 MW; 58FA8368C313471 CRC64;

Query Match 53.1%; Score 43; DB 2; Length 809;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 NDSPIQDQYTTTG 15
DB 526 NNSPTNSSEPTTG 539

RESULT 9

Q4UFT9_THEAN PRELIMINARY; PRT; 5261 AA.
AC Q4UFT9;

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Sfil-subtelomeric related protein family member, putative.

GN ORFNames=TA16050;

OS Theileria annulata.

OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;

OC Theileria.

OX NCBI_Taxid=5674;

RN [1]

NUCLEOTIDE SEQUENCE.

RC STRAIN=Ankara isolate clone C9;

RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
Hall N., Barrett B.G.;

RA "The chromosome 2 sequence of Theileria annulata.";

RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; CR940348; CAI74027.1; -; Genomic_DNA.

DR InterPro; IPR007480; DUF529.

DR Pfam; PF04385; FAINT; 54.

KM Nucleotide-binding.

SQ SEQUENCE 5261 AA; 603934 MW; 79941BB6659578E CRC64;

Query Match 53.1%; Score 43; DB 2; Length 5261;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQDQYTTT 14
DB 4887 NDNPLTKNDYTTT 4899

RESULT 10

O6MK1_NEUCR PRELIMINARY; PRT; 273 AA.
AC O6MK1;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE Hypothetical protein B8J22.210.

GN Name=B8J22.210;

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OX NCBI_Taxid=5141;

RN [1]

NUCLEOTIDE SEQUENCE.

RP Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
Nyakatura G., Mewes H.W., Mannhaupt G.;

RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

RN [2]

NUCLEOTIDE SEQUENCE.

RA German Neurospora genome project;

RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX842627; CAE76297.1; -; Genomic_DNA.

KM Hypothetical protein.

SQ SEQUENCE 273 AA; 29666 MW; 86F5D7647F13873 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 273;
Best Local Similarity 57.1%; Pred. No. 59;

```
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 2 NDSP1QTDQYTTG 15
Db 151 NTDH1HDSYTSYG 164

RESULT 11
Q88D16_PSEPK PRELIMINARY; PRT; 455 AA.
AC Q88D16_1
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Membrane protein, putative.
GN OrderedLocustNames=PP4839;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22423060; PubMed=12534463;
RX DOI=10.1046/j.1462-2920.2002.00366.x;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Bauman M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chis Lee P., Holtzapfe E.K., Scanlan D., Tran K.,
RA Maizel A., Utechtack T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Medler H., Lauber J., Stjepandic D., Hohnsbeil J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tummeler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016792; AAN70408.1; -; Genomic_DNA.
DR TIGR; PP4839; -.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006508; P:protein binding and peptidolysis; IEA.
DR InterPro; IPR005625; Pepsy tm.
DR InterPro; IPR005075; Propyl_Pepsy.
DR Pfam; PF03413; Pepsy; 2.
DR Pfam; PF03923; Pepsy_TM; 5.
DR Complete proteome.
DR KW
SQ SEQUENCE 455 AA; 50581 MW; 9DDC64470ED713A5 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 455;
Best Local Similarity 58.3%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNDSP1QTDQYTTG 12
Db 325 RNDATLHVQYTTG 336

RESULT 12
Q45133_CABEL PRELIMINARY; PRT; 516 AA.
AC Q45133_1
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein COSD2.6.
GN ORFNames=COSD2.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peleodidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
```

```
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AF047651; AAK67208.2; -; Genomic_DNA.
DR Ensembl; COSD2.6; Caenorhabditis elegans.
DR WormBase; WBGene00015468; COSD2.6.
DR WormPep; COSD2.6; CB32115.
DR InterPro; IPR006578; MADF.
DR PROSITE; PS51029; MADF; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 516 AA; 58256 MW; 9596BBSA0855743 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 516;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNDSP1QTDQYTTG 15
Db 41 REDPPVKTQYTTG 52

RESULT 13
Q24781_BACSP PRELIMINARY; PRT; 700 AA.
AC Q24781_1
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Alpha-amylase precursor.
GN Name-baa;
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=No. 195;
RX MEDLINE=20407125; PubMed=10947962; DOI=10.1042/0264-6021.3500477;
RA Sumitani J., Tottori T., Kawaguchi T., Arai M.;
RT "New type of starch-binding domain: the direct repeat motif in the C-
RT terminal region of Bacillus sp. no. 195 alpha-amylase contributes to
RT starch binding and raw starch degrading.";
RL Biochem. J 350:477-484(2000).
DR EMBL; AB006823; BAA22082.1; -; Genomic_DNA.
DR HSSP; P29957; 1801.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_C.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR005085; CBM_25.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; Alpha-amylase; 1.
DR Pfam; PF02806; Alpha-amylase_C; 1.
DR Pfam; PF03423; CBM_25; 2.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Aamy; 1.
DR SMART; SM00632; Aamy; 1.
DR PROSITE; PS00152; ATPase_ALPHA_BETA; UNKNOWN_1.
KW Signal.
FT SIGNAL 1
SQ SEQUENCE 700 AA; 73569 MW; 1A6F3B9218F8A8C0 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 700;
Best Local Similarity 46.7%; Pred. No. 1.7e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNDSP1QTDQYTTG 15
Db 256 RANP1QPEBYTSNG 270
```

RESULT 14
ID 08M105 ARATH PRELIMINARY; PRT; 1049 AA.
AC 08M105-
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE At1G50840/FBA12.8 (Poli-like A DNA polymerase) (putative DNA
DE polymerase A family protein).
GN Name=At1G50840;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15993837; DOI=10.1016/j.brc.2005.06.052;
RA Mori Y., Kimura S., Saotome A., Kasei N., Sakaguchi N., Uchiyama Y.,
RA Ishihashi T., Yamamoto T., Chiku H., Sakaguchi K.;
RT "Placid DNA polymerases from higher plants, Arabidopsis thaliana.";
RL Biochem. Biophys. Res. Commun. 334:43-50(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Tang J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Deng C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shim P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB211532; AAL58915.1; -; mRNA.
DR EMBL: AF462826; AAL58915.1; -; mRNA.
DR EMBL: AY091072; AAM13892.1; -; mRNA.
DR HSSP: P19821; IKTQ.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0008408; F:3'-5' exonuclease activity; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR GO: GO:000260; P:DNA replication; IEA.
DR InterPro: IPR002562; 3_5_exonuclease.
DR InterPro: IPR001098; DNA_pol.
DR InterPro: IPR002298; DNA_pol.
DR InterPro: IPR012337; RNaseH fold.
DR Pfam: PF01612; 3_5_exonuc; I.
DR PRINTS: PR00476; DNA_pol_A; 1.
DR PRINTS: PR00868; DNAPOL.
DR SMART: SM00474; 35XOC; 1.
DR SMART: SM00482; POLAC; 1.
SQ SEQUENCE 1049 AA; 117147 MW; 5D48466D69798DA1 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 1049;
Best Local Similarity 42.9%; Pred. No. 2.8e+02;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 2 NDSPIOTDOYTTTG 15
Db 625 SDSPLSTENTTAGG 638

RESULT 15
ID 052G34 MAGGR PRELIMINARY; PRT; 1056 AA.
AC 052G34;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG01452.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe.
OX NCBI_TaxID=242507;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Alt-Zehra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantansang P., Baldwin J., Barry A.,
RA Bayul T., Blithers E. B., Bloom T., Bye J., Boguslavsky L.,
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Chesantansang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Cornu B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Dufey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gierre S.,
RA Ghitke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Homan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson E.,
RA Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokytsang T., Lokytsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabbitt R., MacDonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Maucelli E.,
RA McCarthy M., McDonough S., Mcghee T., Melrim J., Menes L.,
RA Mesirov J., Mihalovich A., Mihova T., Mikkelson T., Menga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., Neves C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'Donnell P., Okawa O., O'Leary S., Omotosho B.,
RA Orneli K., Osman S., Parker S., Perrin D., Phunhthang P., Pigani B.,
RA Purcell S., Rachupka T., Ramasamy U., Ramau R., Ray V., Raymond C.,
RA Ratta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA Rutman M., Schuppach R., Seaman C., Settillai S., Sharpe T.,
RA Sheridan J., Sherna N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talans J., Tchinga P.,
RA Tenzing P., Testaye S., Theodore J., Thoulutang Y., Topham K.,
RA Towey S., Teamia T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vanson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembek L.,
RA Zimmer A., Zody M., Lander E.;
RL "The genome sequence of Magnaporthe grisea.";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AACU0100053; EAA55801.1; -; Genomic_DNA.
DR Hypothetical protein.
SQ SEQUENCE 1056 AA; 116594 MW; 57BF6982798C69 CRC64;

Query Match 51.9%; Score 42; DB 2; Length 1056;
 Best Local Similarity 52.9%; Pred. NO. 2.8e+02;
 Matches 9; Conservative 3; Mismatches 3; Indels 2; Gaps 1;
 QY 1 RNDSPICQTDQ--YTTTG 15
 :|||:|||||:
 Db 124 KNDVPVQTFDADIQSTTG 140

Search completed: December 12, 2005, 20:41:02
 Job time : 84.4655 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:43:06 ; Search time 112.667 Seconds
(without alignments)
58.497 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNDSPVTEOQATTW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 770462

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	15	8	ADRI0602 Cat IGE e
2	48	56.5	15	8	ADRI0601 Dog IGE e
3	39	45.9	15	8	ADRI0607 Pig IGE e
4	37	43.5	15	8	ADRI0603 Horse IGE
5	35	41.2	15	7	ADCG4568 Horse Imm
6	32	37.6	11	5	AAU79709 Synthetic
7	30	35.3	10	3	AAI38098 Human ABC
8	29	34.1	6	4	AAAS5476 Human ala
9	29	34.1	15	2	AAAS5733 dsDNA-dep
10	29	34.1	15	8	ADR97089 Cysteine
11	28.5	33.5	12	2	AAW56548 Toxin fra
12	28	32.9	9	2	AAW76034 LM609 gra
13	28	32.9	9	4	AAI61392 Mutant VL
14	28	32.9	9	6	ABO19830 Enhanced
15	28	32.9	9	6	ABR62303 Surface s
16	28	32.9	9	7	ADG71862 Enhanced
17	28	32.9	9	8	ADJ58043 Murine LM
18	28	32.9	9	8	ADJ73181 CDR3 of t
19	28	32.9	10	5	ABG98755 F protein
20	28	32.9	13	2	AAAR79898 Fusion pr
21	28	32.9	15	7	ADK62291 Human 98P
22	28	32.9	15	7	ADK63829 Human 98P
23	27	31.8	8	2	AAW59312 Non-Polio
24	27	31.8	9	3	AAI10015 H. pylori

25	27	31.8	9	4	ABR86095 H. pylori
26	27	31.8	9	4	ABR86063 H. pylori
27	27	31.8	9	5	ABR99231 CD45RO/RB
28	27	31.8	9	5	AAU72845 Anti-NG2
29	27	31.8	9	5	AAU72853 Anti-NG2
30	27	31.8	9	5	ADY80269 CDR3 from
31	27	31.8	10	5	ABG98754 F protein
32	27	31.8	13	2	AAAR63411 Peptide f
33	27	31.8	13	2	AAAR6483 Hepatitis
34	27	31.8	14	4	AAW97114 Human pep
35	27	31.8	14	8	ADT40356 hSARS vlr
36	27	31.8	14	8	ADT97773 SARS vlr
37	27	31.8	14	8	ADT37886 hSARS vlr
38	26	30.6	8	2	AAV04462 Active m1
39	26	30.6	9	6	ABP74676 Human SCP
40	26	30.6	9	6	AAE38100 Human COU
41	26	30.6	9	7	ADC09535 Epitope w
42	26	30.6	9	8	ADN28303 Human CD3
43	26	30.6	10	2	AAV04464 Active m1
44	26	30.6	10	2	AAV04463 Active m1
45	26	30.6	10	3	AAV51451 AAV VP3 d

ALIGNMENTS

RESULT 1
ADRI0602 standard; peptide, 15 AA.
ID ADRI0602
AC ADR10602;
XX
XX
DT 21-OCT-2004 (first entry)
XX
XX
DE Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.
KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW cat.
XX
XX
OS Felis catus.
XX
XX
PN WO2004065936-A2.
XX
XX
PD 05-AUG-2004.
XX
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
XX
PR 16-JAN-2003; 2003US-0440472P.
XX
XX
PA (UNNC-) UNIV NORTH CAROLINA STATE.
XX
XX
PI Hammerberg B;
XX
XX
DR WPI; 2004-593545/57.
XX
XX
PT Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
XX
PS Example 6; Page 9; 14pp; English.
XX
XX
CC The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC (I) is useful for testing an allergen reactivity of an IGE sample.
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (II) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC cat IGE 5.91 recognition site.

XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 85; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.7e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQOATTW 15
 Db 1 HNDSPVTEQOATTW 15

RESULT 2

ID ADR10601 standard; peptide; 15 AA.

XX ADR10601;

DT 21-OCT-2004 (first entry)

DE Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.

XX Antiaethmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;

KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.

XX Canis familiaris.

PN WO2004065936-A2.

PD 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

DR WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE.

XX Sequence 15 AA;

Query Match 56.5%; Score 48; DB 8; Length 15;
 Best Local Similarity 61.5%; Pred. No. 0.23;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPPVTEQOATT 14
 Db 2 NDSPPVTEQOATT 14

RESULT 3

ID ADR10607 standard; peptide; 15 AA.

XX ADR10607;

DT 21-OCT-2004 (first entry)

DE Pig IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.

XX Antiaethmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;

KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;

XX pig.

OS Sus scrofa.

PN WO2004065936-A2.

PD 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

DR WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC pig IGE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 45.9%; Score 39; DB 8; Length 15;
 Best Local Similarity 46.2%; Pred. No. 9.5;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPPVTEQOATT 14
 Db 2 NDAVQADRHSTT 14

RESULT 4

ID ADR10603 standard; peptide; 15 AA.


```

XX ADR10603;
AC
XX 21-OCT-2004 (first entry)
DT
XX
XX Horse IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 3.
DE
XX Antiaesthetic; Antiallergic; Immunosuppressive; IGF; dog; asthma;
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KM horse.
XX
XX Equus caballus.
OS
XX MO2004065936-A2.
XX
XX 05-AUG-2004.
PD
XX
XX 15-JAN-2004; 2004WO-US003566.
XX
XX 16-JAN-2003; 2003US-0440472P.
XX
XX (UNNC-) UNIV NORTH CAROLINA STRATE.
XX
XX Hammerberg B;
XX
XX WPI; 2004-593545/57.
DR
XX
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
PS
XX
XX The present invention relates to a novel monoclonal antibody (I) that
XX specifically binds to a mammalian IGE epitope, where the epitope is
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX (I) is useful for testing an allergen reactivity of an IGE sample. The
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX and corn allergens. The sample is a biological sample collected from a
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX antibodies recognise epitopes on canine IGE corresponding to amino acid
XX residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
XX cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
XX 3.76 were observed to have good cross-reactivity with the epsilon-chain
XX of IGE from cat and horse, but did not exhibit cross-reactivity with
XX either pig or human epsilon-chains of IGE. The present sequence is the
XX horse IGE 5.91 recognition site.
XX
XX Sequence 15 AA;
SQ
Query Match 43.5%; Score 37; DB 8; Length 15;
Best Local Similarity 53.8%; Pred. No. 22;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 2 NDSVRTQOQATT 14
Db 2 NNVLITDQOQATT 14

```

```

OS Equus caballus.
XX
XX US2003087314-A1.
XX
XX 08-MAY-2003.
PD
XX
XX 08-NOV-2001; 2001US-00052788.
XX
XX 08-NOV-2001; 2001US-00052788.
XX
XX 08-NOV-2001; 2001US-00052788.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Gershwin LJ, Pettigrew HD, Kalina WV;
XX
XX WPI; 2003-765437/72.
XX
XX Immunogenic composition comprising an isolated equine immunoglobulin E
PT polypeptide that induces production of antibodies which specifically bind
PT to equine immunoglobulin E.
XX
XX Example 1; Page 8; 14pp; English.
PS
XX
XX The invention relates to an immunogenic composition comprising an
XX isolated polypeptide having an amino acid sequence that is at least 80%
XX identical to 6 (S1-S6), 15 amino acid peptide sequences derived from
XX equine immunoglobulin E (the composition induces production of an
XX antibody that specifically binds to equine immunoglobulin (Ig)E), the six
XX polypeptides are not explicitly identified in the specification. Also
XX included are a composition comprising an antibody that specifically binds
XX to a polypeptide at least 80% identical to (S1)-(S6), an antibody that
XX specifically binds to equine IGE made by the process of immunising an
XX animal with a polypeptide at least 80% identical to (S1)-(S6), making an
XX antibody that specifically binds to equine IGE (involving immunising an
XX animal with a composition further comprising an isolated polypeptide (the
XX amino acid sequence of the polypeptide is at least 80% identical to (S1)-
XX (S6)), and collecting antiserum from the animal) and a kit for detection
XX of equine IGE in a biological sample comprising the antibody and means
XX for detecting specific binding of the antibody to equine IGE. The
XX antibody is useful for detecting equine IGE protein in a biological
XX sample (serum) which involves contacting the sample with the antibody,
XX thus forming an antigen/antibody complex, and detecting the presence or
XX absence of the antigen/antibody complex. The antibody and antigen are
XX immobilised on a solid surface. The antibody is labelled such that the
XX complex can be detected. The complex is detected using a second labelled
XX antibody. The peptides are useful for generating antibodies specific for
XX IGE which can serve as a diagnostic test for allergy. The present
XX sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic
XX peptide from the early portion of the C4 region.
XX
XX Sequence 15 AA;
SQ
Query Match 41.2%; Score 35; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 6 VRTQOQATT 14
Db 1 IQTDQOQATT 9

```

```

RESULT 5
AD64568
ID ADC64568 standard; peptide; 15 AA.
XX
XX ADC64568;
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P4.
XX
XX Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.
XX
XX

```

```

RESULT 6
AAU79709
ID AAU79709 standard; peptide; 11 AA.
XX
XX AAU79709;
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX Synthetic peptide CPP-2 used in invention of DRL90.
XX
XX Human; tissue-specific secretory polypeptide; DRL90; infection; cancer;
XX immune disease; digestive disease; circulatory disease;
XX endocrine disease; infertility; cytostatic; immunomodulator;
XX
XX

```

KM antimicrobial; vasotropic; antifertility; hormonal; CPP-2.
XX Synthetic.
XX WO200224908-A1.
XX
PD 28-MAR-2002.
XX
XX 21-SEP-2001; 2001WO-JP008223.
XX
PR 22-SEP-2000; 2000JP-00293985.
PR 29-SEP-2000; 2000JP-00302839.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Ito Y, Tanaka H, Nishimura A, Ogi K;
XX
XX WPI; 2002-330018/36.
DR
XX
XX New tissue-specific secretory polypeptides applicable in diagnosis of and
PT remedies for cancer, immune diseases, infection, digestive diseases,
PT circulatory diseases, endocrine diseases and infertility.
XX
PS Example 8; Page 80; 11pp; Japanese.
XX
XX The present invention relates to the isolation of a novel tissue-specific
CC secretory polypeptide, DRJ90, and the polynucleotide sequence encoding
CC it. The DRJ90 polypeptide and encoding DNA are useful for diagnosing and
CC treating cancer, immune diseases, infection, digestive diseases,
CC circulatory diseases, endocrine diseases and infertility. The present
CC sequence for synthetic peptide CPP-2 is used in the examples of the
CC present invention
XX
SQ Sequence 11 AA;
XX
Query Match 37.6%; Score 32; DB 5; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 SPVATEQQA 12
||: ||: ||
Db 2 SPITEKQA 10
XX
RESULT 7
AAB38098
ID AAB38098 standard; peptide; 10 AA.
XX
AC AAB38098;
XX
DT 29-JAN-2001 (first entry)
XX
XX Human ABC1 FHA-3 mutant exon 41-encoded peptide fragment, SEQ ID NO:65.
DE
XX Human ABC1 cholesterol transporter; chromosome 9q31;
KM ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KM Tangier disease; T3; familial HDL deficiency; FHA; polymorphism;
KM cerebrovascular disease; coronary artery disease; coronary restenosis;
KM Alzheimer's disease; peripheral vascular disease;
KM X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KM prognosis; prophylaxis; drug screening; transgenic animal.
XX
XX Homo sapiens.
OS
XX
XX WO200055318-A2.
PN
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-IB000532.
XX
PR 15-MAR-1999; 99US-0124702P.
PR 08-JUN-1999; 99US-0138048P.
XX

PR 17-JUN-1999; 99US-0139600P.
PR 01-SEP-1999; 99US-0151977P.
XX
XX (VYBR-) UNIV BRITISH COLUMBIA.
PA (XENON-) XENON BIORESEARCH INC.
XX
XX Hayden MR, Wilson AR, Pimstone SN;
PI
XX
XX WPI; 2000-587528/55.
DR N-PSDB; AAC69168.
XX
XX
PT New ABC1 polypeptide is useful for treating diseases associated with ABC1
PT biological activity, e.g. Alzheimer's disease, Huntington's disease and
PT cancer.
XX
XX Example; Fig 6E; 229pp; English.
XX
XX The invention relates to the human ABC1 cholesterol transporter protein
CC (B38082) and to nucleic acid sequences (CG9120) which encode it. ABC1 is
CC a member of the ATP-binding cassette (ABC transporter) superfamily of
CC proteins, and plays a crucial role in cholesterol transport, particularly
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC located on chromosome 9q31, and mutations in this gene are associated
CC with two genetic HDL (high density lipoprotein) deficiency disorders,
CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC are distinguishable in that TD is an autosomal recessive disorder, while
CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC cholesterol") in the blood correlate with a high risk of cardiovascular
CC disease, particularly coronary artery disease, but also cerebrovascular
CC disease, coronary restenosis, and peripheral vascular disease.
CC Conversely, a high level of HDL has protective effects against
CC cardiovascular disease. The invention provides genetic constructs and
CC transgenic cells and non-human animals comprising human ABC1 nucleic
CC acids, and methods of gene therapy for the treatment or prevention of
CC cardiovascular disease comprising the administration of an expression
CC vector encoding ABC1 or an active fragment thereof. The invention also
CC encompasses compounds which mimic ABC1 activity, compounds which
CC stimulate ABC1 expression and methods of screening for such compounds. It
CC further relates to methods for determining whether a patient has an
CC increased risk for cardiovascular disease due to polymorphisms in the
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or
CC prevent cardiovascular disease, especially coronary artery disease,
CC cerebrovascular disease, coronary restenosis or peripheral vascular
CC disease. They may also be used in the treatment of diseases associated
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC The invention specifically excludes proteins with the exact amino acid
CC sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic
CC acid with the exact sequence as Genbank Accession No: AU012376.1. The
CC present sequence represents a human ABC1 cholesterol transporter peptide
CC fragment used in the exemplifications of the invention
XX
SQ Sequence 10 AA;
XX
Query Match 35.3%; Score 30; DB 3; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 NDSPVATEQ 11
||: ||: ||
Db 1 NDEVRRERQ 10
XX
RESULT 8
AAB55476
ID AAB55476 standard; peptide; 6 AA.
XX
AC AAB55476;
XX
DT 07-MAR-2001 (first entry)
XX
XX Human elastase variant segment peptide SEQ ID NO:46.
DE

XX Human; elastase; variant; substrate; mutant; mutagenesis; histidine;
 KM human neutrophil elastase; H43A; cytosolic; proteolysis; ADEPT;
 KM antibody-directed enzyme activated prodrug therapy.
 XX OS Homo sapiens.
 XX PN WO20068363-A2.
 XX PD 16-NOV-2000.
 XX PF 04-MAY-2000; 2000WO-US006692.
 XX PR 05-MAY-1999; 99US-0132640P.
 XX PA (GETH) GENENTECH INC.
 XX PI Carter PJ, Dall'Aquila W, Rodrigues M;
 XX DR WPI; 2001-007389/01.
 XX PT Elastase variant (H43A) having altered substrate specificity useful for
 PT antibody-directed enzyme activated prodrug therapy.
 XX PS Example 4; Fig 3; 79pp; English.
 XX CC The present invention describes a purified elastase variant (I) with an
 CC amino acid sequence different from that of a precursor elastase, the
 CC difference comprising a substitution of an active site histidine residue
 CC corresponding to residue 43 in human neutrophil elastase with a different
 CC amino acid residue so that (I) has substrate specificity substantially
 CC different from the precursor elastase. (I) has cytosolic activity, and
 CC can be used in antibody-directed enzyme activated prodrug therapy. The
 CC elastase variant can be used to cleave a particulate substrate, especially
 CC those containing histidine residues at the substrate site. Site-specific
 CC proteolysis is useful in therapeutic applications, e.g. for antibody-
 CC directed enzyme activated prodrug therapy (ADEPT). AAc8022, AAc8023 and
 CC AAc55432 to AAc55526 represent sequences used in the exemplification of
 CC the present invention
 XX SQ Sequence 6 AA;
 XX
 XX Query Match 34.1%; Score 29; DB 4; Length 6;
 XX Best Local Similarity 83.3%; Pred. No. 2e+06; 1; Indels 0; Gaps 0;
 XX Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 10 QOATTW 15
 Db 1 QOATTW 6
 RESULT 9
 AAc55733
 ID AAc55733 standard; peptide; 15 AA.
 XX AAc55733;
 XX AAc55733;
 DT 25-MAR-2003 (revised)
 DT 16-NOV-1994 (first entry)
 XX dedNA-dependent kinase inhibitor.
 XX dedNA-dependent kinase inhibitor.
 KM dadNA-dependent kinase inhibitor; fatty acyl-peptide; conjugate;
 KM antiproliferative; tumor; psoriasis; docosahexaenoic acid; DNA;
 KM eicosapentaenoic acid; EPA; antitumor.
 XX Synthetic.
 XX OS
 XX PN WO9412530-A1.
 XX PD 09-JUN-1994.
 XX PF 29-NOV-1993; 93WO-HU000065.

XX 30-NOV-1992; 92US-00984293.
 XX (BIOS-) BIOSIGNAL KUTATO PEPTIDESZTO KFT.
 XX (SYNT-) SYNTHETIC PEPTIDES INC.
 XX PI Keri G, Hodges RS, Cachia PJ, Szederkenyi F, Horvath A, Balogh A;
 XX Vadasz Z;
 XX WPI; 1994-200194/24.
 XX New fatty acyl-peptide conjugates for inhibiting cell proliferation -
 PT more active than free peptide, partic. for treating tumours, virus-
 PT infected cells, psoriasis, etc.
 XX PS Disclosure; Fig 1; 45pp; English.
 XX CC The peptides given in AAc55718-48 can each be conjugated through an amide
 CC linkage with a polyunsaturated fatty acid moiety, such as docosahexaenoic
 CC acid or eicosapentaenoic acid, to improve antiproliferative activity. The
 CC dedNA-dependent kinase inhibitor given in AAc55733 competes with native
 CC kinases associated with neoplastic cell proliferation or transformation,
 CC psoriasis, etc. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 15 AA;
 XX
 XX Query Match 34.1%; Score 29; DB 2; Length 15;
 XX Best Local Similarity 40.0%; Pred. No. 5.8e+02; 2; Indels 0; Gaps 0;
 XX Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 OY 1 HNDSPVRETEQ 10
 Db 6 YNDNPMEEEE 15
 RESULT 10
 AAc97089
 ID AAc97089 standard; peptide; 15 AA.
 XX AAc97089;
 XX AAc97089;
 DT 02-DEC-2004 (first entry)
 DE Cysteine protease inhibitory protein fragment #2.
 XX antiinflammatory; vasotropic; immunostimulator;
 KM cysteine protease inhibitory protein; diagnosis; Behcet's disease;
 KM Harada's disease.
 XX OS Homo sapiens.
 XX PN WO2004078975-A1.
 XX 16-SEP-2004.
 XX 05-MAR-2004; 2004WO-JP002902.
 XX 05-MAR-2003; 2003JP-00059082.
 XX (SENP) SENJU PHARM CO LTD.
 XX Katunuma N, Shiota H;
 XX WPI; 2004-668624/65.
 XX Novel cysteine protease inhibitory protein, useful as diagnostic marker
 PT for diagnosing Behcet's disease and Harada's disease.
 XX Disclosure; SEQ ID NO 4; 64pp; Japanese.
 XX A cysteine protease inhibitory protein (I) having the amino acid sequence
 CC AAc97086 at its N-terminal and exhibiting the molecular weight of 31 kDa,
 CC is new. (I) is useful for screening a compound or its salt having

CC activity of promoting or inhibiting the function of (I). (I) enables
CC diagnosis, prevention or treatment of Behcet's disease or Harada's
CC disease. This sequence is a fragment of the cysteine protease inhibitory
CC protein.

XX Sequence 15 AA;

Query Match 34.1%; Score 29; DB 8; Length 15;
Best Local Similarity 38.5%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Dy 3 DSPVTEQOATW 15
Db 3 DRPRHPQEPPLW 15

RESULT 11

AAW56548
ID AAW56548 standard; peptide; 12 AA.

AC AAW56548;

DT 07-AUG-1998 (first entry)

DE Toxin fragment of Tcac of the bacterium Photorhabdus luminescens.

XX Photorhabdus luminescens W-14; nematode; symbiotic; Heterorhabditis; tca;
XX tcb; tcc; tcd; insecticidal activity; toxin; Lepidoptera; Coleoptera;
XX Hymenoptera; Diptera; Dictyoptera; Acarina; Homoptera; Southern;
XX Western corn rootworm; Colorado potato beetle; mealworm; boll weevil;
XX turf grub; beetle armyworm; black cutworm; cabbage looper; codling moth;
XX corn earworm; European corn borer; Tobacco hornworm; budworm.
XX Photorhabdus luminescens.

XX W09808932-A1.

PD 05-MAR-1998.

PF 05-MAY-1997; 97WO-US007657.

PR 28-AUG-1996; 96US-00705484.

PR 06-NOV-1996; 96US-00743699.

PR 06-NOV-1996; 96WO-US018003.

PA (DOWC) DOWELANCO.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

PI Ensign JC, Bowen DJ, Petrell J, Faticig R, Schoonover S;
PI French-Constant RH, Rochelleau TA, Blackburn MB, Hey TD, Merlo DJ;
PI Orr GL, Roberts JR, Strickland JA, Guo L, Cliche TA, Sukhapinda K;
XX WPI; 1998-179427/16.

PT Isolated toxins from Photorhabdus luminescens strains - useful for
PT control of insect pests.

PS Claim 30; Page 151; 321pp; English.

XX The present sequence represents a fragment of the toxic protein Tcac
CC (encoded by gene tcaC) of the bacterium Photorhabdus luminescens (W-14).
CC This is a symbiotic bacterium of the nematodes of the Heterorhabditis
CC genus. The bacterium has at least 4 distinct genomic regions, tca, tcb,
CC tcc, and tcd. Peptide products are produced from these regions that are
CC associated with insecticidal activity. The native toxins are secreted
CC proteins. The proteins are toxic to insects upon exposure and especially
CC when ingested. The nucleic acid sequence can be used to produce
CC transgenic plants, baculoviruses or microbial hosts for toxin production.
CC They can be used to control insects pests from the Lepidoptera.
CC Coleoptera, Hymenoptera, Diptera, Dictyoptera, Acarina or Homoptera
CC orders, especially the Southern or Western corn rootworm, Colorado potato
CC beetle, mealworm, boll weevil, turf grub, beetle armyworm, black cutworm,
CC cabbage looper, codling moth, corn earworm, European corn borer or

CC tobacco hornworm or budworm
XX Sequence 12 AA;

Query Match 33.5%; Score 28.5; DB 2; Length 12;
Best Local Similarity 53.8%; Pred. No. 5.5e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Dy 3 DSPVTEQOATW 15
Db 3 DSP---EVSITW 12

RESULT 12

AAW76034
ID AAW76034 standard; protein; 9 AA.

AC AAW76034;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-L region CDR3 protein fragment #3.

XX Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
XX LM609; inhibitor; integrin-mediated signal transduction; treatment;
XX diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
XX neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
XX macular degeneration; osteoporosis; primer; V-L region; CDR;
XX complementarity determining region.

XX Mus sp.

XX W09833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; 98WO-US001826.

PR 30-JAN-1997; 97US-00791391.

PA (IXSY-) IXSYS INC.

XX Huse WD, Glaeser SM;

XX WPI; 1998-437472/37.

DR N-PSDB; AAV49871.

PT Humanised antibody, vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis.

XX Claim 62; Page 41; 129pp; English.

XX AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block integrin-
CC mediated signal transduction. This is useful in the treatment, prevention
CC and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis
CC and restenosis (but also e.g. (non-)immune inflammation, diabetic
CC retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody

XX Sequence 9 AA;

Query Match 32.9%; Score 28; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0;

OY 10 QOATW 15
DB 1 QOSTSW 6

RESULT 13
AAB61392
ID AAB61392 standard; peptide; 9 AA.
XX
AC AAB61392;
XX
DT 03-APR-2001 (first entry)
XX
DE Mutant VL CDR3 peptide #2.
XX
KW LM609; grafted antibody; alphaVbeta.3 integrin; angiogenesis;
KW inflammatory; cancer; retina; restenosis; osteoporosis.
XX
OS Unidentified.
XX
PN WO200078815-A1.
XX
PD 28-DEC-2000.
XX
PF 23-JUN-2000; 2000WO-US017454.
XX
PR 24-JUN-1999; 99US-00339922.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Huse WD, Wu H;
XX
DR WPI; 2001-050110/06.
XX
PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
PT to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
PT angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
PT osteoporosis.
XX
XX
PS Disclosure; Page 41; 132pp; English.
XX
CC The present invention relates to enhanced LM609 grafted antibodies
CC exhibiting selective binding affinity to alphaVbeta.3 integrin or their
CC functional fragments. The antibodies or their functional fragments can be
CC used in the diagnosis and treatment of alphaVbeta.3-mediated diseases
CC such as angiogenesis, inflammatory diseases (such as psoriasis and
CC chronic articular rheumatism), disorders associated with inappropriate or
CC inoprotune invasion of vessels (such as diabetic retinopathy,
CC neovascular glaucoma and cancer disorders such as tumours and Kaposi's
CC sarcoma), retinal diseases (such as macular degeneration), restenosis and
CC osteoporosis
CC
SQ Sequence 9 AA;

OY 10 QOATW 15
DB 1 QOSTSW 6

Query Match 32.9%; Score 28; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
ABO19830
ID ABO19830 standard; peptide; 9 AA.
XX
AC ABO19830;
XX
DT 28-AUG-2003 (first entry)
XX
DE Enhanced LM609 light chain variable region CDR3 #2.
XX

KW LM609; antibody; grafted antibody; alpha_vbeta.3; angiogenesis; CDR;
KW alpha_vbeta.3-mediated disease; complementarity determining region;
KW restenosis.
XX
OS Unidentified.
XX
PN US2003028009-A1.
XX
PD 06-FEB-2003.
XX
PF 06-JUL-2001; 2001US-00900590.
XX
PR 30-JAN-1998; 98US-00016061.
XX
PA (IXSY-) IXSYS INC.
XX
PI Huse WD;
XX
DR WPI; 2003-492042/46.
DR N-PSDB; ACD30189.
XX
PT New Vitaxin or LM609 grafted antibody exhibiting selective binding
PT affinity to alphaVbeta3, useful for treating an alphaVbeta3-mediated
PT disease e.g., angiogenesis or restenosis.
XX
PS Claim 65; Page 12; 71pp; English.
XX
CC The invention relates to a Vitaxin or LM609 grafted antibody, exhibiting
CC selective binding affinity to alpha_vbeta.3. The Vitaxin or LM609 grafted
CC antibody is useful for treating an alpha_vbeta.3-mediated disease e.g.
CC angiogenesis or restenosis. The present sequence represents the amino
CC acid sequence of a LM609 complementarity determining region
XX
SQ Sequence 9 AA;

OY 10 QOATW 15
DB 1 QOSTSW 6

Query Match 32.9%; Score 28; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
ABR62303
ID ABR62303 standard; peptide; 9 AA.
XX
AC ABR62303;
XX
DT 22-SEP-2003 (first entry)
XX
DE Surface simulation synthetic peptide useful in HIV-1 vaccine.
XX
KW Surface simulation synthetic peptide; SSSP; HIV-1; vaccine; anti-HIV;
KW vitruclide; eptlope.
XX
OS Human immunodeficiency virus 1.
OS Synthetic.
XX
PN WO2003048186-A2.
XX
PD 12-JUN-2003.
XX
PF 23-NOV-2002; 2002WO-US037664.
XX
PR 01-DEC-2001; 2001US-00012806.
XX
PA (CREV/) CREVECOEUR H.
XX
PI Crevecoeur H;
XX
DR WPI; 2003-558941/52.

XX Configuration of synthetic peptides useful for treating hyper-variable
PT viral pathogen e.g. HIV, involves identifying non-sequential conserved
PT residues in selected viral proteins and designing a sequence from image
PT scan of the residues.

XX
PS Disclosure; Page 27; 55pp; English.

XX
CC The present sequence is that of a surface simulation synthetic peptide
CC (SSSP) corresponding to a non-sequential conserved residue epitope of HIV
CC -1 glycoprotein gp120 required for viral pathogenicity. It is an example
CC of SSSPs of the invention, which incorporate amino acid sequences that
CC simulate the 3-dimensional spatial positions of non-sequential conserved
CC residues necessary for viral pathogenicity. The SSSPs are useful for
CC incorporation into vaccines effective in eliciting an effective broad
CC spectrum immune response against hyper-variable viral pathogens such as
CC HIV-1, and in diagnostic kits. SSSPs provide a reliable strategy for
CC allowing the immune system to process and recognise discontinuous
CC epitopes and to mount immune responses to the 3-dimensional
CC configurations of targeted proteins

XX
SQ Sequence 9 AA;

Query Match 32.9%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPV RTEQ 11
:| |||:
Db 1 NPCTREKQ 8

Search completed: December 12, 2005, 21:11:36
Job time : 114.667 secs

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: December 12, 2005, 20:20:00 ; Search time 27 Seconds
(without alignments)
45.931 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNDSPVTEQQATTW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 186887

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*

- 1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	35.3	10	2	US-09-526-193A-65
2	28.5	33.5	12	2	US-08-851-567B-2
3	28	32.9	9	2	US-09-339-922A-88
4	28	32.9	9	2	US-09-016-061-88
5	28	32.9	13	6	5223254-6
6	27	31.8	13	2	US-08-836-075A-166
7	27	31.8	13	2	US-09-878-281A-244
8	27	31.8	15	1	US-08-221-583-56
9	27	31.8	15	4	PCR-US95-04018-56
10	26	30.6	10	2	US-08-981-392-53
11	26	30.6	10	2	US-09-620-091-436
12	26	30.6	10	2	US-09-908-322-53
13	26	30.6	12	2	US-09-620-091-172
14	26	30.6	14	1	US-08-321-668-28
15	26	30.6	14	1	US-08-837-941-28
16	26	30.6	15	2	US-09-148-712-23
17	25	29.4	10	1	US-08-203-716-13
18	25	29.4	10	1	US-08-383-434-7
19	25	29.4	10	1	US-08-649-197-7
20	25	29.4	10	1	US-08-440-179-13
21	25	29.4	10	1	US-08-748-117A-1
22	25	29.4	10	1	US-08-597-346-1
23	25	29.4	10	1	US-08-679-350-1
24	25	29.4	10	2	US-09-039-657-13
25	25	29.4	10	2	US-09-421-954-1
26	25	29.4	10	2	US-09-623-548A-1263
27	25	29.4	10	2	US-09-657-276-1263

28	25	29.4	10	6	5422425-8	Patent No. 5422425
29	25	29.4	11	1	US-08-456-670B-38	Sequence 38, Appl
30	25	29.4	11	2	US-09-372-036-38	Sequence 38, Appl
31	25	29.4	12	1	US-08-203-716-21	Sequence 21, Appl
32	25	29.4	12	1	US-08-440-179-21	Sequence 21, Appl
33	25	29.4	12	2	US-09-039-657-21	Sequence 21, Appl
34	25	29.4	13	2	US-08-354-685-3	Sequence 2, Appl
35	25	29.4	14	1	US-08-665-643A-2	Sequence 3, Appl
36	25	29.4	14	2	US-09-693-746-93	Sequence 93, Appl
37	25	29.4	15	1	US-07-616-910-55	Sequence 55, Appl
38	25	29.4	15	4	PCR-US91-08497-55	Sequence 55, Appl
39	25	29.4	8	1	US-08-203-716-22	Sequence 22, Appl
40	24	28.2	8	1	US-08-440-179-22	Sequence 22, Appl
41	24	28.2	8	2	US-09-039-657-22	Sequence 2, Appl
42	24	28.2	9	1	US-08-232-081B-6	Sequence 6, Appl
43	24	28.2	10	1	US-08-203-716-17	Sequence 17, Appl
44	24	28.2	10	1	US-08-203-716-19	Sequence 19, Appl
45	24	28.2	10	1	US-08-203-716-17	Sequence 19, Appl

ALIGNMENTS

```
RESULT 1
US-09-526-193A-65
; Sequence 65, Application US/09526193A
; Patent No. 6617122
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; APPLICANT: Pimstone, Simon N.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; FILE REFERENCE: 50110/002005
; CURRENT APPLICATION NUMBER: US/09/526,193A
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-526-193A-65

Query Match      35.3%   Score 30;   DB 2;   Length 10;
Best Local Similarity 60.0%;   Pred. No. 58;
Matches 6;   Conservative 1;   Mismatches 3;   Indels 0;   Gaps 0;

CY      2      NDSPTREQ 11
DB      1      NDEVRRERQ 10

RESULT 2
US-08-851-567B-2
; Sequence 2, Application US/08851567B
; Patent No. 6528484
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Pettig, James
; APPLICANT: Faticg, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: Firench-Constant, Richard
; APPLICANT: Rocheleau, Thomas A.
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; APPLICANT: Blackburn, Michael B.
; APPLICANT: Hey, Timothy D.
; APPLICANT: Merlo, Donald J.
; APPLICANT: Orr, Gregory L.
; APPLICANT: Roberts, Jean L.
; APPLICANT: Strickland, James A.
; APPLICANT: Guo, Lining
; APPLICANT: Cliche, Todd A.
; APPLICANT: Sukhapiinda, Kitiari
; TITLE OF INVENTION: Insecticidal Protein Toxins From Photobabdu
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosiences Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,567B
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,615
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/395,497
; FILING DATE: 28-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/007,255
; FILING DATE: 06-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,423
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/705,484
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.93804
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; US-08-851-567B-2

Query Match      33.5%; Score 28.5; DB 2; Length 12;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy      3 DSPVTEQQTW 15
      ||| |
      ||| |
Db      3 DSP---EVSITW 12

RESULT 3
US-09-339-922A-88
; Sequence 88, Application US/09339922A
; Patent No. 6531580
; GENERAL INFORMATION:

```

```

; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Anti-Alpha Beta3 Recombinant Human Antibodies, Nucleic
; FILE REFERENCE: P-IX 3536
; CURRENT APPLICATION NUMBER: US/09/339,922A
; CURRENT FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mutated
; US-09-339-922A-88

Query Match      32.9%; Score 28; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      10 QOATW 15
      |||:|
      |||:|
Db      1 QOSTW 6

RESULT 4
US-09-016-061-88
; Sequence 88, Application US/09016061
; Patent No. 6596850
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; APPLICANT: Glaeser, Scott M.
; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,061
; FILING DATE: 30-JAN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/791,391
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 2965
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9901
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-016-061-88

Query Match      32.9%; Score 28; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;

```


Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 QOATW 15
|||:|
Db 1 QOSTW 6

RESULT 5
5223254-6
Patent No. 5223254
APPLICANT: PARADISO, PETER R.; HILDETH, STEPHEN W.; HU,
BRANDA T.; MARTIN-GALLARDO, ANTONIA; ARMUGHAM, RASAPPA
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/247,017
FILING DATE: 20-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 102,180
FILING DATE: 29-SEP-1987
SEQ ID NO: 6:
LENGTH: 13
5223254-6

Query Match 32.9%; Score 28; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPTREQ 11
|||:|
Db 2 NDMPTINDOK 11

RESULT 6
US-08-836-075A-166
Sequence 166; Application US/08836075A
Patent No. 6180768
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: STUYVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,075A
FILING DATE: 21 Apr 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/04155
FILING DATE: 23 Oct 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 Oct 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 Jun 1995
ATTORNEY/AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS:004
INFORMATION FOR SEQ ID NO: 166:

SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-075A-166

Query Match 31.8%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 VRTGQATW 15
|||:|
Db 1 VRTGQSRWC 10

RESULT 7
US-09-878-281A-244
Sequence 244; Application US/09878281A
Patent No. 6762024
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph
FILE REFERENCE: 35
CURRENT APPLICATION NUMBER: US/09/878,281A
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn version 3.1
SEQ ID NO 244
LENGTH: 13
TYPE: PRT
ORGANISM: hepatitis C virus
US-09-878-281A-244

Query Match 31.8%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 VRTGQATW 15
|||:|
Db 1 VRTGQSRWC 10

RESULT 8
US-08-221-583-56
Sequence 56; Application US/08221583
Patent No. 5486595
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595stis
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25.mdetcmcd.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCO-0185
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-56

Query Match 31.8%; Score 27; DB 1; Length 15;
Best Local Similarity 46.2%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQT 13
Db 1 HLPQPVSTRSQHT 13

RESULT 9
PCT-US95-04018-56
Sequence 56, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heavner, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-56
Query Match 31.8%; Score 27; DB 4; Length 15;
Best Local Similarity 46.2%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQT 13
Db 1 HLPQPVSTRSQHT 13

RESULT 10
US-08-981-392-53
Sequence 53, Application US/08981392
Patent No. 6262025
GENERAL INFORMATION:
APPLICANT: Ieh-Horowicz, David
APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Altavanti-Tsakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-981-392-53
Query Match 30.6%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 VRTEQQ 11
Db 5 VRTEGE 10

RESULT 11
US-09-620-091-436
Sequence 436, Application US/09620091
Patent No. 6716811
GENERAL INFORMATION:
APPLICANT: CWIRLA, STEVEN E.
APPLICANT: BALU, PALANI
APPLICANT: DUFFIN, DAVID J.
APPLICANT: PIPLANI, SONILA
APPLICANT: MERRILL, BARBARA MCEOWEN
APPLICANT: SCHATZ, PETER JOSEPH
TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY

;; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
;; FILE REFERENCE: 0300-0014
;; CURRENT APPLICATION NUMBER: US/09/620,091
;; CURRENT FILING DATE: 2000-07-20
;; NUMBER OF SEQ ID NOS: 491
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO: 436
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: peptide
US-09-620-091-436

Query Match 30.6%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HNDSPV 6
|||:
1 HNSSPM 6

Db 1 HNSSPM 6

RESULT 12
US-09-908-322-53
; Sequence 53, Application US/09908322
; Patent No. 6783956
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowicz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/908,322
; FILING DATE: 17-JUL-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,392
; FILING DATE: 22-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7336-123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:

US-09-908-322-53

Query Match 30.6%; Score 26; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 VRTEQ 11
|||:
5 VRTEQ 10

Db 5 VRTEQ 10

RESULT 13
US-09-620-091-172
; Sequence 172, Application US/09620091
; Patent No. 6716811
; GENERAL INFORMATION:
; APPLICANT: CWRILA, STEVEN E.
; APPLICANT: BALU, PALANI
; APPLICANT: DUFFIN, DAVID J.
; APPLICANT: PIPLANI, SUNILA
; APPLICANT: MERRILL, BARBARA MCEOWEN
; APPLICANT: SCHATZ, PETER JOSEPH
; TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
; TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
; FILE REFERENCE: 0300-0014
; CURRENT APPLICATION NUMBER: US/09/620,091
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 172
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-620-091-172

Query Match 30.6%; Score 26; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HNDSPV 6
|||:
2 HNSSPM 7

Db 2 HNSSPM 7

RESULT 14
US-08-321-668-28
; Sequence 28, Application US/08321668
; Patent No. 3663859
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BRAKEBUSCH, Cord
; APPLICANT: VARPOLOMEY, Eugene
; APPLICANT: BATKIN, Michael
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/321,668
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: /note= hu p55 TNF-R mutant
OTHER INFORMATION: construct V 173 P
US-08-321-668-28

Query Match 30.6%; Score 26; DB 1; Length 14;
Best Local Similarity 41.7%; Pred. No. 4.2e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 DSPVTEQOATT 14
::|||
Db 2 ENPKGTDSGTT 13

RESULT 15
US-08-837-941-28
Sequence 28, Application US/08837941
Patent No. 5766917
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BRAKEBUSCH, Cord
APPLICANT: VARFOLOMEV, Eugene
APPLICANT: BATKIN, Michael
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF
TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,941
FILING DATE: 28-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/321,668
FILING DATE: 12-OCT-1994
APPLICATION NUMBER: IL 107268
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=13
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: /note= hu p55 TNF-R mutant
OTHER INFORMATION: construct V 173 P
US-08-837-941-28

Query Match 30.6%; Score 26; DB 1; Length 14;
Best Local Similarity 41.7%; Pred. No. 4.2e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 DSPVTEQOATT 14
::|||
Db 2 ENPKGTDSGTT 13

Search completed: December 12, 2005, 21:00:45
Job time : 27 secs

GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: December 12, 2005, 20:30:45 ; Search time 92.6667 Seconds
(without alignments)
67.634 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNDSPVTEQQATTW 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 324073

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	15	US-10-758-165-2	Sequence 2, Appl1
2	48	56.5	15	US-10-758-165-1	Sequence 1, Appl1
3	39	45.9	15	US-10-758-165-7	Sequence 7, Appl1
4	37	43.5	15	US-10-758-165-3	Sequence 3, Appl1
5	35	41.2	15	US-10-052-788-4	Sequence 4, Appl1
6	32	37.6	11	US-10-381-089-18	Sequence 18, Appl1
7	32	37.6	15	US-10-381-089-8	Sequence 8, Appl1
8	30	35.3	10	US-10-452-510-65	Sequence 65, Appl1
9	30	35.3	10	US-10-617-334-65	Sequence 65, Appl1
10	30	35.3	10	US-10-744-465-65	Sequence 65, Appl1
11	30	35.3	10	US-10-833-679-65	Sequence 65, Appl1
12	30	35.3	10	US-10-818-279-65	Sequence 65, Appl1
13	28.5	33.5	12	US-10-262-794A-2	Sequence 2, Appl1
14	28	32.9	9	US-09-900-590-88	Sequence 88, Appl1
15	28	32.9	9	US-10-012-806A-39	Sequence 39, Appl1
16	28	32.9	9	US-10-305-231-88	Sequence 88, Appl1
17	28	32.9	9	US-10-463-847-88	Sequence 88, Appl1
18	28	32.9	10	US-10-432-234A-250	Sequence 250, Appl1
19	27	31.8	9	US-09-842-776A-39	Sequence 39, Appl1
20	27	31.8	9	US-10-239-656-31	Sequence 31, Appl1
21	27	31.8	9	US-10-239-656-41	Sequence 41, Appl1
22	27	31.8	9	US-10-467-546-21	Sequence 21, Appl1
23	27	31.8	9	US-10-666-332-21	Sequence 21, Appl1
24	27	31.8	10	US-10-432-234A-249	Sequence 249, Appl1
25	27	31.8	13	US-09-851-138-166	Sequence 166, Appl1
26	27	31.8	13	US-09-899-046-244	Sequence 244, Appl1
27	27	31.8	13	US-09-878-281-244	Sequence 244, Appl1

28	27	31.8	13	3	US-09-873-224-244	Sequence 244, App
29	27	31.8	14	5	US-10-808-187-1344	Sequence 1344, App
30	27	31.8	14	5	US-10-807-807-1344	Sequence 1344, App
31	26	30.6	9	4	US-10-117-937-560	Sequence 560, App
32	26	30.6	9	4	US-10-428-335-103	Sequence 103, App
33	26	30.6	9	5	US-10-883-020-19	Sequence 19, App
34	26	30.6	9	6	US-11-067-064-560	Sequence 560, App
35	26	30.6	9	6	US-11-067-159-560	Sequence 560, App
36	26	30.6	10	3	US-09-908-332-53	Sequence 53, App
37	26	30.6	10	3	US-09-783-931-53	Sequence 53, App
38	26	30.6	10	4	US-10-117-937-561	Sequence 561, App
39	26	30.6	10	5	US-10-659-207-436	Sequence 436, App
40	26	30.6	10	6	US-11-067-064-561	Sequence 561, App
41	26	30.6	10	6	US-11-067-159-561	Sequence 561, App
42	26	30.6	11	4	US-10-203-754A-7	Sequence 7, Appl1
43	26	30.6	11	4	US-10-607-834-11	Sequence 11, Appl1
44	26	30.6	12	5	US-10-468-543-9	Sequence 9, Appl1
45	26	30.6	12	5	US-10-659-207-172	Sequence 172, App

ALIGNMENTS

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RESULT 1
US-10-758-165-2
; Sequence 2, Application US/10758165
; Publication No. US20050196616A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-2

Query Match      100.0%; Score 85; DB 5; Length 15;
Beet Local Similarity 100.0%; Pred. NO. 6.3e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HNDSPVTEQQATTW 15
      |||||
Db      1 HNDSPVTEQQATTW 15

RESULT 2
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196616A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1

Query Match      56.5%; Score 48; DB 5; Length 15;
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Best Local Similarity 61.5%; Pred. No. 0.23;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 NDSFVTEQOATT 14
|||:|:|
Db 2 NDSPIQTDQYTT 14

RESULT 3
US-10-758-165-7
; Sequence 7, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammetberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-7

Query Match 45.9%; Score 39; DB 5; Length 15;
Best Local Similarity 46.2%; Pred. No. 9;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFVTEQOATT 14
|||:|:|
Db 2 NDAVQADRHSTT 14

RESULT 4
US-10-758-165-3
; Sequence 3, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammetberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-3

Query Match 43.5%; Score 37; DB 5; Length 15;
Best Local Similarity 53.8%; Pred. No. 20;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFVTEQOATT 14
|||:|:|
Db 2 NNVLQTDQOATT 14

RESULT 5
US-10-052-788-4
; Sequence 4, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
; APPLICANT: Gershwin, Laurel J.
; APPLICANT: Pettigrew, Howard David

; APPLICANT: Kalina, Warren V.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; TITLE OF INVENTION: Induction of Anti-IgE Antibodies
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052,788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:epitope peptide
; OTHER INFORMATION: P4, early portion of C4 of equine IgE epsilon
US-10-052-788-4

Query Match 41.2%; Score 35; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 VTEQOATT 14
|||:|:|
Db 1 IQTDQOATT 9

RESULT 6
US-10-381-089-18
; Sequence 18, Application US/10381089
; Publication No. US20040053276A1
; GENERAL INFORMATION:
; APPLICANT: ITO, Yasuaki
; APPLICANT: TANAKA, Hideyuki
; APPLICANT: NISHIMURA, Ateushi
; APPLICANT: OGI, Kazuhito
; TITLE OF INVENTION: Tissue specific novel secretory polypeptide and its DNA
; FILE REFERENCE: 2789 USOP
; CURRENT APPLICATION NUMBER: US/10/381,089
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2000-293985
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: JP 2000-302839
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide Cpp1-2
US-10-381-089-18

Query Match 37.6%; Score 32; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 11e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPVTEQQA 12
|||:|:|
Db 2 SPVTEKQA 10

RESULT 7
US-10-381-089-8
; Sequence 8, Application US/10381089
; Publication No. US20040053276A1
; GENERAL INFORMATION:
; APPLICANT: ITO, Yasuaki
; APPLICANT: TANAKA, Hideyuki
; APPLICANT: NISHIMURA, Ateushi
; APPLICANT: OGI, Kazuhito
; TITLE OF INVENTION: Tissue specific novel secretory polypeptide and its DNA

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FILE REFERENCE: 2789 USOP
; CURRENT APPLICATION NUMBER: US/10/361,089
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2000-293985
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: JP 2000-302839
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human
US-10-381-089-8

Query Match      37.6%; Score 32; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 SPVTEQQA 12
      ||| |||
Db      1 SPILTEKQA 9

RESULT 8
US-10-452-510-65
; Sequence 65, Application US/10452510
; Publication No. US20040005666A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
; FILE REFERENCE: 760050-93
; CURRENT APPLICATION NUMBER: US/10/452,510
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 09/526,193
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-452-510-65

Query Match      35.3%; Score 30; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSPVTEQQA 11
      ||| |||
Db      1 NDEVTRERQ 10

RESULT 9
US-10-617-334-65
; Sequence 65, Application US/10617334
; Publication No. US20040058869A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
; FILE REFERENCE: 760050-91
; CURRENT APPLICATION NUMBER: US/10/617,334
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 09/526,193
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; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: PatentIn 3.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-334-65

Query Match      35.3%; Score 30; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSPVTEQQA 11
      ||| |||
Db      1 NDEVTRERQ 10

RESULT 10
US-10-744-465-65
; Sequence 65, Application US/10744465
; Publication No. US20040157250A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; APPLICANT: Pinstone, Simon N.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
; FILE REFERENCE: 760050-92
; CURRENT APPLICATION NUMBER: US/10/744,465
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: 10/617,334
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 09/526,193
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-744-465-65

Query Match      35.3%; Score 30; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSPVTEQQA 11
      ||| |||
Db      1 NDEVTRERQ 10

RESULT 11
US-10-833-679-65
; Sequence 65, Application US/10833679
; Publication No. US20040185508A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
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SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
US-10-262-794A-2

Query Match 33.5% Score 28.5; DB 4; Length 12;
Best Local Similarity 53.8%; Pred. No. 5.1e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy 3 DSPVTEQOATW 15
|||
3 DSP---EVSITW 12

RESULT 14

US-09-900-590-88
Sequence 88, Application US/09900590
Publication No. US20030028009A1

GENERAL INFORMATION:
APPLICANT: Huse, William D.

GLaser, Scott M.

TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

Antibodies, Nucleic Acids Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/900,590

FILING DATE: 06-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/016,061

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IX 2965

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 88:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 88:

US-09-900-590-88

Query Match 32.9% Score 28; DB 3; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.7e+06;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 QOATW 15
||:|:|
1 QOATW 6

RESULT 15

US-10-012-806A-39
Sequence 39, Application US/10012806A
Publication No. US20030125518A1

GENERAL INFORMATION:

APPLICANT: CREVICOER, HARRY

TITLE OF INVENTION: SURFACE SIMULATION SYNTHETIC PEPTIDES USEFUL IN THE

TITLE OF INVENTION: TREATMENT OF HYPER-VARIABLE VIRAL PATHOGENS

FILE REFERENCE: 2001-Crev1

CURRENT APPLICATION NUMBER: US/10/012,806A

CURRENT FILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 39

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-012-806A-39

Query Match 32.9% Score 28; DB 4; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.7e+06;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SPVTEQ 11
:|:|:|
Db 1 NPCRTEQ 8

Search completed: December 12, 2005, 21:05:29
Job time : 93.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 12, 2005, 21:00:56 ; Search time 4.66667 Seconds
(without alignments)
17,950 Million cell updates/sec

Title: US-10-758-165a-2
Perfect score: 85
Sequence: 1 HNDSPVTEQQTW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 8641

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCCT_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	31.8	9	US-11-108-135-12	Sequence 12, Appl
2	24	28.2	13	US-10-511-559-627	Sequence 627, App
3	24	28.2	13	US-10-511-559-628	Sequence 628, App
4	23	27.1	13	US-10-511-559-626	Sequence 626, App
5	22	25.9	9	US-11-010-748A-270	Sequence 270, App
6	22	25.9	12	US-11-058-735-37	Sequence 37, Appl
7	22	25.9	13	US-10-511-559-625	Sequence 625, App
8	21	24.7	9	US-10-997-201A-39	Sequence 39, Appl
9	21	24.7	9	US-11-093-274-18	Sequence 752, Appl
10	21	24.7	13	US-10-511-559-752	Sequence 752, App
11	21	24.7	13	US-10-511-559-753	Sequence 753, App
12	21	24.7	13	US-10-511-559-754	Sequence 754, App
13	21	24.7	13	US-10-511-559-755	Sequence 755, App
14	21	24.7	15	US-11-006-119-37	Sequence 37, Appl
15	20	23.5	6	US-11-129-143-161	Sequence 161, App
16	20	23.5	6	US-11-129-143-162	Sequence 162, App
17	20	23.5	6	US-11-129-143-163	Sequence 163, App
18	20	23.5	6	US-11-129-143-164	Sequence 164, App
19	20	23.5	6	US-11-129-143-165	Sequence 165, App
20	20	23.5	8	US-11-129-143-166	Sequence 166, App
21	20	23.5	8	US-10-989-226-49	Sequence 49, Appl
22	20	23.5	9	US-10-989-226-50	Sequence 50, Appl
23	20	23.5	9	US-11-010-748A-265	Sequence 265, App
24	20	23.5	9	US-11-010-748A-266	Sequence 266, App
25	20	23.5	9	US-11-010-748A-267	Sequence 267, App

26	20	23.5	9	7	US-11-010-748A-268	Sequence 268, App
27	20	23.5	9	7	US-11-010-748A-271	Sequence 271, App
28	20	23.5	10	7	US-11-053-076-242	Sequence 242, App
29	20	23.5	10	7	US-11-053-076-247	Sequence 247, App
30	20	23.5	10	7	US-11-093-274-16	Sequence 16, Appl
31	20	23.5	10	7	US-11-093-274-17	Sequence 17, Appl
32	20	23.5	12	6	US-11-054-515-3189	Sequence 3189, App
33	20	23.5	12	6	US-11-073-457-84	Sequence 84, Appl
34	20	23.5	13	6	US-10-511-559-882	Sequence 882, App
35	20	23.5	13	6	US-10-511-559-883	Sequence 883, App
36	20	23.5	13	6	US-10-511-559-200	Sequence 200, App
37	20	23.5	13	6	US-10-511-559-201	Sequence 201, App
38	20	23.5	13	6	US-10-511-559-202	Sequence 202, App
39	20	23.5	13	6	US-10-511-559-203	Sequence 203, App
40	20	23.5	13	6	US-10-511-559-882	Sequence 882, App
41	20	23.5	13	6	US-10-511-559-883	Sequence 883, App
42	20	23.5	15	7	US-11-022-562-105	Sequence 105, App
43	20	23.5	15	7	US-11-022-562-106	Sequence 106, App
44	20	23.5	15	7	US-11-022-562-107	Sequence 107, App
45	19	22.4	8	6	US-10-416-047-7	Sequence 7, Appl

ALIGNMENTS

```

RESULT 1
US-11-108-135-12
; Sequence 12, Application US/11108135
; Publication No. US20050260213A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Veri, Maria Concetta
; APPLICANT: Tuailon, Nadine
; APPLICANT: Bonvini, Ezio
; APPLICANT: Stavenhagen, Jeffrey
; APPLICANT: Rankin, Christopher
; TITLE OF INVENTION: Fc-gamma-RIIb-specific antibodies and methods of use thereof
; FILE REFERENCE: 11183-014-999
; CURRENT APPLICATION NUMBER: US/11/108,135
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/562,804
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/582,044
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/582,045
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/654,713
; PRIOR FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 286 Light chain variable region - CDR3
US-11-108-135-12

Query Match      31.8%   Score 27;   DB 7;   Length 9;
Best Local Similarity 66.7%;   Pred. No. 2.8e+04;
Matches 4;   Conservative 1;   Mismatches 1;   Indels 0;   Gaps 0;

QY      10 COATTW 15
Db      1 QOSNTW 6

RESULT 2
US-10-511-559-627
; Sequence 627, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim

```

```
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 627
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
; US-10-511-559-627
```

```
Query Match      28.2%; Score 24; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 NDSVPRTQ 10
Db      5 NDSTNRTK 13
```

```
RESULT 3
; US-10-511-559-628
; Sequence 628, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
; US-10-511-559-628
```

```
Query Match      28.2%; Score 24; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 NDSVPRTQ 10
Db      4 NDSTNRTK 12
```

```
RESULT 4
; US-10-511-559-626
; Sequence 626, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
```

```
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 626
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
; US-10-511-559-626
```

```
Query Match      27.1%; Score 23; DB 6; Length 13;
Best Local Similarity 62.5%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 NDSVPRT 9
Db      6 NDSTNRTK 13
```

```
RESULT 5
; US-11-010-748A-270
; Sequence 270, Application US/11010748A
; Publication No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHAW, Burhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 270
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of seq. No. 263
; US-11-010-748A-270
```

```
Query Match      25.9%; Score 22; DB 7; Length 9;
Best Local Similarity 33.3%; Pred. No. 2; Seq+04;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 HNSDPVTE 9
Db      1 HNESLISSQ 9
```

```
RESULT 6
; US-11-058-735-37
; Sequence 37, Application US/11058735
; Publication No. US20050261475A1
; GENERAL INFORMATION:
```

APPLICANT: TSENG, HUANG-CHUN
APPLICANT: TSAI, LI-HUEI
TITLE OF INVENTION: SOLID-PHASE CAPTURE-RELEASE-TAG METHODS FOR
FILE REFERENCE: PHOSPHOPROTEOMIC ANALYSES
CURRENT APPLICATION NUMBER: US/11/058,735
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,748
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 37
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-058-735-37

Query Match 25.9%; Score 22; DB 7; Length 12;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 DSPVTEQO 11
| : ||| :
Db 2 DAAVTTEER 10

RESULT 7
US-10-511-559-625
Sequence 625, Application US/10511559
Publication No. US20050256304A1
GENERAL INFORMATION:
APPLICANT: JONES, Tim
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis, J.
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: MER-133
CURRENT APPLICATION NUMBER: US/10/511,559
CURRENT FILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: PCT/EP03/04063
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: EP 02008712.8
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: EP 03006554.4
PRIOR FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 1147
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 625
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-625

Query Match 25.9%; Score 22; DB 6; Length 13;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSPT 8
| : ||| :
Db 7 NDSTRT 13

RESULT 8
US-10-997-201A-39
Sequence 39, Application US/10997201A
Publication No. US20050249739A1
GENERAL INFORMATION:
APPLICANT: Marasco, Wayne
APPLICANT: Sui, Jianhua

TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
FILE REFERENCE: 20363-026
CURRENT APPLICATION NUMBER: US/10/997,201A
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: 60/524,840
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 39
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-997-201A-39

Query Match 24.7%; Score 21; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 QOATW 15
| : ||| :
Db 1 QORSNW 6

RESULT 9
US-11-093-274-18
Sequence 18, Application US/11093274
Publication No. US20050266008A1
GENERAL INFORMATION:
APPLICANT: Graziano, Robert
APPLICANT: Cardarelli, Josephine M.
APPLICANT: Kempe, Thomas
APPLICANT: Cutler, Beth
APPLICANT: Srinivasan, Mohan
TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
FILE REFERENCE: 04280/1201101-US1
CURRENT APPLICATION NUMBER: US/11/093,274
CURRENT FILING DATE: 2005-03-28
PRIOR APPLICATION NUMBER: 60/557,741
PRIOR FILING DATE: 2004-03-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.2
SEQ ID NO 18
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-11-093-274-18

Query Match 24.7%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 QOATW 15
| : ||| :
Db 1 QORSNW 6

RESULT 10
US-10-511-559-752
Sequence 752, Application US/10511559
Publication No. US20050256304A1
GENERAL INFORMATION:
APPLICANT: JONES, Tim
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis, J.
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: MER-133
CURRENT APPLICATION NUMBER: US/10/511,559
CURRENT FILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: PCT/EP03/04063
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: EP 02008712.8
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: EP 03006554.4

```
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 752
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-752
```

```
Query Match      24.7%; Score 21; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```
Qy      6 VRTSEQOATT 14
Db      5 VATESSAKT 13
```

RESULT 11

```
US-10-511-559-753
; Sequence 753, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 753
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-753
```

```
Query Match      24.7%; Score 21; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      6 VRTSEQOATT 14
Db      4 VATESSAKT 12
```

RESULT 12

```
US-10-511-559-754
; Sequence 754, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
```

```
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 754
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-754
```

```
Query Match      24.7%; Score 21; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      6 VRTSEQOATT 14
Db      3 VATESSAKT 11
```

RESULT 13

```
US-10-511-559-755
; Sequence 755, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 755
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-755
```

```
Query Match      24.7%; Score 21; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      6 VRTSEQOATT 14
Db      1 VATESSAKT 9
```

RESULT 14

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US-11-006-119-37
; Sequence 37, Application US/11006119
; Publication No. US20050260691A1
; GENERAL INFORMATION:
; APPLICANT: Ndao, Brian
; APPLICANT: Carey, Rebecca
; APPLICANT: Spithill, Terry
; APPLICANT: Li, Hongshan
; APPLICANT: Podust, Vladimir
; APPLICANT: Perichon, Regis
; APPLICANT: Ciplergen Biocystems, Inc.
; TITLE OF INVENTION: Serum Biomarkers for Chagas Disease
; FILE REFERENCE: 016866-012130US
```

```

; CURRENT APPLICATION NUMBER: US/11/006,119
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 60/527,153
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US 60/565,093
; PRIOR FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/625,519
; PRIOR FILING DATE: 2004-11-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:C-terminal
; OTHER INFORMATION: truncation 24.7 kDa fragment of Apolipoprotein A-I
; OTHER INFORMATION: (APOA-I) Chagas disease biomarker tryptic digest
; OTHER INFORMATION: fragment peptide
US-11-006-119-37

```

```

Query Match          24.7%  Score 21;  DB 7;  Length 15;
Best Local Similarity 57.1%  Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

OY      5  PVTEQQ 11
        | : | | |
Db       5  PLRAELQ 11

```

```

RESULT 15
US-11-129-143-161
; Sequence 161, Application US/11/29143
; Publication No. US20050266518a1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: YELISEEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOL PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Bradyrhizobium japonicum
US-11-129-143-161

```

```

Query Match          23.5%  Score 20;  DB 7;  Length 6;
Best Local Similarity 60.0%  Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

OY      1  HNDSP 5
        | : | |
Db       2  HDDLP 6

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Search completed: December 12, 2005, 21:17:40
Job time : 4.66667 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 12, 2005, 21:05:42 ; Search time 18 Seconds

(without alignments)
80.181 Million cell updates/sec

Title: US-10-758-165A-2

Perfect score: 85

Sequence: 1 HNDSPVTEQQTW 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	27.1	11	2	S71304
2	22	25.9	15	2	PA0062
3	21	24.7	12	2	141235
4	21	24.7	13	2	PH0138
5	20	23.5	11	2	I52980
6	20	23.5	15	2	S39012
7	20	23.5	15	2	B60763
8	19	22.4	9	2	A61357
9	19	22.4	10	2	A61337
10	19	22.4	11	2	A29806
11	19	22.4	11	2	A49037
12	19	22.4	12	2	ES8502
13	19	22.4	13	2	A60458
14	19	22.4	13	2	S36887
15	19	22.4	14	2	S74128
16	19	22.4	14	2	PN0147
17	19	22.4	15	2	JN0263
18	19	22.4	15	2	A36527
19	18	21.2	6	2	S78764
20	18	21.2	11	2	UQ2317
21	18	21.2	12	2	PD0021
22	18	21.2	12	2	C30503
23	18	21.2	13	2	S33273
24	18	21.2	13	2	S47376
25	18	21.2	14	2	PH1625
26	18	21.2	14	2	PH1627
27	18	21.2	15	2	PD0195
28	18	21.2	15	2	S32677
29	18	21.2	15	2	PA0020

ALIGNMENTS

30	18	21.2	15	2	PA0058	protein QF200022 -
31	18	21.2	15	2	A49177	22K protein p1, m
32	18	21.2	15	2	A53594	calnexin - mouse (
33	17	20.0	5	2	PT0580	T-cell receptor be
34	17	20.0	6	2	A31263	dihydrofolate redu
35	17	20.0	7	2	S33246	neuroendocrine pe
36	17	20.0	8	2	PT0030	inulinase (EC 3.2.
37	17	20.0	8	2	I57018	gene Cfr protein
38	17	20.0	9	2	PT0247	Ig heavy chain CRD
39	17	20.0	10	2	S66248	processing enzyme,
40	17	20.0	10	2	A60722	cryptic fibrillar p
41	17	20.0	10	2	S39030	lysoyl-bradykinin -
42	17	20.0	11	2	H54346	pyruvate synthase
43	17	20.0	11	2	B49037	TCR gamma V-J regi
44	17	20.0	11	2	C49037	TCR gamma V-J regi
45	17	20.0	11	2	A61512	variant surface gl

RESULT 1

S71304 amine oxidase (copper-containing) (EC 1.4.3.6) II - *Aspergillus niger* (fragment)
C:Species: *Aspergillus niger*
C:Date: 12-Feb-1998 #sequence_revision 01-May-1998 #text_change 09-Jul-2004

C:Accession: S71304

R:Frederick, I.; Tamaki, H.; Ishida, H.; Pec, P.; Luhova, L.; Tanno, H.; Halata, M.; Asano

Bur, J. Biochem. 237, 255-265, 1996

A>Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the myc

A:Reference number: S71303; PMID:96203933; PMID:8620882

A:Accession: S71304

A:Molecule type: protein

A:Residues: 1-11 <FR>

A:Cross-References: UNIPROT:Q7M504; UNIPARC:UPI000017B3B7

C:Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquione

Query Match 27.1%; Score 23; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 6,7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 NDSF 4

RESULT 2

PA0062 fumarate hydratase (EC 4.2.1.2) - fungus (*Fusarium sporotrichioides*) (fragment)
C:Species: *Fusarium sporotrichioides*
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: PA0062

R:Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichi*

A:Reference number: PA0051

A:Accession: PA0062

A:Molecule type: protein

A:Residues: 1-15 <CHO>

A:Cross-References: UNIPROT:Q7M4Z3; UNIPARC:UPI000017B3FD

C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 25.9%; Score 22; DB 2; Length 15;

Best Local Similarity 55.6%; Pred. No. 1.4e+03;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DB 4 SPVTEQQA 12

1 SOTRTESDA 9

RESULT 3

IA1235

glutamine-tRNA ligase (EC 6.1.1.18) - Escherichia coli (fragment)
C/Species: Escherichia coli
C/Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 03-Jun-2002
C/Accession: 141235
R/Hoben, P.; Uemura, H.; Yamao, F.; Cheung, A.; Swanson, R.; Summer-Smith, M.; Soli, D.
Fed. Proc. 43, 2972-2976, 1984
A/Title: Misaminoacylation by glutamyl-tRNA synthetase: relaxed specificity in wild-type
A/Reference number: 141235; PMID:85051900; PMID:6389180
A/Accession: 141235
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-12 <RES>
A/Cross-references: UNIPARC:UPI000016F1B4; GB:M16470; NID:G146170; PIDN:AAA69006.1; PID:
C/Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 24.7%; Score 21; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 QATW 15
Db 3 EAETW 7

RESULT 4
PH0138
T-cell receptor beta chain V-D-J region C8 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-May-1997
C/Accession: PH0138
R/Martin, R.; Howell, M.D.; Jaraquemada, D.; Flierlge, M.; Richert, J.; Brostoff, S.; Le
J. Exp. Med. 173, 19-24, 1991
A/Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the context
A/Reference number: PH0135; PMID:91086843; PMID:1702137
A/Accession: PH0138
A/Molecule type: mRNA
A/Residues: 1-13 <MAR>
A/Cross-references: UNIPARC:UPI000017C3AC
C/Keywords: T-cell receptor

Query Match 24.7%; Score 21; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 ATTW 15
Db 4 ASTW 7

RESULT 5
I52980
glucocerebrosidase - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C/Accession: I52980; I59771
R/Reiner, O.; Wigderson, M.; Horowitz, M.
DNA 7, 107-116, 1988
A/Title: Structural analysis of the human glucocerebrosidase genes.
A/Reference number: I52980; MUID:88195776; PMID:3359914
A/Accession: I52980
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-11 <RES>
A/Cross-references: UNIPARC:UPI000016A981; GB:M18916; NID:G183023; PIDN:AAA35878.1; PID:
A/Accession: I65971
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-11 <RES>
A/Cross-references: UNIPARC:UPI000016A981; GB:M18917; NID:G183025; PIDN:AAA35879.1; PID:

Query Match 23.5%; Score 20; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SPVR 7
Db 5 SPVR 8

RESULT 6
S39012
proteinnase - Thermus sp.
C/Species: Thermus sp.
C/Date: 18-Feb-1994 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C/Accession: S39012
R/Freeman, S.A.; Peek, K.; Prescott, M.; Daniel, R.
Biochem. J. 295, 463-469, 1993
A/Title: Characterization of a chelator-resistant proteinase from Thermus strain Rt4A2.
A/Reference number: S39012; MUID:94058984; PMID:8240244
A/Accession: S39012
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-15 <FRE>
A/Cross-references: UNIPARC:UPI00000BFF9
A/Note: 13-Ala was also found

Query Match 23.5%; Score 20; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 QATW 15
Db 3 QSPVTW 8

RESULT 7
B60763
endo-1,3-beta-glucanase (EC 3.2.1.-), 40k - Bacillus circulans (strain WL-12) (fragment)
C/Species: Bacillus circulans
C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C/Accession: B60763
R/Fiske, M.J.; Tobey-Fincher, K.L.; Fuchs, R.L.
J. Gen. Microbiol. 136, 2377-2383, 1990
A/Title: Cloning of two genes from Bacillus circulans WL-12 which encode 1,3-beta-glucanase
A/Reference number: A60763; MUID:91178514; PMID:2127800
A/Accession: B60763
A/Molecule type: protein
A/Residues: 1-15 <FIS>
A/Cross-references: UNIPROT:Q7M110; UNIPARC:UPI000017AC94
C/Comment: This bacillus produces up to six different 1,3-beta-glucanases for growth on c
C/Keywords: glycosidase; hydrolase

Query Match 23.5%; Score 20; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 ATTW 15
Db 1 ATTW 4

RESULT 8
A61357
phyllotaerulain - Sauvage's leaf frog
C/Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C/Accession: A61357
R/Anastasi, A.; Bertecchini, G.; Cei, J.M.; De Caro, G.; Erspamer, V.; Impicciatore, M.
Br. J. Pharmacol. 37, 198-206, 1969
A/Title: Structure and pharmacological actions of phyllotaerulain, a caerulein-like nona
A/Reference number: A61357; MUID:70005484; PMID:5824931
A/Accession: A61357
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <ANA>
A/Cross-references: UNIPROT:Q7LZC4; UNIPARC:UPI000017668D

C:Superfamily: gaetrin
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotein
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Binding site: sulfate (Tyr) (covalent) #status experimental
F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 22.4% Score 19; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 QOATW 15
DB 1 QDYTGW 6

RESULT 9

A61337 caerulein - frog (Hyla caerulea)

C:Species: Hyla caerulea

C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999

C:Accession: A61337

R:Anastasi, A.; Erxler, V.; Edean, R.

Arch. Biochem. Biophys. 125, 57-68, 1968

A:Title: Isolation and amino acid sequence of caerulein, the active decapeptide of the

A:Reference number: A61337; MUID:68238534; PMID:5649531

A:Accession: A61337

A:Molecule type: protein

A:Residues: 1-10 <ANA>

A:Cross-references: UNIPARC:UPI00001260CC

C:Comment: The last five amino acids and the carboxyl terminal amide group of this neuro

C:Superfamily: gaetrin

C:Keywords: amidated carboxyl end; antihypertensive; neuropeptide; pyroglutamic acid; se

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:4/Binding site: sulfate (Tyr) (covalent) #status experimental

F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 22.4% Score 19; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.1e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 EQOATW 15
DB 1 QOQYTGW 7

RESULT 10

A29806 acidic proline-rich protein HP43b - golden hamster (fragment)

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993

C:Accession: A29806

R:Mechanico, H.; Am, D.K.; Butler, L.G.; Rogler, J.; Carlson, D.M.

J. Biol. Chem. 262, 12344-12350, 1987

A:Title: Induction of proline-rich proteins in hamster salivary glands by isoproterenol

A:Reference number: A29811; MUID:87308247; PMID:3040740

A:Accession: A29806

A:Molecule type: protein

A:Residues: 1-11 <MEH>

A:Cross-references: UNIPARC:UPI000017C60F

Query Match 22.4% Score 19; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HNDSP 5
DB 4 YEDSP 8

RESULT 11

A49037 TCR gamma V-J region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C:Accession: A49037

R:Esquerre, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M.

Bar. J. Immunol. 22, 491-498, 1992

A:Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T

A:Reference number: A49037; MUID:92164730; PMID:1311262

A:Accession: A49037

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-11 <EZO>

A:Cross-references: UNIPARC:UPI00001154FA; GB:S90637; NID:9246288; PIDN:AAB21547.1; PID:

A:Experimental source: dendritic epidermal T-cell lines

A>Note: sequence extracted from NCBI backbone (NCBI:90637, NCBI:90641)

Query Match 22.4% Score 19; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 11 QATW 15
DB 6 RSTW 10

RESULT 12

B58502 43.2K bile stone protein - unidentified bacterium (fragment)

C:Species: unidentified bacterium

C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004

C:Accession: B58502

R:Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A:Description: The proteins of kidney and gallbladder stones.

A:Reference number: A58501

A:Accession: B58502

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <BIN>

A:Cross-references: UNIPROT:Q7MID0; UNIPARC:UPI000017ABD4

A:Experimental source: human bile with stones

A>Note: a secondary sequence DVKIGVAGS was also found

Query Match 22.4% Score 19; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NDSPV 6
DB 6 NEQPV 10

RESULT 13

A60458 protocatechuate 3,4-dioxygenase (EC 1.13.11.3) alpha chain - Moraxella sp. (strain G02)

N:Alternate names: protocatechuate oxygenase

C:Species: Moraxella sp.

C:Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 07-May-1999

C:Accession: A60458

R:Sterjades, R.; Belmont, J.

Appl. Environ. Microbiol. 55, 340-347, 1989

A:Title: Occurrence of two different forms of protocatechuate 3,4-dioxygenase in a Morax

A:Reference number: A60458; MUID:89245845; PMID:2541659

A:Accession: A60458

A:Molecule type: protein

A:Residues: 1-13 <STB>

A:Cross-references: UNIPARC:UPI000017A9FE

A>Note: two forms P and G of the alpha subunit yielded identical amino terminal sequence

Query Match 22.4% Score 19; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 4.1e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 RTEQOATW 15
 | | : | :
 Db 3 RTAKPAPTY 11

RESULT 14

S36887
 ribosomal protein S14 - Mycobacterium bovis (fragments)
 C:Species: Mycobacterium bovis
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
 C:Accession: S36887
 R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
 FEBS Lett. 331, 9-14, 1993
 A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobac
 A:Reference number: S36887; MUID:94009653; PMID:8405418
 A:Accession: S36887
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-2;3-12;13 <OH>
 A:Cross-references: UNIPARC:UPI0000061DAD; UNIPARC:UPI000011EC65; UNIPARC:UPI000017AD47
 C:Keywords: protein biosynthesis; ribosome

Query Match 22.4%; Score 19; DB 2; Length 13;
 Best Local Similarity 37.5%; Pred. No. 4.1e+03;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 6 VRTEQOAT 13
 | : : : :
 Db 6 VKNGRRAT 13

RESULT 15

S74128
 superoxide dismutase (EC 1.15.1.1) 1 (Ni) - Streptomyces coelicolor (fragment)
 C:Species: Streptomyces coelicolor
 C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
 C:Accession: S74128
 R:Kim, B.U.; Kim, H.P.; Hah, Y.C.; Roe, J.H.
 Eur. J. Biochem. 241, 178-185, 1996
 A:Title: Differential expression of superoxide dismutases containing Ni and Fe/Zn in Str
 A:Reference number: S74128; MUID:97054607; PMID:8898904
 A:Accession: S74128
 A:Molecule type: protein
 A:Residues: 1-14 <KIM>
 A:Cross-references: UNIPARC:UPI000017AE10
 A:Experimental source: ATCC 10147
 C:Function:
 A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C:Keywords: metalloprotein; nickel; oxidoreductase; tetramer

Query Match 22.4%; Score 19; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HNDSP 5
 | | : | :
 Db 1 HGDLF 5

Search completed: December 12, 2005, 21:18:42
 Job time : 19 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:59:31 ; Search time 114 Seconds
(without alignments)
92.833 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNDSPVTEQQTW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 7855

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	28.2	10	Q9F9H5_HELPY	Q9F9H5 HELPY
2	24	28.2	11	Q6LBJO_MOUSE	Q6LBJO mus musculus
3	23	27.1	11	Q7M504_ASPNG	Q7M504 aspergillus
4	22	25.9	11	Q47602_ECOLI	Q47602 escherichia
5	22	25.9	13	Q50117_MYCLE	Q50117 mycobacteri
6	22	25.9	15	Q7M423_FUSSP	Q7M423 fusarium sp
7	21.5	25.3	15	Q9TS39_GORILL	Q9TS39 gorilla gor
8	21	24.7	9	Q798K5_STRELI	Q798K5 streptomyce
9	21	24.7	9	Q9R635_CHUTR	Q9R635 chlamydia t
10	21	24.7	11	Q5ERD3_LBGRN	Q5ERD3 legionella
11	21	24.7	13	EPE5_HUMAN	EPE5 homo sapien
12	21	24.7	13	Q9SB03_ORISA	Q9SB03 oryza sativ
13	21	24.7	14	Q7IGS6_9HYME	Q7IGS6 andrena n.
14	21	24.7	14	Q9LCS1_AZOVI	Q9LCS1 azotobacter
15	21	24.7	14	Q6SCH4_9GEMI	Q6SCH4 tomato leaf
16	20.5	24.1	14	R1PL_LUPCY	R1PL lupinus cylin
17	20	23.5	8	Q9T2W0_YEAST	Q9T2W0 saccharomyc
18	20	23.5	9	Q71066_CANEA	Q71066 canine dist
19	20	23.5	10	Q86D30_TRYCR	Q86D30 trypanosoma
20	20	23.5	11	Q8TDA8_HUMAN	Q8TDA8 homo sapien
21	20	23.5	12	Q6JDGO_CANFA	Q6JDGO canis famli
22	20	23.5	12	Q9EQV3_MOUSE	Q9EQV3 mus musculu
23	20	23.5	13	Q718T2_9PARA	Q718T2 newcastle d
24	20	23.5	14	SODN_STRGR	SODN streptomyce
25	20	23.5	14	Q7IGM6_9HYME	Q7IGM6 andrena eri
26	20	23.5	14	Q6LDN2_BACST	Q6LDN2 bacillus st
27	20	23.5	15	Q71GV6_9HYME	Q71GV6 andrena sim
28	20	23.5	15	Q71H38_9HYME	Q71H38 andrena aur
29	20	23.5	15	Q9RS31_9DEIN	Q9RS31 thermus ch
30	20	23.5	15	Q7M110_BACCI	Q7M110 bacillus ci
31	19	22.4	7	Q8JEB1_9HIV1	Q8JEB1 human immun

32	19	22.4	9	1	CAER_PHYSA	Q71ZC4 phyllomedus
33	19	22.4	9	2	Q71H00_9HYME	Q71H00 andrena iso
34	19	22.4	10	1	CAE12_LITCI	P62540 litorea cit
35	19	22.4	10	1	CAE12_LITSP	P62541 litorea sp1
36	19	22.4	10	1	CAER_LITXA	P56264 litorea xan
37	19	22.4	10	2	Q9QV65_9MURI	Q9QV65 mus sp. pro
38	19	22.4	10	2	Q33EAI_9NEOB	Q33EAI eleutheroda
39	19	22.4	10	2	P84487_LITCE	P84487 litorea cae
40	19	22.4	12	2	Q7M1D0_9BACT	Q7M1D0 unidentified
41	19	22.4	12	2	Q98Z40_9HIV1	Q98Z40 human immun
42	19	22.4	13	2	Q7YRDI_BISBO	Q7YRDI bison bonas
43	19	22.4	13	2	Q7YR14_BOVIN	Q7YR14 bos taurus
44	19	22.4	13	2	P97140_BORBU	P97140 botreilia bu
45	19	22.4	13	2	Q53557_9PERC	Q53557 channa argu

ALIGNMENTS

```
RESULT 1
Q9F9H5_HELPY PRELIMINARY; PRT; 10 AA.
ID Q9F9H5_HELPY
AC Q9F9H5_
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Glutamate racemase (Fragment).
GN Name=glr;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Indiat75A;
RX MEDLINE=20270152; PubMed=10809702;
RX DOI=10.1128/JB.182.11.3210-3218.2000;
RA Keruliyte D., Mukhopadhyay A.K., Velapattino B., Su W.W., Pan Z.J.,
RA Garcia C., Hernandez V., Valdez Y., Mistry R.S., Gilman R.H., Yuan Y.,
RA Gao H., Alarcon T., Lopez-Brea M., Balakrish Nair G., Chowdhury A.,
RA Datta S., Shirai M., Nakazawa T., Ally R., Segal I., Wong B.C.,
RA Lam S.K., Olat F.O., Boren T., Engstrand L., Torres O., Schneider R.,
RA Thomas J.E., Czinn S., Berg D.E.;
RT "Differences in genotypes of Helicobacter pylori from different human
RT populations."
RL U. Bacteriol. 182:3210-3218(2000).
DR EMBL; AF190663; AAG18486.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 10 AA; 1273 MW; CAD126337B133DC6 CRC64;

Query Match 28.2%; Score 24; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 3.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 EQQTW 15
|:|:|
Db 1 EKQAKW 7

RESULT 2
Q6LBJO_MOUSE PRELIMINARY; PRT; 11 AA.
ID Q6LBJO_MOUSE
AC Q6LBJO_
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Topoisomerase I (Fragment).
GN Name=Top1; Synonyms=TOP;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

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RN [1]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=Balb/c; TISSUE=Liver;
RX MEDLINE=94250690; PubMed=8193161;
RA Baumgartner B., Heiland S., Kunze N., Richter A., Knippers R.;
RT "Conserved regulatory elements in the type I DNA topoisomerase gene
RT promoter of mouse and man.";
RL Biochim. Biophys. Acta 1218:123-127(1994).
RN [2]
RC NUCLEOTIDE SEQUENCE.
RP STRAIN=Balb/c; TISSUE=Liver;
RA Baumgartner B.; PubMed=1995588;
RX MEDLINE=91139577; PubMed=1995588;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL, M63620; AAA24558.1; -, Genomic_DNA.
KM NON_TER 11 11
SQ SEQUENCE 11 AA; 1240 MW; 95183AD41E721EA CRC64;

Query Match 28.2%; Score 24; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDS 4
Db 7 HNDS 10

RESULT 3
Q7M504_ASPNG PRELIMINARY; PRT; 11 AA.
AC Q7M504;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE Amino oxidase (Copper-containing) (EC 1.4.3.6) II (Fragment).
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiaceae; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RC PROTEIN SEQUENCE.
RP Fiebert I., Tamaki H., Ishida H., Pec P., Luhova L., Tsuno H.,
RA Halata M., Asano Y., Kato Y., Matsushita K., Toyana H., Kumagai H.,
RA Adachi O.;
RT "Two distinct quinoprotein amino oxidases are induced by n-butylamine
RT in the mycelia of Aspergillus niger AKU 3392: purification,
RT characterization, cDNA cloning and sequencing.";
RL Eur. J. Biochem. 237:255-265(1996).
DR GO; GO:0008131; F:amine oxidase activity; IEA.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1158 MW; 21BBPDC4472DC7 CRC64;

Query Match 27.1%; Score 23; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NDSP 5
Db 1 NDSP 4

RESULT 4
Q47602_ECOLI PRELIMINARY; PRT; 11 AA.
AC Q47602;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Release protein (Fragment).

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GN Name=Rease;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL, M63620; AAA24558.1; -, Genomic_DNA.
KM NON_TER 11 11
SQ SEQUENCE 11 AA; 1412 MW; 80ABBI90C736DAAA CRC64;

Query Match 25.9%; Score 22; DB 2; Length 11;
Best Local Similarity 44.4%; Pred. No. 7.7e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 7 RTEQATTW 15
Db 3 RDDQLFTLW 11

RESULT 5
Q50117_MYCLE PRELIMINARY; PRT; 13 AA.
AC Q50117;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE U650W.
OS Mycobacterium lepreae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RC NUCLEOTIDE SEQUENCE.
RA Robinson K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U15184; AAA63055.1; -, Genomic DNA.
SQ SEQUENCE 13 AA; 1503 MW; CAABP1429DED5412 CRC64;

Query Match 25.9%; Score 22; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 9.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DSPVR 7
Db 3 DEPRV 7

RESULT 6
Q7M423_FUSSP PRELIMINARY; PRT; 15 AA.
AC Q7M423;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Fumarate hydratase (EC 4.2.1.2) (Fragment).
OS Fusarium sporotrichioides.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocremycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5514;
RN [1]
RC PROTEIN SEQUENCE.
RA Chow L.P., Fukaya N., Sugiyura Y., Ueno Y., Tabuchi K., Tsugita A.;
RL Submitted (OCT-1994) to the PIR data bank.

```

DR PIR: PA0062; PA0062.
DR GO: GO:0004333; F: fumarate hydratase activity; IEA.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1668 MW; 805C8118C239DE05 CRC64;
Query Match 25.9%; Score 22; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 SPVTEQQA 12
DB 1 SQRTESDA 9
RESULT 7
ID Q9TS39_9PRIM PRELIMINARY; PRT; 15 AA.
AC Q9TS39;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Dopamine D5 (Fragment).
OS Gorilla gorilla (Gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Gorilla.
OX NCBI_TaxID=9593;
RN NCBI
RP NUCLEOTIDE SEQUENCE.
RX NGUYEN T., Sunahara R., Marchese A., Van Tol H.H., Seeman P.,
RA O'Dowd B.F.;
RT "Transcription of a human dopamine D5 pseudogene";
RL Biochem. Biophys. Res. Commun. 181:16-21(1991).
FT NON_TER 1
SQ SEQUENCE 15 AA; 1637 MW; 39D8326BA63BB90B CRC64;
Query Match 25.3%; Score 21.5; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 7; Gaps 1;
QY 1 HNDSPVTEQOATW 15
DB 1 HRD-----QNASW 8
RESULT 8
ID Q798K5_STRLI PRELIMINARY; PRT; 9 AA.
AC Q798K5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE AmlB protein (Fragment).
GN Name=AmlB.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1916;
RN NCBI
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96332731; PubMed=9666116; DOI=10.1016/S0378-1119(98)00265-0;
RA Yin X.H., Getraud C., Franco F.X., Guerin M., Virolle M.J.;
RT "amC, another amyloid gene maps close to the amlB locus in
ST Streptomyces lividans RK24.";
RL Gene 215:171-180(1998).
DR EMBL; Z86113; CAB06815.1; -; Genomic_DNA.
FT NON_TER 9
SQ SEQUENCE 9 AA; 970 MW; F334C75A1A44871 CRC64;
Query Match 24.7%; Score 21; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 NDSPVR 7
DB 4 NTSPAR 9
RESULT 9
ID Q9R635_CHLTR PRELIMINARY; PRT; 9 AA.
AC Q9R635;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Major outer membrane protein variable domain IV, MOMP VD IV
DE (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN NCBI
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92040090; PubMed=1718870;
RA Peterson E.M., Cheng X., Markoff B.A., Fielder T.J., de la Maza L.M.;
RT "Functional and structural mapping of Chlamydia trachomatis species-
RT specific major outer membrane protein epitopes by use of neutralizing
RT monoclonal antibodies";
RL Infect. Immun. 59:4147-4153(1991).
DR PIR: S16034; S16034.
FT NON_TER 1
SQ SEQUENCE 9 AA; 976 MW; 9C61B041B7645361 CRC64;
Query Match 24.7%; Score 21; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 TTW 15
DB 1 TTW 3
RESULT 10
ID Q5EDJ3_LEGN PRELIMINARY; PRT; 11 AA.
AC Q5EDJ3;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE Putative acyl carrier protein (Fragment).
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN NCBI
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=02/41;
RA Newton H.V., Hartland E.L.;
RT "Subtractive hybridization reveals DNA fragments present in Legionella
RT pneumophila, strain 02/41, and absent in Legionella micdadei, strain
RT 02/42.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY902880; AA083806.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1159 MW; DCC78E8601ADC66 CRC64;
Query Match 24.7%; Score 21; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 9 EQOAT 13
DB 3 QOQAT 7

```
RESULT 11
EP65 HUMAN STANDARD; PRT; 13 AA.
AC P54963;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Erythrocyte 65 kDa protein (P65) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=90004678; PubMed=2507249;
RA Hart G.W., Haltiwanger R.S., Holt G.D., Kelly W.G.;
RT "Nucleoplasmic and cytoplasmic glycoproteins.";
RL Ciba Found. Symp. 145:102-118(1989);
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR GO: GO:0005737; C:cytoplasm; NAS.
KW Direct protein sequencing; Glycoprotein.
FT CARBOHYD 2
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1300 MW; D0B873344C61A776 CRC64;

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DSPV 6
Db 1 DSPV 4

RESULT 12
Q9SB03 ORYSA PRELIMINARY; PRT; 13 AA.
ID Q9SB03 ORYSA PRELIMINARY;
AC Q9SB03;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Waxy (Fragment).
GN Name=Waxy;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98384837; PubMed=9718725;
RA Hirano H., Eiyunghi M., Sano Y.;
RT "A single base change altered the regulation of the Waxy gene at the
RT post-transcriptional level during domestication of rice.";
RL Mol. Biol. Evol. 15:978-987(1998).
DR EMBL; AB008794; BAA32471.1; -; Genomic_DNA.
DR Gramene; Q9SB03; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1281 MW; 999F8DEB570FC5A1 CRC64;

Query Match
Best Local Similarity 24.7%; Score 21; DB 2; Length 13;
Matches 45.5%; Pred. No. 1.4e+04;
```

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Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 SPVTEGOAT 14
Db 2 SALTSQLATS 12

RESULT 13
Q7IGS6 9HYME PRELIMINARY; PRT; 14 AA.
ID Q7IGS6 9HYME PRELIMINARY;
AC Q7IGS6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena n. sp. 'goth'.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena; Callandrena.
OX NCBI_TaxID=205171;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Iarkin L.L., Neff J.L., Simpson B.B.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF04376; AAQ07723.1; -; Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1692 MW; 79E3B922A4E7BE5B CRC64;

Query Match
Best Local Similarity 24.7%; Score 21; DB 2; Length 14;
Matches 37.5%; Pred. No. 1.5e+04;

QY 2 NDSPV RTE 9
Db 6 NEIPIMTK 13

RESULT 14
Q9LCS1 AZOVI PRELIMINARY; PRT; 14 AA.
ID Q9LCS1 AZOVI PRELIMINARY;
AC Q9LCS1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Levan sucrase (Fragment).
GN Name=sacB;
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=DWI136;
RA Maldonado R., Casadesus J.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ249381; CAB76429.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1623 MW; 8DC9108BA1B18745 CRC64;

Query Match
Best Local Similarity 24.7%; Score 21; DB 2; Length 14;
Matches 40.0%; Pred. No. 1.5e+04;

QY 2 NDSPV RTEQ 11
Db 5 NDSILMDQTO 14

RESULT 15
```


Q6SCH4_9GEMI
 ID Q6SCH4_9GEMI PRELIMINARY; PRT; 14 AA.
 AC Q6SCH4;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Coat protein (Fragment).
 GN Name=AV1;
 OS Tomato leaf curl Sinaloa virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=71186;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Nil;
 RX PubMed=15789265; DOI=10.1007/s00705-005-0509-x;
 RA Rojas A., Kvarnheden A., Marcenaro D., Valkonen J.P.T.;
 RT "Sequence characterization of Tomato leaf curl Sinaloa virus and
 RT Tomato bevere leaf curl virus: Phylogeny of New World begomoviruses
 RT and detection of recombination.";
 RL Arch. Virol. 150:1281-1291(2005).
 DR EMBL; AJ508778; CAD48516.1; -; Genomic_DNA.
 KW Capsid protein.
 FT NON_TER 14 14
 SO SEQUENCE 14 AA; 1573 MW; 571284313A0594D3 CRC64;
 QY 11 QATTW 15
 :|||
 Db 7 KATAW 11

Search completed: December 12, 2005, 21:17:23
 Job time : 116 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:37:19 ; Search time 81.3362 Seconds
(without alignments)
81.030 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNSDPVREOCATTW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	15	ADRI0602	Adri0602 Cat IGE e
2	85	100.0	431	ADG73237	Adg73237 Cat immun
3	85	100.0	496	ABP96580	Abp96580 Cat IGE h
4	85	100.0	496	ABU09338	Abu09338 Feline Ig
5	85	100.0	496	ABU09336	Abu09336 Feline Ig
6	85	100.0	496	ADG73251	Adg73251 Cat parti
7	85	100.0	496	ADG73225	Adg73225 Cat parti
8	48	56.5	15	ADRI0601	Adri0601 Dog IGE e
9	48	56.5	312	AAI79995	Aai79995 Dog immun
10	48	56.5	417	AAW23067	Aaw23067 Canine Ig
11	48	56.5	426	AAK97753	Aak97753 Canine Ig
12	48	56.5	426	ABP96583	Abp96583 Dog IGE h
13	47	55.3	84	ABU55745	Abu55745 Tree coct
14	47	54.1	449	ABR60974	Abbr60974 Drosophil
15	45	52.9	321	AAE12007	Aae12007 Streptomy
16	45	52.9	321	ABG73760	Abg73760 S. catlie
17	44	51.8	673	ABR71738	Abbr71738 Drosophil
18	43	50.6	470	ADG27897	Adg27897 Bacterial
19	43	50.6	696	ADK67175	Adk67175 Plant ful
20	42	49.4	87	AAU55965	Aau55965 Propionib
21	42	49.4	87	ABM52485	Abm52485 Propionib
22	42	49.4	178	ABR83494	Abbr83494 Human zin
23	42	49.4	178	ADB65732	Adb65732 Human pro
24	42	49.4	197	ABO60445	Abob60445 Human gen

25	42	49.4	296	ADA54799	Ada54799 Human pro
26	42	49.4	296	AAO27216	Aao27216 Human zin
27	42	49.4	349	AAW79729	Aaw79729 Human pro
28	42	49.4	430	AAW78745	Aaw78745 Human pro
29	42	49.4	536	ADY18750	Ady18750 PRO polyp
30	42	49.4	537	AAE33775	Aae33775 Human nuc
31	41	48.2	70	AAU59982	Aau59982 Propionib
32	41	48.2	152	ABM56501	Abm56501 Propionib
33	41	48.2	152	AAI18098	Aai18098 Peptide #
34	41	48.2	152	ABR37133	Abbr37133 Peptide #
35	41	48.2	152	AAAM3068	Aam3068 Peptide #
36	41	48.2	152	ABR22444	Abbr22444 Protein #
37	41	48.2	152	AAW70271	Aaw70271 Human bon
38	41	48.2	152	AAAM57851	Aam57851 Human bra
39	41	48.2	152	AAAM5733	Aam05733 Peptide #
40	41	48.2	349	AAU30476	Aau30476 Novel hum
41	41	48.2	647	AAAG92695	Aag92695 C glutami
42	41	48.2	812	ABG19065	Abg19065 Novel hum
43	41	48.2	1194	ADP29882	Adp29882 Human sec
44	41	48.2	1527	ABG08603	Abg08603 Novel hum
45	41	48.2	1664	ABG14228	Abg14228 Novel hum

ALIGNMENTS

RESULT 1	ADRI0602	standard; peptide, 15 AA.
ID	ADRI0602	
XX	ADRI0602;	
AC	21-OCT-2004	(first entry)
XX		
DT		
XX		
DE	Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.	
KW	Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma; anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody; cat.	
KM		
XX		
OS	Felis catus.	
XX		
PN	WO2004065936-A2.	
XX		
PD	05-AUG-2004.	
XX		
PF	15-JAN-2004; 2004WO-US003566.	
XX		
PR	16-JAN-2003; 2003US-0440472P.	
XX		
XX	(UNNC-) UNIV NORTH CAROLINA STATE.	
XX		
PI	Hammerberg B,	
XX		
DR	WPI; 2004-593545/57.	
XX		
PT	Novel antibody that specifically binds to mammalian IGE epitope, useful for testing an allergen reactivity of IGE sample, detecting mammalian IGE or treating asthma or anaphylactic shock.	
PT		
XX		
PS	Example 6; Page 9; 14pp; English.	
XX		
CC	The present invention relates to a novel monoclonal antibody (I) that specifically binds to a mammalian IGE epitope, where the epitope is between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.	
CC	(I) is useful for testing an allergen reactivity of an IGE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (I) is also useful for detecting mammalian IGE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine IGE corresponding to amino acid residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from	

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IgE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IgE. The present sequence is the
CC cat IgE 5.91 recognition site.

XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 85; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HNDSPVTEQOATW 15
Db 1 HNDSPVTEQOATW 15
|||||

RESULT 2

ADG73237 standard; protein; 431 AA.

XX
AC ADG73237;

DT 11-MAR-2004 (first entry)

DE Cat immunoglobulin E (IgE) constant region.

XX antiallergic; IgE-modulator; vaccine; feline; IgE; immunoglobulin E;
KM immune response; IgE-mediated response; allergy; cat; constant region.

XX
OS Felis catus.

XX
PN US2003216565-A1.

XX
PD 20-NOV-2003.

XX
PF 07-APR-2003; 2003US-00409772.

XX
PR 07-JAN-1999; 99US-0115033P.

XX
PR 07-JAN-2000; 2000US-00479614.

XX
PA (MCCA/) MCCALL C.

XX
PA (WEBE/) WEBER E.

XX
PI McCall C, Weber E;

XX
DR WPI; 2004-010802/01.

XX
DR N-PSDB; ADG73236.

PT New isolated nucleic acid molecule encoding a portion of a feline IgE
PT heavy chain protein, useful for treating and/or eliciting feline immune
PT responses for IgE-mediated responses, such as allergies.

XX
PS Claim 12; SEQ ID NO 14; 44pp; English.

CC The invention describes an isolated nucleic acid molecule (I) encoding a
CC portion of a feline IgE heavy chain protein. The methods and compositions
CC of the present invention are useful for eliciting feline immune responses
CC for and/or treating IgE-mediated responses, such as allergies. This is
CC the amino acid sequence of a cat immunoglobulin E (IgE) constant region.

XX
SQ Sequence 431 AA;

Query Match 100.0%; Score 85; DB 8; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HNDSPVTEQOATW 15
Db 362 HNDSPVTEQOATW 376
|||||

RESULT 3

ABP96580
ID ABP96580 standard; protein; 496 AA.

XX
AC ABP96580;

DT 28-MAY-2003 (first entry)

DE Cat IgE heavy chain amino acid sequence SEQ ID NO:25.

XX Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
KM immune response; major histocompatibility complex; MHC; immunogenic;
KM antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
KM dermatological; antiinflammatory; IgE-mediated condition; food allergy;
KM atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KM atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
KM urticaria hives.

XX
OS Felis catus.

XX
PN WO2003015716-A2.

XX
PD 27-FEB-2003.

XX
PF 08-AUG-2002; 2002WO-US026986.

XX
PR 13-AUG-2001; 2001US-0312120P.

XX
PR (IGET-) IGE THERAPEUTICS INC.

XX
PI Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX
DR WPI; 2003-268242/26.

PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
PT against IgE, by identifying peptide eliciting CTL response to IgE
PT peptides naturally presented by major histocompatibility complex class I
PT protein.

XX
PS Example 7; Page 145-147; 187pp; English.

CC The present invention describes a method (M1) for identifying peptides
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
CC E (IgE), comprising providing a test peptide (T) suspected of being able
CC to bind to major histocompatibility complex (MHC) class I molecule, and
CC evaluating (T) for ability to elicit in a mammal a CTL response to
CC naturally processed and presented IgE peptides, where a peptide that
CC induces such a response is identified. Also described are compositions:
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
CC (C2) comprising at least one isolated polynucleotide encoding (I); and
CC (C3) comprising antigen-presenting cells that recognise at least one (I).
CC Where C1-3 are able to bind to at least one MHC class I molecule and to
CC elicit in a mammal a CTL response to naturally processed and presented
CC IgE peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive,
CC vasotropic, dermatological, antiinflammatory and cyostatic activities,
CC and can be used as inducers of a CTL response against IgE, and in
CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as
CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic
CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
CC useful for treating atopic hypersensitivity conditions (such as allergic
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
CC hives). The present sequence represents an IgE heavy chain amino acid
CC sequence, which is given in an example from the present invention

XX
SQ Sequence 496 AA;

Query Match 100.0%; Score 85; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HNDSPVTEQOATW 15
|||||

Db 427 HNDSFVTEQOATW 441

RESULT 4
ABU09338
ID ABU09338 standard; protein; 496 AA.
XX
XX ABU09338;
XX
XX 27-JUN-2003 (first entry)
XX
XX Feline IGE epsilon heavy chain #2.
XX
XX Feline IGE epsilon heavy chain; parasitic infection;
XX IGE-mediated immune response; allergy; neoplasia; vaccine technology;
XX antibody technology; antiallergic; antiparasitic; cytostatic.
XX
XX Felis catus.
XX
XX US2003013183-A1.
XX
XX 16-JAN-2003.
XX
XX 07-JAN-2000; 2000US-00479614.
XX
XX 07-JAN-1999; 99US-0115033P.
XX
XX (MCCA/) MCCALL C.
XX (WEBER/) WEBER E.
XX
XX Mccall C, Weber E;
XX
XX WPI; 2003-391997/37.
XX N-PSDB; ABX95715.
XX
XX New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or
XX light chain protein, useful for treating feline IGE-mediated responses
XX e.g. allergies, parasitic infections or neoplasia.
XX
XX Claim 1; Page 37-39; 45pp; English.
XX
XX The present invention relates to the isolation of feline immunoglobulin E
XX (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the
XX polynucleotide sequences encoding them. The sequences of the invention
XX are useful for treating feline IGE-mediated immune responses (e.g.
XX allergies, parasitic infections or neoplasia), in vaccine technology,
XX small molecule/antibody technology, molecular biology, and various
XX immunological techniques related to feline IGE and its functions. The
XX present sequence represents feline IGE epsilon heavy chain #2
XX
XX Sequence 496 AA;
XX
XX Query Match 100.0%; Score 85; DB 6; Length 496;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-06;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HNDSFVTEQOATW 15
Db 427 HNDSFVTEQOATW 441

RESULT 5
ABU09336
ID ABU09336 standard; protein; 496 AA.
XX
XX ABU09336;
XX
XX 27-JUN-2003 (first entry)
XX
XX Feline IGE epsilon heavy chain #1.
XX
XX Feline IGE epsilon heavy chain; parasitic infection;
XX IGE-mediated immune response; allergy; neoplasia; vaccine technology;
XX

KW antibody technology; antiallergic; antiparasitic; cytostatic.
XX
XX Felis catus.
XX
XX Key Location/Qualifiers
XX Region 66. .496
XX /note= "This sequence is given as SEQ ID No:14 and is
XX specifically claimed in Claim 12"
XX Region 284. .309
XX /note= "This sequence is given as SEQ ID No:11 and is
XX specifically claimed in Claim 9"
XX Region 288. .305
XX /note= "This sequence is given as SEQ ID No:8 and is
XX specifically claimed in Claim 10"
XX Region 291. .302
XX /note= "This sequence is given as SEQ ID No:5 and is
XX specifically claimed in Claim 11"
XX
XX US2003013183-A1.
XX
XX 16-JAN-2003.
XX
XX 07-JAN-2000; 2000US-00479614.
XX
XX 07-JAN-1999; 99US-0115033P.
XX
XX (MCCA/) MCCALL C.
XX (WEBER/) WEBER E.
XX
XX Mccall C, Weber E;
XX
XX WPI; 2003-391997/37.
XX N-PSDB; ABX95713.
XX
XX New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or
XX light chain protein, useful for treating feline IGE-mediated responses
XX e.g. allergies, parasitic infections or neoplasia.
XX
XX Claim 1; Page 24-25; 45pp; English.
XX
XX The present invention relates to the isolation of feline immunoglobulin E
XX (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the
XX polynucleotide sequences encoding them. The sequences of the invention
XX are useful for treating feline IGE-mediated immune responses (e.g.
XX allergies, parasitic infections or neoplasia), in vaccine technology,
XX small molecule/antibody technology, molecular biology, and various
XX immunological techniques related to feline IGE and its functions. The
XX present sequence represents feline IGE epsilon heavy chain #1
XX
XX Sequence 496 AA;
XX
XX Query Match 100.0%; Score 85; DB 6; Length 496;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-06;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HNDSFVTEQOATW 15
Db 427 HNDSFVTEQOATW 441

RESULT 6
ADG73251
ID ADG73251 standard; protein; 496 AA.
XX
XX ADG73251;
XX
XX 11-MAR-2004 (first entry)
XX
XX Cat partial immunoglobulin E (IGE) heavy chain #2.
XX
XX antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;
XX immune response; IGE-mediated response; allergy; cat; heavy chain.
XX

```

OS   Felis catus.
PN   US2003216565-A1.
XX   20-NOV-2003.
PD   XX
XX   PF   07-APR-2003; 2003US-00409772.
XX   PR   07-JAN-1999; 99US-0115033P.
XX   PR   07-JAN-2000; 2000US-00479614.
XX   PA   (MCCA/) MCCALL C.
XX   PA   (WEBER/) WEBER E.
XX   PI   Mccall C, Weber E;
XX   DR   WPI: 2004-010802/01.
XX   DR   N-PSDB; ADG73250.
XX   PT   New isolated nucleic acid molecule encoding a portion of a feline IGE
XX   PT   heavy chain protein, useful for treating and/or eliciting feline immune
XX   PT   responses for IGE-mediated responses, such as allergies.
XX   PS   Claim 8; SEQ ID NO 29; 44pp; English.
XX   CC   The invention describes an isolated nucleic acid molecule (I) encoding a
XX   CC   portion of a feline IGE heavy chain protein. The methods and compositions
XX   CC   of the present invention are useful for eliciting feline immune responses
XX   CC   for and/or treating IGE-mediated responses, such as allergies. This is
XX   CC   the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy
XX   CC   chain.
XX   SQ   Sequence 496 AA;

Query Match      100.0%; Score 85; DB 8; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 HNDSPVRTSEQATTW 15
      |||||
Db   427 HNDSPVRTSEQATTW 441

RESULT 7
ADG73225
ID   ADG73225 standard; protein; 496 AA.
XX
XX   AC   ADG73225;
XX   DT   11-MAR-2004 (first entry)
XX   DE   Cat partial immunoglobulin E (IGE) heavy chain #1.
XX   KM   anti allergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;
XX   KM   immune response; IGE-mediated response; allergy; cat; heavy chain.
XX   OS   Felis catus.
XX   PN   US2003216565-A1.
XX   PD   20-NOV-2003.
XX   PF   07-APR-2003; 2003US-00409772.
XX   PR   07-JAN-1999; 99US-0115033P.
XX   PR   07-JAN-2000; 2000US-00479614.
XX   PA   (MCCA/) MCCALL C.
XX   PA   (WEBER/) WEBER E.
XX   PI   Mccall C, Weber E;
XX   DR   WPI: 2004-010802/01.

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DR   N-PSDB; ADG73224.
XX
XX   PT   New isolated nucleic acid molecule encoding a portion of a feline IGE
XX   PT   heavy chain protein, useful for treating and/or eliciting feline immune
XX   PT   responses for IGE-mediated responses, such as allergies.
XX   PS   Claim 8; SEQ ID NO 2; 44pp; English.
XX   CC   The invention describes an isolated nucleic acid molecule (I) encoding a
XX   CC   portion of a feline IGE heavy chain protein. The methods and compositions
XX   CC   of the present invention are useful for eliciting feline immune responses
XX   CC   for and/or treating IGE-mediated responses, such as allergies. This is
XX   CC   the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy
XX   CC   chain.
XX   SQ   Sequence 496 AA;

Query Match      100.0%; Score 85; DB 8; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 HNDSPVRTSEQATTW 15
      |||||
Db   427 HNDSPVRTSEQATTW 441

RESULT 8
ADRI0601
ID   ADRI0601 standard; peptide; 15 AA.
XX
XX   AC   ADRI0601;
XX   DT   21-OCT-2004 (first entry)
XX   DE   Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.
XX   KM   Antiaethmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
XX   KM   anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
XX   OS   Canis familiaris.
XX   PN   WO2004065936-A2.
XX   PD   05-AUG-2004.
XX   PF   15-JAN-2004; 2004WO-US003566.
XX   PR   16-JAN-2003; 2003US-0440472P.
XX   PA   (UYNC-) UNIV NORTH CAROLINA STATE.
XX   PI   Hammerberg B;
XX   DR   WPI: 2004-593545/57.
XX   PT   Novel antibody that specifically binds to mammalian IGE epitope, useful
XX   PT   for testing an allergen reactivity of IGE sample, detecting mammalian IGE
XX   PT   or treating asthma or anaphylactic shock.
XX   PS   Example 6; Page 9; 14pp; English.
XX   CC   The present invention relates to a novel monoclonal antibody (I) that
XX   CC   specifically binds to a mammalian IGE epitope, where the epitope is
XX   CC   between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX   CC   (I) is useful for testing an allergen reactivity of an IGE sample. The
XX   CC   allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX   CC   and corn allergens. The sample is a biological sample collected from a
XX   CC   dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
XX   CC   treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX   CC   antibodies recognise epitopes on canine IGE corresponding to amino acid
XX   CC   residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
XX   CC   canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
XX   CC   cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and

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CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE.

XX Sequence 15 AA;

Query Match 56.5%; Score 48; DB 8; Length 15;
 Best Local Similarity 61.5%; Pred. No. 0.23;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVTEQQAAT 14
 |||::|:
 Db 2 NDSPVTEQQAAT 14

RESULT 9
 ID AAY79995 standard; protein; 312 AA.

XX AAY79995;

DT 15-MAY-2000 (first entry)

XX Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.

XX Immunoglobulin E; IGE; epsilon heavy chain; antigenic; antigen;
 KM immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
 KM antibody; allergy; allergic disease; immunization; anti-allergic;
 KM anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Canis sp.

XX MO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013959.

XX 20-JUN-1998; 98US-00100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
 PT for immunization against allergy.

PS Example 1; Page 66-68; 155pp; English.

XX The present invention describes immunoglobulin E (IGE)-CH3 domain
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
 CC a target effector site on the epsilon-heavy chain of IGE, and so
 CC preventing triggering and activation of mast cells and basophils and
 CC downregulation of IGE synthesis. Conjugates, or fusion peptides,
 CC containing (I) are used for active immunisation against IGE-mediated
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
 CC dermatitis. Nucleic acids that encode these compounds are useful for
 CC recombinant production of corresponding peptides or in DNA vaccines.
 CC Conjugates of (I) that include a promiscuous T helper cell epitope
 CC (functional in genetically diverse subjects), in addition to a B cell
 CC target epitope, have increased immunogenicity and may include cyclic
 CC constraints (disulfide bridge) to stabilise conformational features and
 CC maximize cross-reactivity to the natural target. They induce safe (non-
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid
 CC sequences used in the exemplification of the present invention

XX Sequence 312 AA;

Query Match 56.5%; Score 48; DB 3; Length 312;
 Best Local Similarity 61.5%; Pred. No. 7;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 NDSPVTEQQAAT 14
 |||::|:
 Db 256 NDSPVTEQQAAT 268

RESULT 10
 ID AAW23067 standard; protein; 417 AA.

XX AAW23067;

DT 30-JUN-2005 (revised)

DT 16-JUN-2005 (revised)

DT 19-FEB-1998 (first entry)

XX Canine IGE heavy chain constant region (exon 1-4 product).
 KM IGE; immunoglobulin; antibody; heavy chain constant region; allergy;
 KM hypersensitivity; therapy; dog; antiserum; immunomodulation.

XX Canis familiaris.

XX Key Location/Qualifiers

FT Misc-difference 55 /note= "encoded by ACC"

FT Misc-difference 56 /note= "encoded by TAC"

FT Misc-difference 67 /note= "encoded by GCC"

FT Misc-difference 83 /note= "encoded by NNT"

FT Misc-difference 174 /note= "encoded by GGN"

FT Misc-difference 175 /note= "encoded by NNG"

FT Misc-difference 176 /note= "encoded by TGN"

FT Misc-difference 203 /note= "encoded by TCC"

FT Misc-difference 204 /note= "encoded by GAC"

XX WO9730156-A2.

XX 21-AUG-1997.

XX 14-FEB-1997; 97WO-US002322.

XX 14-FEB-1996; 96US-00601197.

XX (IDEX-) IDEXX LAB INC.

XX Mermer B, Harris RA, Sieffring AE;

XX WPI; 1997-425031/39.

XX N-PSDB; AAT79278.

XX Isolated canine IGE heavy chain constant region DNA - useful to develop
 PT products for treatment of canine allergies and for immunomodulation in
 PT dogs.

XX Disclosure; Page 35-39; 59pp; English.

XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IGE
 CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,
 CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant
 CC peptides encoded by exons 1-6 can be produced in eukaryotic or
 CC prokaryotic cells. Such peptides, and antibodies raised against them, are
 CC used in methods to treat the manifestation of allergy in dogs, e.g. to
 CC treat Type I immediate hypersensitivity, and for immunomodulation

CC Revised record issued on 30-JUN-2005 : Typo in comments
XX Sequence 417 AA;
SQ

Query Match 56.5%; Score 48; DB 2; Length 417;
Best Local Similarity 61.5%; Pred. No. 9.8;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSFPRTEQQAAT 14
|||::|||
Db 353 NDSPIQTDQYTT 365

RESULT 11
AAR97753
ID AAR97753 standard; protein; 426 AA.
XX
AC AAR97753;
XX
DT 28-AUG-1996 (first entry)
XX
DE Canine IgE.
XX
KM IgE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
XX
OS Canis familiaris.
XX
PN MO9614867-A1.
XX
PD 23-MAY-1996.
XX
PF 03-NOV-1995; 95WO-US013795.
XX
PR 09-NOV-1994; 94US-00336583.
PR 09-NOV-1994; 94US-00336891.
XX
PA (MERI) MERCK & CO INC.
XX
PI Hollis GF, Patel MD;
XX
DR WPI: 1996-277321/28.
DR N-PSDB; AAT29824.
XX
KT New DNA encoding canine IgE and IGA - useful in vaccines, anti-sense
PT therapy, assays, drug screening, etc.
XX
PS Claim 11; Page 29-30; 49pp; English.
XX
CC The canine IgE amino acid sequence (AAR97753) was deduced from an
CC isolated gene (AAR29824) obtd. from a canine liver DNA library. The
CC cloning of the IgE gene allows produ. of large quantities of recombinant
CC IgE using bacterial, yeast, mammalian, insect or viral systems. The IgE
CC can be used in drug development (e.g. small molecule screening, assay
CC development and anti-IgE antibody generation). Fragments of IgE can be
CC used in vaccines or to prevent IgE-mediated hypersensitivity. The new
CC sequence information permits targeted modulation of IgE-mediated immune
CC responses
XX
SQ Sequence 426 AA;

Query Match 56.5%; Score 48; DB 2; Length 426;
Best Local Similarity 61.5%; Pred. No. 10;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSFPRTEQQAAT 14
|||::|||
Db 358 NDSPIQTDQYTT 370

RESULT 12
ABP96583
ID ABP96583 standard; protein; 426 AA.
XX

AC ABP96583;
XX
DT 28-MAY-2003 (first entry)
XX
DE Dog IgE heavy chain amino acid sequence SEQ ID NO:28.
XX
KM Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response;
KM immune response; major histocompatibility complex; MHC; immunogenic;
KM anti-allergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic;
KM dermatological; antiinflammatory; IgE-mediated condition; food allergy;
KM atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KM atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
KM urticaria hives.
XX
XX Canis familiaris.
XX
EN WO2003015716-A2.
XX
PD 27-FEB-2003.
XX
PF 08-AUG-2002; 2002WO-US026986.
XX
PR 13-AUG-2001; 2001US-0312120P.
XX
PA (IGET-) IGE THERAPEUTICS INC.
XX
PI Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX
DR WPI: 2003-268242/26.
XX
KT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
PT against IgE, by identifying peptide eliciting CTL response to IgE
PT peptides naturally presented by major histocompatibility complex class I
PT protein.
XX
XX
PS Example 7; Page 152-154; 187pp; English.
XX
CC The present invention describes a method (M1) for identifying peptides
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
CC E (IgE), comprising providing a test peptide (T) suspected of being able
CC to bind to major histocompatibility complex (MHC) class I molecule, and
CC evaluating (T) for ability to elicit in a mammal a CTL response to
CC naturally processed and presented IgE peptides, where a peptide that
CC induces such a response is identified. Also described are compositions:
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
CC (C2) comprising at least one isolated polynucleotide encoding (I); and
CC (C3) comprising antigen-presenting cells that recognise at least one (I).
CC where C1-3 are able to bind to at least one MHC class I molecule and to
CC elicit in a mammal a CTL response to naturally processed and presented
CC IgE peptides. C1-3 have anti-allergic, antiasthmatic, immunosuppressive,
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
CC and can be used as inducers of a CTL response against IgE, and in
CC vaccines. C1-3 can be used for modulating an IgE-mediated condition in a
CC mammal. C1-3 are useful for modulating an IgE-mediated condition such as
CC IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic
CC hypersensitivity condition, IgE myeloma in a mammal. Preferably, C1-3 are
CC useful for treating atopic hypersensitivity conditions (such as allergic
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
CC hives). The present sequence represents an IgE heavy chain amino acid
CC sequence, which is given in an example from the present invention
XX
SQ Sequence 426 AA;

Query Match 56.5%; Score 48; DB 6; Length 426;
Best Local Similarity 61.5%; Pred. No. 10;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSFPRTEQQAAT 14
|||::|||
Db 358 NDSPIQTDQYTT 370

RESULT 13
ID ABL055745
XX ABL055745 standard; protein; 84 AA.
XX
AC ABL055745;
XX
DT 17-MAR-2003 (first entry)
XX
DE Tree cotton growth regulating protein, GAGREPI.
XX
KM ss; plant; growth regulating protein; PSK; phytoosulphokine-alpha;
XX transgenic; marker-assisted breeding; agriculture; horticulture.
XX
OS Gossypium arboreum.
XX
PN WO200283901-A2.
XX
PD 24-OCT-2002.
XX
PE 11-APR-2002; 2002WO-EP004035.
XX
PR 12-APR-2001; 2001US-0283313P.
XX
PA (CROP-) CROPDISEIGN NV.
XX (SAUT/) SAUTER M.
PI Sauter M, Lonbiecke R, Mironov V, Frankard V, Dillen W;
PI Lejeune P, Broekaert W;
XX
DR WPI; 2003-093023/08.
DR N-PSDB; ABX74222.
XX
XX
PT New isolated GREP nucleic acids and polypeptides controlling or modifying
PT the growth characteristics of a plant, useful for a wide application in
PT agricultural and horticultural practices, and in vitro plant cell and
PT tissue culture.
XX
XX
PS Claim 5; Fig 22; 156pp; English.
XX
XX The invention relates to a new isolated nucleic acid encoding a growth
XX regulating protein (GREP), where the protein conforms to the GREP
XX signature sequence appearing as ABL055722, and the GREP proteins. Also
XX included are a vector comprising a GREP nucleic acid, or a vector
XX encoding the rice growth regulating polypeptide OsPSK (phytoosulphokine-
XX alpha) where the growth regulating proteins regulate growth and/or
XX development response in intact plants, a GREP transgenic plant, a
XX transgenic plant comprising the vector, seed/pollen and a harvestable
XX part of propagation material from the transgenic plant, a host cell
XX comprising the GREP nucleic acid, an antisense molecule consisting of 14-
XX 100 nucleotides targeted to the GREP signature nucleotide sequence
XX appearing as ABLX74197, an anti-GREP antibody which specifically
XX recognises a GREP or its fragment, a method for altering growth and/or
XX activity of a plant or plant cell/storage organ comprising modulating the
XX level and/or activity of a GREP or the rice growth regulating peptide
XX OsPSK, a method for downregulating levels of a GREP or OsPSK gene product
XX or its activity (comprising administering or exposing GREP or OsPSK
XX antibodies or gene products to cells, tissues or organs of a plant) a
XX method for identifying an allele with desired features of a gene encoding
XX a GREP which comprises isolating alleles for a GREP and testing the
XX features of the allele by expression in a transgenic plant, a method for
XX identifying an allele of GREP and selecting an allele with desired
XX features which comprises the use of genes encoding GREP, or sequences
XX located in the genome in the neighbourhood of GREP genes, as molecular
XX markers for different GREP alleles and selecting specific GREP alleles by
XX marker-assisted breeding and a method for identifying regulatory
XX sequences of GREP growth regulating polypeptide genes. The methods and
XX compositions are for controlling or modifying the growth characteristics
XX of a plant or its organs and tissues, useful for a wide application in
XX agricultural and horticultural practices, and in vitro plant cell and
XX tissue culture. The present sequence is a growth regulating protein
SQ Sequence 84 AA;

Query Match 55.3%; Score 47; DB 6; Length 84;
Best Local Similarity 61.5%; Pred. No. 2.4;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 NDSPVTEQOATT 14
DB 32 NDSPAKTQSGGT 44

RESULT 14
ID ABB60974
XX ABB60974 standard; protein; 449 AA.
XX
AC ABB60974;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 9714.
XX
KM Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PE 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
PI Venter JC, Adams M, Li PWD, Myers EW;
PI
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL05077.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions.
XX
PS Disclousure; SEQ ID NO 9714; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737-
XX ABB872072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 449 AA;
Query Match 54.1%; Score 46; DB 4; Length 449;
Best Local Similarity 53.3%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 HNDSPVTEQOATTW 15
DB 133 HNDGFVRCPEBALTW 147
RESULT 15
ID AAE12007
XX AAE12007 standard; protein; 321 AA.
XX
AC AAE12007;

```

XX 18-DEC-2001 (first entry)
DT
XX Streptomyces cattleya modified isopenicillin N synthetase (IPNS).
DE
XX Isopenicillin N synthetase; IPNS; antibiotic; penicillin; oxygenase;
XX non-haeme iron (II) dependent family; oxidase; mutant; mutacin.
XX Streptomyces cattleya.
OS
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 211 /note= "wild type Glu substituted with Arg"
XX
XX US6284483-B1.
XX
XX 04-SEP-2001.
XX
XX 06-OCT-1999; 99US-00413231.
XX
XX 06-OCT-1999; 99US-00413231.
XX
XX (UNMS ) UNIV MICHIGAN STATE.
XX
XX Dilley DR, Kadyrzhanova DK, Wang Z, Warner TM;
XX
XX WPI; 2001-615433/71.
XX
XX Method for producing antibiotics, particularly penicillin G or V,
XX comprises employing a modified isopenicillin N synthetase, in either an
XX organism or a cell-free system under the control of bicarbonate.
XX
XX Claim 2; Col 37-38; 27p; English.
XX
XX The invention relates to a modified enzyme of a non-haeme iron (II)
XX dependent family of oxygenases and oxidases which renders the enzyme
XX dependent on bicarbonate for activity. The invention also related to a
XX method for producing penicillin G or V comprises employing a modified
XX enzyme, particularly isopenicillin N synthetase (IPNS), in either an
XX organism or a cell-free system, under the control of bicarbonate. The
XX modified enzymes are IPNS, deacetoxycephalosporin C synthetase (DAOCS)
XX and deacetylcephalosporin C synthetase (IDACS). The method is useful for
XX producing antibiotics, particularly penicillin G or V. The method is
XX useful for making organisms useful for making an antibiotic dependent on
XX bicarbonate to make the antibiotic. The present sequence is Streptomyces
XX cattleya modified isopenicillin N synthetase showing an Arg211 in place
XX of Glu211
XX
XX Sequence 321 AA;
SQ

```

```

Query Match 52.9%; Score 45; DB 4; Length 321;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
OY 2 NDSFRTQOATTW 15
|:|:|:|:|:|
Db 61 NESTTMTDRSTW 74

```

Search completed: December 12, 2005, 20:30:27
 Job time : 83.3362 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:23:41 ; Search time 20.431 Seconds
(without alignments)
60.699 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNDSPVTEQOATW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	431	2	US-09-479-614-14
2	85	100.0	496	2	US-09-479-614-2
3	85	100.0	496	2	US-09-479-614-29
4	48	56.5	108	2	US-09-281-760E-37
5	48	56.5	312	2	US-09-701-623C-2
6	48	56.5	426	1	US-08-336-583-2
7	46	54.1	426	4	PCT-US95-13795-2
8	46	54.1	210	2	US-09-270-767-45299
9	45	52.9	321	2	US-09-413-231-8
10	44	51.8	181	2	US-09-270-767-43758
11	42	49.4	178	2	US-10-104-047-3886
12	41	48.2	384	2	US-09-605-703B-1364
13	41	48.2	534	2	US-09-605-703B-1362
14	40	47.1	540	2	US-09-949-016-8465
15	40	47.1	540	2	US-09-949-016-9052
16	39	45.9	225	2	US-09-252-991A-17094
17	39	45.9	655	2	US-08-556-422A-3
18	39	45.9	771	1	US-08-121-713D-54
19	39	45.9	771	1	US-08-835-268-54
20	39	45.9	771	1	US-09-060-692-54
21	39	45.9	771	2	US-08-833-391-54
22	39	45.9	771	2	US-09-060-610-54
23	39	45.9	771	4	PCT-US94-10151A-54
24	38	44.7	127	2	US-09-270-767-3906
25	38	44.7	127	2	US-09-270-767-54223
26	38	44.7	528	2	US-09-356-806-8
27	38	44.7	528	2	US-09-949-016-6999

28	38	44.7	530	2	US-09-180-852-2	Sequence 2, Appli
29	38	44.7	649	2	US-09-489-039A-11880	Sequence 11880, A
30	38	44.7	704	2	US-09-532A-5612	Sequence 5612, Ap
31	38	44.7	1092	2	US-09-134-000C-6291	Sequence 6291, Ap
32	37.5	44.1	447	2	US-09-252-991A-25916	Sequence 25916, A
33	37.5	44.1	1124	2	US-09-605-703B-2576	Sequence 2576, Ap
34	37	43.5	113	2	US-09-902-540-11153	Sequence 11193, A
35	37	43.5	116	2	US-09-513-959C-8156	Sequence 8156, Ap
36	37	43.5	236	2	US-09-248-796A-15717	Sequence 15717, A
37	37	43.5	249	2	US-09-134-001C-4442	Sequence 4442, Ap
38	37	43.5	249	2	US-09-710-279-106	Sequence 306, App
39	37	43.5	424	2	US-08-248-796A-16232	Sequence 16232, A
40	37	43.5	865	2	US-08-842-382-2	Sequence 2, Appli
41	37	43.5	865	2	US-09-608-821-2	Sequence 13, Appli
42	37	43.5	3546	2	US-09-679-279-13	Sequence 24760, A
43	36.5	42.9	188	2	US-09-252-991A-24760	Sequence 957, App
44	36.5	42.9	439	2	US-09-538-092-852	Sequence 8063, Ap
45	36.5	42.9	493	2	US-09-949-016-8063	

ALIGNMENTS

```
RESULT 1
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match          100.0%; Score 85; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 9.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HNDSPVTEQOATW 15
      |||||
DB      362 HNDSPVTEQOATW 376

RESULT 2
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2
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Query Match 100.0%; Score 85; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNDSPVTEQOATW 15
|||||
Db 427 HNDSPVTEQOATW 441

RESULT 3

US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match 100.0%; Score 85; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNDSPVTEQOATW 15
|||||
Db 427 HNDSPVTEQOATW 441

RESULT 4

US-09-281-760E-37
; Sequence 37, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Mermer, Brian
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (413)..(414)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (451)..(451)
; OTHER INFORMATION: "n" stands for any nucleic acid

;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (460)..(462)
;; OTHER INFORMATION: "n" stands for any nucleic acid
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (500)..(500)
;; OTHER INFORMATION: "n" stands for any nucleic acid
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (530)..(530)
;; OTHER INFORMATION: "n" stands for any nucleic acid
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (568)..(568)
;; OTHER INFORMATION: "n" stands for any nucleic acid
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (847)..(849)
;; OTHER INFORMATION: "n" stands for any nucleic acid
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (853)..(853)
;; OTHER INFORMATION: "n" stands for any nucleic acid
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1382)..(1382)
;; OTHER INFORMATION: "n" stands for any nucleic acid
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1832)..(1832)
;; OTHER INFORMATION: "n" stands for any nucleic acid
US-09-281-760E-37

Query Match 56.5%; Score 48; DB 2; Length 108;
Best Local Similarity 61.5%; Pred. No. 0.6;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVTEQOATT 14
|||:|:|
Db 44 NDSPVTEQOATT 56

RESULT 5

US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog Ige
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-09-701-623C-2

Query Match 56.5%; Score 48; DB 2; Length 312;
Best Local Similarity 61.5%; Pred. No. 2;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 NDSFPRTEQQT 14
|||:::|
Db 256 NDSFPRTEQQT 268

RESULT 6

US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-336-583-2

Query Match 56.5%; Score 48; DB 1; Length 426;
Best Local Similarity 61.5%; Pred. No. 2.8;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 NDSFPRTEQQT 14
|||:::|
Db 358 NDSFPRTEQQT 370

RESULT 7

PCT-US95-13795-2
; Sequence 2, Application PC/TUS9513795
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
; CITY: RAHWAY
; STATE: NEW JERSEY

COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-13795-2

Query Match 56.5%; Score 48; DB 4; Length 426;
Best Local Similarity 61.5%; Pred. No. 2.8;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 NDSFPRTEQQT 14
|||:::|
Db 358 NDSFPRTEQQT 370

RESULT 8

US-09-270-767-45299
; Sequence 45299, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45299
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45299

Query Match 54.1%; Score 46; DB 2; Length 210;
Best Local Similarity 53.3%; Pred. No. 2.8;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HNSFPRTEQQT 15
|||:::|
Db 149 HNSFPRTEQQT 163

RESULT 9

US-09-413-231-8
; Sequence 8, Application US/09413231
; Patent No. 6284483
; GENERAL INFORMATION:
; APPLICANT: Dilley, David R.
; APPLICANT: Kadyrzhanova, Dina K
; APPLICANT: Wang, Zhenyong
; APPLICANT: Warner, Toni M
; TITLE OF INVENTION: Modified Synthetases To Produce Penicillins and

```
; TITLE OF INVENTION: Cephalosporins under the Control of Bicarbonate
; FILE REFERENCE: MS041-453
; CURRENT APPLICATION NUMBER: US/09/413,231
; CURRENT FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: modified IPNS
; NAME/KEY: MUTAGEN
; LOCATION: (211)
; OTHER INFORMATION: Glu211 in native IPNS modified to Arg
; US-09-413-231-8

Query Match      52.9%; Score 45; DB 2; Length 321;
Best Local Similarity 50.0%; Pred. No. 6.8;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSFVTEQOATW 15
DB      61 NESTMTDQSTTW 74

RESULT 10
; US-09-270-767-43758
; Sequence 43758, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43758
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURES:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-43758

Query Match      51.8%; Score 44; DB 2; Length 181;
Best Local Similarity 57.1%; Pred. No. 5.3;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 NDSFVTEQOATW 15
DB      62 NCSPIQTEVQAIQW 75

RESULT 11
; US-10-104-047-3886
; Sequence 3886, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3886
; LENGTH: 178
; TYPE: PRT
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; ORGANISM: Homo sapiens
; US-10-104-047-3886

Query Match      49.4%; Score 42; DB 2; Length 178;
Best Local Similarity 40.0%; Pred. No. 12;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 HNSFVTEQOATW 15
DB      8 HODFPVKRKRLSTW 22

RESULT 12
; US-09-605-703B-1364
; Sequence 1364, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1364
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-605-703B-1364

Query Match      48.2%; Score 41; DB 2; Length 381;
Best Local Similarity 40.0%; Pred. No. 41;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1 HNSFVTEQOATW 15
DB      185 HSDKPIRHEALKGW 199

RESULT 13
; US-09-605-703B-1362
; Sequence 1362, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1362
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-605-703B-1362
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Query March	48.2%	Score 41;	DB 2;	Length 534;
Best Local Similarity	40.0%	Pred. No. 60;		
Matches	6;	Conservative	3;	Mismatches 6;
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				Gaps 0.
QY	1	HNDSPVTEQCAATW	15	
Db	185	HSDKIRHEALDKGW	199	

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Db          461 HHDQPVKLERAYFW 475
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Search completed: December 12, 2005, 19:37:04
Job time : 21.431 secs

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RESULT 14
US-09-949-016-8465
: Sequence 8465, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001307
: CURRENT APPLICATION NUMBER: US/09/949, 016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241, 755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237, 768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231, 498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8465
: LENGTH: 540
: TYPE: prt
: ORGANISM: Human
US-09-949-016-8465

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Query Match	47.1%	Score 40;	DB 2;	Length 540;
Best Local Similarity	40.0%	Pred. No. 91;		
Matches	6;	Conservative	4;	Mismatches 5;
				Indels 0;
				Gaps 0

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RESULT 15
US-09-949-016-9052
; Sequence 9052; Application US/09949016
; Patent No. 6812359
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9052
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9052

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Query Match	47.1%	Score 40;	DB 2;	Length 540;
Best Local Similarity	40.0%	Pred. No. 91;		
Matches	6;	Conservative	4;	Mismatches 5;
				Indels 0;
				Gaps 0

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OM protein - protein search, using BW model

Run on: December 12, 2005, 19:33:42 ; Search time 66.9828 Seconds
(without alignments)
93.568 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNDSPVTEQQTW 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.dep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.dep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.dep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	US-10-758-165-2	Sequence 2, Appl1
2	85	100.0	431	US-09-479-614-14	Sequence 14, Appl
3	85	100.0	431	US-10-409-772-14	Sequence 14, Appl
4	85	100.0	496	US-09-479-614-2	Sequence 2, Appl1
5	85	100.0	496	US-09-479-614-29	Sequence 29, Appl
6	85	100.0	496	US-10-214-524-25	Sequence 25, Appl
7	85	100.0	496	US-10-409-772-2	Sequence 2, Appl1
8	85	100.0	496	US-10-409-772-29	Sequence 29, Appl
9	48	56.5	15	US-10-758-165-1	Sequence 1, Appl1
10	48	56.5	426	US-10-214-524-28	Sequence 28, Appl
11	47	55.3	68	US-10-425-115-203123	Sequence 203123
12	47	55.3	84	US-10-474-691-101	Sequence 101, Appl
13	47	55.3	1083	US-10-732-923-13976	Sequence 13976, A
14	46	54.1	2360	US-10-732-923-13960	Sequence 13960, A
15	46	54.1	449	US-11-097-143-9714	Sequence 9714, Ap
16	45	53.9	321	US-09-924-841-8	Sequence 8, Appl1
17	44	51.8	194	US-10-437-963-145550	Sequence 145550
18	44	51.8	673	US-11-097-143-42006	Sequence 42006, A
19	43	50.6	151	US-10-425-115-283053	Sequence 283053
20	43	50.6	425	US-10-425-115-190849	Sequence 190849
21	43	50.6	433	US-10-425-115-189170	Sequence 189170
22	43	50.6	435	US-10-425-115-320857	Sequence 320857
23	43	50.6	459	US-10-425-115-184927	Sequence 184927
24	43	50.6	461	US-10-425-115-320858	Sequence 320858
25	43	50.6	470	US-10-369-493-16930	Sequence 16930, A
26	43	50.6	493	US-10-425-115-190842	Sequence 190842
27	43	50.6	503	US-10-425-115-351700	Sequence 351700

28	43	50.6	505	4	US-10-425-115-184928	Sequence 184928
29	43	50.6	506	4	US-10-425-115-189173	Sequence 189173
30	43	50.6	696	4	US-10-425-114-38018	Sequence 38018, A
31	43	50.6	716	4	US-10-425-115-336115	Sequence 336115
32	42.5	50.0	188	4	US-10-437-963-201785	Sequence 201785
33	42	49.4	68	4	US-10-425-115-233639	Sequence 233639
34	42	49.4	197	4	US-10-104-047-3886	Sequence 3886, Ap
35	42	49.4	197	4	US-10-029-386-34079	Sequence 34079, A
36	42	49.4	262	4	US-10-425-115-220304	Sequence 220304
37	42	49.4	296	4	US-10-094-749-2367	Sequence 2367, Ap
38	42	49.4	537	4	US-10-479-435-15	Sequence 15, Appl
39	41	48.2	152	3	US-09-864-761-37742	Sequence 37742, A
40	41	48.2	473	4	US-10-424-599-153291	Sequence 153291
41	41	48.2	647	3	US-09-738-626-6449	Sequence 6449, Ap
42	41	48.2	671	4	US-10-767-701-45175	Sequence 45175, A
43	41	48.2	750	5	US-10-732-923-11093	Sequence 11093
44	41	48.2	812	5	US-10-450-763-49424	Sequence 49424, A
45	41	48.2	1527	5	US-10-450-763-38962	Sequence 38962, A

ALIGNMENTS

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RESULT 1
US-10-758-165-2
; Sequence 2, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-2

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Query Match 100.0%; Score 85; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 HNDSPVTEQQTW 15
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DB 1 HNDSPVTEQQTW 15

RESULT 2
US-09-479-614-14
; Sequence 14, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

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Query Match 100.0%; Score 85; DB 3; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEOQATTW 15
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Db 362 HNDSPVTEOQATTW 376

RESULT 3
US-10-409-772-14
; Sequence 14, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-14

Query Match 100.0%; Score 85; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEOQATTW 15
|||
Db 362 HNDSPVTEOQATTW 376

RESULT 4
US-09-479-614-2
; Sequence 2, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match 100.0%; Score 85; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEOQATTW 15
|||
Db 427 HNDSPVTEOQATTW 441

RESULT 5
US-09-479-614-29
; Sequence 29, Application US/09479614
; Publication No. US20030013183A1

; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

Query Match 100.0%; Score 85; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEOQATTW 15
|||
Db 427 HNDSPVTEOQATTW 441

RESULT 6
US-10-214-524-25
; Sequence 25, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Cat (Felis catus)
US-10-214-524-25

Query Match 100.0%; Score 85; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNDSPVTEOQATTW 15
|||
Db 427 HNDSPVTEOQATTW 441

RESULT 7
US-10-409-772-2
; Sequence 2, Application US/10409772
; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2
LENGTH: 496
TYPE: PRT
ORGANISM: Felis catus
US-10-409-772-2

Query Match 100.0%; Score 85; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNDSPVTEQOATTW 15
DB 427 HNDSPVTEQOATTW 441

RESULT 8
US-10-409-772-29
Sequence 29, Application US/10409772
Publication No. US20030216565A1

GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047

CURRENT APPLICATION NUMBER: US/10/409,772
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US/09/479,614
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 29
LENGTH: 496
TYPE: PRT
ORGANISM: Felis catus
US-10-409-772-29

Query Match 100.0%; Score 85; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNDSPVTEQOATTW 15
DB 427 HNDSPVTEQOATTW 441

RESULT 9
US-10-758-165-1
Sequence 1, Application US/10758165
Publication No. US20050196816A1

GENERAL INFORMATION:
APPLICANT: Hammerberg, Bruce
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
FILE REFERENCE: 5051-661
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: US 60/440,472
PRIOR FILING DATE: 2003-01-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.2

SEQ ID NO 1
LENGTH: 15
TYPE: PRT
ORGANISM: Canis familiaris
US-10-758-165-1

Query Match 56.5%; Score 48; DB 5; Length 15;
Best Local Similarity 61.5%; Pred. No. 0.23;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVTEQOATT 14
DB 2 NDSPIQTDQYTTT 14

RESULT 10
US-10-214-524-28
Sequence 28, Application US/10214524
Publication No. US20030073142A1

GENERAL INFORMATION:
APPLICANT: Chen, Sway-Shen Alex
APPLICANT: Yang, Yong-Min
APPLICANT: Barankiewicz, Theresa J.
APPLICANT: Chen, Zhong

TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
FILE REFERENCE: IGE-00101.P.1.1
CURRENT APPLICATION NUMBER: US/10/214,524
CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: 60/312,120
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.1

SEQ ID NO 28
LENGTH: 426
TYPE: PRT
ORGANISM: Dog (Canis familiaris)
US-10-214-524-28

Query Match 56.5%; Score 48; DB 4; Length 426;
Best Local Similarity 61.5%; Pred. No. 8.9;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVTEQOATT 14
DB 358 NDSPIQTDQYTTT 370

RESULT 11
US-10-425-115-203123
Sequence 203123, Application US/10425115
Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 203123

LENGTH: 68
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MWT4577_116836C.1.pcp
US-10-425-115-203123

Query Match 55.3%; Score 47; DB 4; Length 68;
Best Local Similarity 69.2%; Pred. No. 1.8;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPVTEQOATT 14
DB 38 NDSPIQTDQYTTT 50

RESULT 12
US-10-474-691-101
Sequence 101, Application US/10474691
Publication No. US20040221332A1

GENERAL INFORMATION:
APPLICANT: Cropdesign N.V.
TITLE OF INVENTION: Plant growth regulating genes, proteins and uses thereof
FILE REFERENCE: CROP-028-PCT

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; CURRENT APPLICATION NUMBER: US/10/474,691
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: US 60/283,313
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Gossypium arboreum
US-10-474-691-101
```

```
Query Match          55.3%; Score 47; DB 5; Length 84;
Best Local Similarity 61.5%; Pred. No. 2.3;
Matches      8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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```
QY      2  HNDSPVTEOQATW 14
Db      32  NDSPAKTOSQGT 44
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```
RESULT 13
US-10-732-923-13976
; Sequence 13976, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13976
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans var. neoformans
US-10-732-923-13976
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```
Query Match          55.3%; Score 47; DB 5; Length 1083;
Best Local Similarity 53.3%; Pred. No. 37;
Matches      8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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```
QY      1  HNDSPVTEOQATW 15
Db      202  HADPARQEMQRTW 216
```

```
RESULT 14
US-10-732-923-13960
; Sequence 13960, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13960
; LENGTH: 2360
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans var. grubii
US-10-732-923-13960
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Query Match          55.3%; Score 47; DB 5; Length 2360;
Best Local Similarity 53.3%; Pred. No. 87;
Matches      8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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.QY      1  HNDSPVTEOQATW 15
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Db      1479  HADPARQEMQRTW 1493
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RESULT 15
US-11-097-143-9714
; Sequence 9714, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CLO00728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9714
; LENGTH: 449
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-9714
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Query Match          54.1%; Score 46; DB 6; Length 449;
Best Local Similarity 53.3%; Pred. No. 21;
Matches      8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
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QY      1  HNDSPVTEOQATW 15
Db      133  HNDGFVRCPEALTW 147
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Search completed: December 12, 2005, 20:19:23
Job time : 66.9828 secs
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OM protein - protein search, using SW model

Run on: December 12, 2005, 19:34:33 ; Search time 2.4569 Seconds
(without alignments)
34.094 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNDSPVTEQQTW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues
Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	56.5	312	6	US-10-723-207-2
2	37	43.5	249	6	US-10-793-626-306
3	37	43.5	865	7	US-11-080-991-110
4	36	42.4	339	7	US-11-010-874-3
5	36	42.4	1275	6	US-11-056-621-4
6	35	41.2	467	6	US-10-821-234-1598
7	35	41.2	737	6	US-10-878-556A-99
8	34	40.0	735	6	US-10-467-657-6990
9	34	40.0	7968	7	US-11-186-731-5
10	33	38.8	136	7	US-11-055-822-966
11	33	38.8	146	6	US-11-055-822-994
12	33	38.8	248	6	US-10-467-657-7696
13	33	38.8	568	6	US-10-510-386-104
14	33	38.8	568	7	US-11-055-822-240
15	33	38.8	568	7	US-11-055-822-1134
16	33	38.8	680	6	US-10-467-657-7612
17	33	38.8	716	6	US-10-467-657-8370
18	33	38.8	716	6	US-10-510-386-108
19	32.5	38.2	259	6	US-10-467-657-2814
20	32	37.6	139	6	US-10-485-517-162
21	32	37.6	216	6	US-10-467-657-482
22	32	37.6	233	6	US-10-467-657-5470
23	32	37.6	244	6	US-10-510-386-110
24	32	37.6	353	7	US-11-137-465-44
25					

26	32	37.6	448	7	US-11-137-465-45	Sequence 45, Appl
27	32	37.6	505	6	US-10-467-657-6228	Sequence 6228, Ap
28	32	37.6	518	6	US-10-878-556A-156	Sequence 156, App
29	32	37.6	840	7	US-11-108-172-1102	Sequence 1102, Ap
30	32	37.6	886	6	US-10-821-234-1329	Sequence 1329, Ap
31	32	37.6	919	6	US-10-858-730-206	Sequence 206, App
32	32	37.6	1155	6	US-10-793-626-1780	Sequence 1780, Ap
33	32	37.6	1184	6	US-10-131-826A-412	Sequence 412, App
34	31	36.5	146	7	US-11-000-463-881	Sequence 881, App
35	31	36.5	181	7	US-11-000-463-409	Sequence 409, App
36	31	36.5	270	6	US-10-467-657-7100	Sequence 7100, Ap
37	31	36.5	273	6	US-10-467-657-7462	Sequence 7462, Ap
38	31	36.5	278	6	US-10-495-597-9	Sequence 9, Appl
39	31	36.5	341	6	US-10-515-481-3	Sequence 3, Appl
40	31	36.5	341	6	US-10-515-481-6	Sequence 6, Appl
41	31	36.5	341	6	US-10-515-481-9	Sequence 9, Appl
42	31	36.5	341	6	US-10-515-481-12	Sequence 12, Appl
43	31	36.5	344	6	US-10-567-527A-24	Sequence 24, Appl
44	31	36.5	362	6	US-10-467-657-6880	Sequence 6880, Ap
45	31	36.5	434	6	US-10-467-657-4482	Sequence 4482, Ap

ALIGNMENTS

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RESULT 1
US-10-723-207-2
; Sequence 2, Application US/10723207
; Publication NO. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE OF INVENTION: ALLERGY
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723,207
; PRIOR FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: 09/701,623
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3 of dog Ige
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
; US-10-723-207-2

Query Match      56.5%  Score 48;  DB 6;  Length 312;
Best Local Similarity 61.5%  Pred. No. 0.063;
Matches 8;  Conservative 3;  Mismatches 2;  Indels 0;  Gaps 0;

QY      2  NDSPIRTDQQT 14
Db      256 NDSPIRTDQYTT 268

RESULT 2
US-10-793-626-306
; Sequence 306, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
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; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 306
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-306

Query Match      43.5%; Score 37; DB 6; Length 249;
Best Local Similarity 46.7%; Pred. No. 5.1;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy      1  NDSFVPRTEQOATTW 15
Db      54  HNDSTFYKXEQKHTGW 68

RESULT 3
US-11-080-991-110
; Sequence 110, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Vealby, Petteer Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-110

Query Match      43.5%; Score 37; DB 7; Length 865;
Best Local Similarity 53.8%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2  NDSFVPRTEQOATT 14
Db      365  NDIPDRVQRQT 377

RESULT 4
US-11-010-874-3
; Sequence 3, Application US/11010874
; Publication No. US20050250694A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Jian-Xing
; TITLE OF INVENTION: COMPOUNDS USEFUL IN INHIBITING VASCULAR LEAKAGE, INFLAMMATION AND
; TITLE OF INVENTION: FIBROSIS AND METHODS OF MAKING AND USING SAME
; FILE REFERENCE: 5820,656
; CURRENT APPLICATION NUMBER: US/11/010,874
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: 10/963,115
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: 60/510,620
; PRIOR FILING DATE: 2003-10-10
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; PRIOR APPLICATION NUMBER: 60/528,647
; PRIOR FILING DATE: 2003-12-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Version 3.3
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-010-874-3

Query Match      42.4%; Score 36; DB 7; Length 339;
Best Local Similarity 61.5%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2  NDSFVPRTEQOATT 14
Db      256  DSSPVSTEQALPT 268

RESULT 5
US-11-056-621-4
; Sequence 4, Application US/11056621
; Publication No. US20050262592A1
; GENERAL INFORMATION:
; APPLICANT: Spencer, David
; APPLICANT: Dickey, Lynn F.
; APPLICANT: Gasdaska, John R.
; APPLICANT: Cox, Kevin M.
; APPLICANT: Wang, Xiaowei
; APPLICANT: Peele, Charles G.
; TITLE OF INVENTION: EXPRESSION OF PLASMINOGEN AND
; TITLE OF INVENTION: MICROPLASMINOGEN IN DUCKWEED
; FILE REFERENCE: 40989/274646
; CURRENT APPLICATION NUMBER: US/11/056,621
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/543,487
; PRIOR FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of mature human plasminogen
US-11-056-621-4

Query Match      42.4%; Score 36; DB 7; Length 791;
Best Local Similarity 61.5%; Pred. No. 26;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2  NDSFVPRTEQOATT 14
Db      334  DSSPVSTEQALPT 346

RESULT 6
US-10-821-234-1598
; Sequence 1598, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
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SEQ ID NO 1598
LENGTH: 1275
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1598

Query Match 42.4%; Score 36; DB 6; Length 1275;
Best Local Similarity 38.5%; Pred. No. 44;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 DSPVTEQATW 15
Db 1024 ETTIRVNQPTW 1036

RESULT 7
US-10-821-234-904
Sequence 904, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andaman, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presenclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PL_SEQ_Genes Version 1.0
SEQ ID NO 904
LENGTH: 467
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-904

Query Match 41.2%; Score 35; DB 6; Length 467;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HNDSPVTE 9
Db 251 YNDSPVKDE 259

RESULT 8
US-10-878-556A-99
Sequence 99, Application US/10878556A
Publication No. US20050266399A1
GENERAL INFORMATION:
APPLICANT: Hoffmann La-Roche, Inc.
TITLE OF INVENTION: HCV regulated protein expression
FILE REFERENCE: 21762
CURRENT APPLICATION NUMBER: US/10/878,556A
CURRENT FILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 199
SOFTWARE: PatentIn version 3.1
SEQ ID NO 99
LENGTH: 737
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (98)..(98)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (242)..(242)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE

LOCATION: (259)..(259)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (262)..(262)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (263)..(263)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (264)..(264)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (269)..(269)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
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NAME/KEY: MISC_FEATURE
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OTHER INFORMATION: Xaa is an undetermined amino acid residue
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NAME/KEY: MISC_FEATURE
LOCATION: (283)..(283)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (284)..(284)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (337)..(337)
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FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (368)..(368)
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FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (418)..(418)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (419)..(419)
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FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (425)..(425)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (428)..(428)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (429)..(429)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (430)..(430)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (432)..(432)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (439)..(439)
OTHER INFORMATION: Xaa is an undetermined amino acid residue
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (443)..(443)

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; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (499)..(499)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (500)..(500)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (502)..(502)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (506)..(506)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC FEATURE
; LOCATION: (507)..(507)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
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; NAME/KEY: MISC FEATURE
; LOCATION: (511)..(511)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (513)..(513)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: haugp/075309-23-0
; DATABASE ENTRY DATE: 2003-02-16
; US-10-878-556A-99
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Query Match 41.2%; Score 35; DB 6; Length 737;
Best Local Similarity 54.5%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY 5 PVRTEQATTW 15
Db 322 PLRLRVGATTW 332
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```
RESULT 9
US-10-467-657-6990
; Sequence 6990, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWIn99, version 1.04
; SEQ ID NO 6990
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-6990
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Query Match 40.0%; Score 34; DB 6; Length 735;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 HNSPVTQEQ 10
|:|:|:|
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```
Db 275 HIDAPVKLEQ 284
```

```
RESULT 10
US-11-186-731-5
; Sequence 5, Application US/11186731
; Publication No. US20050255521A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Roseana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MP12001-047P1RCP1(M)
; CURRENT APPLICATION NUMBER: US/11/186,731
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/077,130
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 7968
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-186-731-5
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```
Query Match 40.0%; Score 34; DB 7; Length 7968;
Best Local Similarity 54.5%; Pred. No. 78;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 NDSPVTEQQA 12
Db 4376 DDEPVRTSEVA 4386
```

```
RESULT 11
US-11-055-822-966
; Sequence 966, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Heberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
```


SEQ ID NO 966
LENGTH: 136
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-11-055-822-966

Query Match 38.8% Score 33; DB 7; Length 136;
Best Local Similarity 35.7% Pred. No. 14;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 NDSPTREQQATW 15
DB 119 SDSPEASEREISIW 132

RESULT 12
US-11-055-822-994
Sequence 994, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Krieger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberdauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
FILE REFERENCE: BGI-121CPN
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 09/606,740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142,101
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148,613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187,970
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE 19930476.9
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931415.2
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931418.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931420.9
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 994
LENGTH: 136
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-11-055-822-994

Query Match 38.8% Score 33; DB 7; Length 136;
Best Local Similarity 35.7% Pred. No. 14;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 NDSPTREQQATW 15
DB 119 SDSPEASEREISIW 132

RESULT 13
US-10-467-7696
Sequence 7696, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA

APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 7696
LENGTH: 248
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7696

Query Match 38.8% Score 33; DB 6; Length 248;
Best Local Similarity 87.5% Pred. No. 27;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPVRTQQ 11
DB 144 SPVRTQQ 151

RESULT 14
US-10-510-386-104
Sequence 104, Application US/10510386
Publication No. US20050244922A1
GENERAL INFORMATION:
APPLICANT: Andersen, Jens Tonne
APPLICANT: Clausen, Ib Groth
APPLICANT: Jorgensen, Steen Troels
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294, 204-US
CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.3
SEQ ID NO 104
LENGTH: 252
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-510-386-104

Query Match 38.8% Score 33; DB 6; Length 252;
Best Local Similarity 50.0% Pred. No. 28;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 VRTREQQATW 15
DB 174 IRTREQQATW 183

RESULT 15
US-11-055-822-240
Sequence 240, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Krieger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberdauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
FILE REFERENCE: BGI-121CPN
CURRENT APPLICATION NUMBER: US/11/055,822
CURRENT FILING DATE: 2005-02-11

```
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 240
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-240
```

```
Query Match          38.8%; Score 33; DB 7; Length 568;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
QY          3 DSPVTEQQAAT 14
          : : : : :
Db          398 ETPVTVARSAT 409
```

Search completed: December 12, 2005, 20:19:48
Job time : 2.4569 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 12, 2005, 20:10:49 ; Search time 12.6724 Seconds
(without alignments)
113.889 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNSDPVTEQOATW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	52.9	321	2	isopenicillin N sy
2	43.5	51.2	403	2	D-galactose-bindin
3	43	50.6	375	2	gag protein - malz
4	43	50.6	470	2	glutaryl-L-lysine
5	42	49.4	247	2	hypothetical prote
6	42	49.4	283	2	glucosyltransferas
7	42	49.4	319	2	glucosyltransferas
8	42	49.4	319	2	exon protein - Rhl
9	41	48.2	101	2	hypothetical prote
10	41	48.2	259	2	hypothetical prote
11	41	48.2	1449	2	hypothetical prote
12	41	48.2	1584	2	hypothetical prote
13	41	48.2	1586	2	hypothetical prote
14	40	47.1	151	2	probable exported
15	40	47.1	270	2	glucosamine-6-phos
16	40	47.1	215	2	probable pol polyp
17	40	47.1	410	2	probable integral
18	40	47.1	513	2	probable RNA-dirac
19	40	47.1	557	2	methy-accepting c
20	40	47.1	631	2	hypothetical prote
21	40	47.1	635	2	hypothetical prote
22	39	45.9	88	2	hypB protein - Bac
23	39	45.9	113	2	T-cell receptor de
24	39	45.9	156	2	conserved hypothet
25	39	45.9	166	2	T-cell receptor de
26	39	45.9	166	2	T-cell receptor de
27	39	45.9	295	2	int protein - phag
28	39	45.9	316	2	multidrug resistan
29	39	45.9	514	2	

30	39	45.9	666	2	semaphorin III - m
31	39	45.9	771	2	semaphorin III pre
32	39	45.9	772	2	collapsin - chicke
33	39	45.9	772	2	semaphorin D - mou
34	39	45.9	772	2	gene 16 protein -
35	38	44.7	393	2	cytochrome P450 10
36	38	44.7	410	1	regulatory protein
37	38	44.7	437	2	glucuronosyltransf
38	38	44.7	460	2	glucuronosyltransf
39	38	44.7	527	2	glucuronosyltransf
40	38	44.7	528	2	glucuronosyltransf
41	38	44.7	529	2	methy-accepting c
42	38	44.7	533	1	methy-accepting c
43	38	44.7	533	2	methy-accepting c
44	38	44.7	551	1	serine chemorecept
45	38	44.7	554	2	methy-accepting c

ALIGNMENTS

RESULT 1
A58458
isopenicillin N synthase (EC 1.14.11.-) [similarity] - Streptomyces cattleya
C:Species: Streptomyces cattleya
C:Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C:Accession: A58458
R:Wang, Y.G.; Li, R.F.
Acta Microbiol. Sin. 36, 87-92, 1996
A:Title: Cloning and sequencing the isopenicillin N synthetase (IPNS) gene from Streptom
A:Reference number: A58458
A:Accession: A58458
A:Molecule type: DNA
A:Residues: 1-321 <MAN>
A:Cross-References: UNIPROT:O53932; UNIPARC:UPI000012D7FD
C:Superfamily: isopenicillin N synthase
C:Keywords: antibiotic biosynthesis; ascorbic acid; iron; metalloprotein; oxidoreductase
P:49,213,269/Binding site: Iron (His) #status predicted

Query Match 52.9%; Score 45; DB 2; Length 321;
Best Local Similarity 50.0%; Pred. No. 3.4;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 2 NDSPPVTEQOATW 15
61 NESTMTDQKSTW 74

RESULT 2
JCS171
D-galactose-binding periplasmic protein mglB-2 - syphilis spirochete
N:Alternate names: carbonhydrate receptor; methylgalactoside transport galactose-binding
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 16-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C:Accession: JCS171; D71295
R:Porcella, S.F.; Popova, T.G.; Hagman, K.E.; Penn, C.W.; Radolf, J.D.; Norgard, M.V.
Gene 177, 115-121, 1996
A:Title: A mgl-like operon in Treponema pallidum, the syphilis spirochete.
A:Reference number: JCS171; MUID:97080510; PMID:8921855
A:Accession: JCS171
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-403 <POB>
A:Cross-References: UNIPROT:O08255; UNIPARC:UPI000012F062; GB:U46416; NID:91230600; PIDN
R:Freaser, C.M.; Norris, S.J.; Weinlock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
R.J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Ulfersback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: D71295
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A;Reference number: A95842; MUID:21396508; PMID:11481431
 A;Accession: A95976
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-319 <KUR>
 A;Cross-references: UNIPROT:P33702; UNIPARC:UPI000012A384; GB:AL591985; PIDN:CMC49473.1;
 A;Experimental source: strain 1021, megaplasmid pSymB
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Adola, P.; Ampe, F.; Barloy-Hubler, P.; Chail, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: exow; SMD21690
 A;Genome: plasmid
 C;Superfamily: Rhizobium succinoglycan biosynthesis glycosyltransferase
 C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 49.4%; Score 42; DB 2; Length 319;
 Best Local Similarity 57.1%; Pred. No. 12;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 NDSFVTEQOATW 15
 ||||| :||| :||
 Db 232 NDSFQFLKQOFNTW 245

RESULT 8
 S40175
 Exow protein - Rhizobium meliloti
 C;Species: Rhizobium meliloti
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S40175
 R;Becker, A.; Kleickmann, A.; Kuester, H.; Keller, M.; Arnold, W.; Puhler, A.
 submitted to the EMBL Data Library, April 1993
 A;Description: Analysis of the Rhizobium meliloti genes exuI, exoV, exow, exoT and exoI
 res.
 A;Reference number: S40173
 A;Accession: S40175
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-319 <BEC>
 A;Cross-references: UNIPROT:P33702; UNIPARC:UPI000012A384; EMBL:222646; NID:g605659; PID
 C;Superfamily: Rhizobium succinoglycan biosynthesis glycosyltransferase

Query Match 49.4%; Score 42; DB 2; Length 319;
 Best Local Similarity 57.1%; Pred. No. 12;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 NDSFVTEQOATW 15
 ||||| :||| :||
 Db 232 NDSFQFLKQOFNTW 245

RESULT 9
 B97851
 hypochlorite protein RCL210 [imported] - Rickettsia conorii (strain Malish 7)
 C;Species: Rickettsia conorii
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C;Accession: B97851
 R;Ogata, H.; Audic, S.; Reneato-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
 Science 293, 2093-2098, 2001
 A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
 A;Reference number: A97700; MUID:21442074; PMID:11557893
 A;Accession: B97851
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-101 <KUD>
 A;Cross-references: UNIPROT:Q92GB3; UNIPARC:UPI00000CC02C; GB:AE006914; PIDN:AAL03748.1;

C;Genetics:
 A;Gene: RCL210

Query Match 48.2%; Score 41; DB 2; Length 101;
 Best Local Similarity 60.0%; Pred. No. 4.9;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 HNDSPVTEQ 10
 ||||| :||| :||
 Db 41 HNDSPVTEQ 50

RESULT 10
 B85066
 hypochlorite protein AT4G05260 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C;Accession: B85066
 R;Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
 Nature 402, 769-777, 1999
 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A;Reference number: A85001; MUID:20083488; PMID:10617198
 A;Accession: B85066
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-259 <STO>
 A;Cross-references: UNIPROT:Q9MOW9; UNIPARC:UPI00000A640D; GB:NC_001268; NID:g7267286; P
 C;Genetics:
 A;Gene: AT4G05260
 A;Map position: 4

Query Match 48.2%; Score 41; DB 2; Length 259;
 Best Local Similarity 63.6%; Pred. No. 14;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 HNDSPVTEQ 11
 ||||| :||| :||
 Db 140 HNDSPVTEQ 150

RESULT 11
 T20181
 hypochlorite protein C53B4.4c - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
 C;Accession: T20181
 R;Berks, M.
 submitted to the EMBL Data Library, December 1995
 A;Reference number: Z19233
 A;Accession: T20181
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1449 <WIL>
 A;Cross-references: UNIPROT:Q9UJ12; UNIPARC:UPI00001641A7; EMBL:268215; PIDN:CAB54213.1;
 A;Experimental source: clone C53B4
 C;Genetics:
 A;Gene: C53B4.4c
 A;Map position: 4
 A;introns: 15/3; 92/2; 252/3; 306/1; 477/2; 571/1; 605/1; 720/3; 880/3; 1008/2; 1091/1;

Query Match 48.2%; Score 41; DB 2; Length 1449;
 Best Local Similarity 58.3%; Pred. No. 92;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 NDSFVTEQOAT 13
 ||||| :||| :||
 Db 423 NNVPIRSERQAT 434

RESULT 12
 T20180
 hypochlorite protein C53B4.4a - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans

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CjDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CjAccession: T20180
RjBerk: M.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19233
A:Accession: T20180
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1584 <N1>
A:Cross-references: UNIPROT:Q18798, UNIPARC:UPI000002A219, EMBL:Z68215, PIDD:CAA92457.1,
A:Experimental source: clone C53B4
CjGenetics:
A:Gene: CESP:C53B4.4a
A:Map position: 4
A:Introns: 61/2, 150/3, 227/2, 387/3, 441/1, 612/2, 706/1, 740/1, 855/3, 1015/3, 1143/2, 1143/2, 1143/2
CjSuperfamily: Caenorhabditis elegans hypothetical protein C53B4.4c

Query Match
Best Local Similarity 48.2% Score 41; DB 2; Length 1584;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 NDSPVTEQOAT 13
Db 558 NNVPFIRSERQAT 569
|:|:|:|:|
|:|:|:|:|

RESULT 13
T20179
hypothetical protein C53B4.4b - Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CjAccession: T20179
RjBerk: M.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19233
A:Accession: T20179
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1586 <N1>
A:Cross-references: UNIPROT:Q18798, UNIPARC:UPI00000866B7, EMBL:Z68215, PIDD:CAA92456.1,
A:Experimental source: clone C53B4
CjGenetics:
A:Gene: CESP:C53B4.4b
A:Map position: 4
A:Introns: 61/2, 150/3, 227/2, 387/3, 441/1, 612/2, 706/1, 740/1, 855/3, 1015/3, 1145/2, 1145/2
CjSuperfamily: Caenorhabditis elegans hypothetical protein C53B4.4c

Query Match
Best Local Similarity 48.2% Score 41; DB 2; Length 1586;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 NDSPVTEQOAT 13
Db 558 NNVPFIRSERQAT 569
|:|:|:|:|
|:|:|:|:|

RESULT 14
AF0931
probable exported protein [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
CjSpecies: Salmonella enterica subsp. enterica serovar Typhimurium
A>Note: this species has also been called Salmonella typhi
CjDate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
CjAccession: AF0931
RjPackhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
th, T.; Comercon, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A:Reference number: AB0502, MUID:21534947, PMID:11677608
A:Accession: AF0931
A:Status: preliminary
A:Molecule type: DNA

```

```

A:Residues: 1-151 <PAR>
A:Cross-references: UNIPARC:UPI000013C475; GB:AL513382; PDB:CAD09472.1; PID:G16504589; C
C:Genetics:
A:Gene: STY3713

Query Match      47.1%; Score 40; DB 2; Length 151;
Best Local Similarity 80.0%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 SPVTEQQQAT 13
      ||:|||||
DB      42 SPLTTEQQAT 51

RESULT 15
FE4050
Glucosamine-6-phosphate deaminase (EC 3.5.99.6) - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: FE4050
R:RFLSICSchmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman, J
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrman, J.L.; Geoghegan, N.S.M.
Science 269, 436-512, 1995
A:Author: Ghem, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: Ae4000; MUID:95350630; PMID:7542800
A:Accession: FE4050
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-270 <TIGR>
A:Cross-references: UNIPROT:P44538; UNIPARC:UPI000012FDD6; GB:U32700; GB:L42023; NID:g321
C:Superfamily: glucosamine-6-phosphate isomerase
C:Keywords: hydrolase; isomerase

Query Match      47.1%; Score 40; DB 2; Length 270;
Best Local Similarity 54.5%; Pred. No. 22;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      5 PVTEQQQATW 15
      ||:|||||
DB      5 PLQTEQQVSCW 15

```

Search completed: December 12, 2005, 20:42:47
Job time : 14.6724 secs

	Query Match	Score	DB	Length	270;
	Best Local Similarity	54.5%			
Matches	6;	Conservative	3;	Mismatches	2;
				Indels	0;
				Gaps	0;
Qy	5	PARTEQQATW	15		
	: :				
Db	5	PLDTEQOVSCW	15		

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:41 ; Search time 81.4655 Seconds
(without alignments)
129.907 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNDSPVTEQOATW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	50	58.8	397	2	Q6Q4A6_TETTH
2	50	58.8	1522	2	Q5C0B3_CRYPV
3	48	56.5	735	2	Q8XXG1_PALSO
4	47	55.3	84	2	Q7RCB5_GOSAR
5	47	55.3	1083	2	Q941B9_CRYNE
6	47	55.3	2360	2	Q941B8_CRYNE
7	47	55.3	2360	2	Q55R83_CRYNE
8	47	55.3	2360	2	Q5KEY7_CRYNE
9	46	54.1	425	2	Q9VGS4_DROME
10	46	54.1	449	2	Q8W7Z6_DROME
11	46	54.1	526	2	Q6AWF6_DROME
12	46	54.1	621	2	Q9VGS5_DROME
13	45.5	53.5	700	2	Q8SOK3_ENCCU
14	45	52.9	321	1	IPNS_STRCT
15	45	52.9	407	2	Q4WH6O_ASPFU
16	44	51.8	673	2	Q9VW10_DROME
17	43.5	51.2	403	1	MGJB_TREPA
18	43	50.6	470	1	SYE_CAVCR
19	43	50.6	774	2	Q8JIM9_XENLA
20	43	50.6	832	2	Q5E2F3_VIBF1
21	43	50.6	1378	2	Q4PFR4_USRMA
22	43	50.6	2742	2	Q8XX21_PALSO
23	43	50.6	2742	2	Q4SZV7_TETNG
24	42	49.4	79	2	Q4ZNL8_PSEBSY
25	42	49.4	79	2	Q87WK0_PSEBSY
26	42	49.4	194	2	Q67J75_SYWTH
27	42	49.4	221	2	Q7PK01_ANOGA
28	42	49.4	247	2	Q8YWK3_ANASP
29	42	49.4	260	2	Q7J3Z6_MYCPA
30	42	49.4	262	2	Q7XBD0_MAIZE
31	42	49.4	296	1	ZN75A_HUMAN

32	42	49.4	319	1	EXOW_RHIME	P33702 rhizobium m
33	42	49.4	426	2	Q6C666_YARLI	Q6C666 yarowia li
34	42	49.4	303	2	Q7Q1A0_ANOGA	Q7Q1A0 anophles g
35	42	49.4	646	2	Q6BGK5_PARTE	Q6BGK5 paramesicium
36	42	49.4	732	2	Q6LN06_PROPR	Q6LN06 photobacter
37	42	49.4	817	2	Q6ZPNT_MOUSE	Q6ZPNT mus musculu
38	42	49.4	983	2	Q6VEB8_USRMA	Q6VEB8 usellago ma
39	42	49.4	983	2	Q4P7R6_USRMA	Q4P7R6 mus musculu
40	42	49.4	1727	2	Q68FD9_MOUSE	Q68FD9 mus musculu
41	42	49.4	2316	2	Q58GK8_PIG	Q58GK8 sus scrofa
42	42	49.4	2411	2	Q58G70_PIG	Q58G70 sus scrofa
43	42	49.4	10791	2	Q7U7M8_STNPK	Q7U7M8 bynechococ
44	41	48.2	101	2	Q92GB3_RICCN	Q92GB3 rickettsia
45	41	48.2	249	2	Q7V6M2_PROWM	Q7V6M2 prochloroxo

ALIGNMENTS

RESULT 1					
ID	Q6Q4A6_TETTH	PRELIMINARY;	PRT;	397 AA.	
AC	Q6Q4A6				
DT	05-JUL-2004 (TrEMBLrel. 27, Created)				
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)				
DE	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)				
OS	Tetrahymena thermophila				
OC	Eukaryota; Alveolata; Ciliophora; Oligotrichophorea; Hymenostomatida;				
OC	Tetrahymenina; Tetrahymenidae; Tetrahymena.				
OX	NCBI_TaxID=5911;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Arslanoglu M., Yildiz M.T.;				
RL	Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.				
CC	-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.				
CC	-I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.				
DR	EMBL; AY650586; AAS5515.1; -; Genomic_DNA.				
DR	HSSP; P24941; 1X88.				
DR	GO; GO:0005524; F:ATP binding; IEA.				
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.				
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.				
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.				
DR	InterPro; IPR003527; MAP_kin.				
DR	InterPro; IPR008271; Ser_thr_kin_AS.				
DR	InterPro; IPR002290; Ser_thr_kinase.				
DR	InterPro; IPR001245; Tyr_kinase.				
DR	Pfam; PF00069; Pkinase; 1.				
DR	ProDom; PD000001; Prot_kinase; 1.				
DR	SMART; SM002219; TyrKc; 1.				
DR	SMART; SM001351; MAPK; UNKNOWN_1.				
DR	PROSITE; PS01017; MAPKIN_KINASE_ATP; 1.				
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.				
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.				
KW	ATP-binding; kinase; Nucleotide-Binding;				
KW	Serine/threonine-protein Kinase; Transferase.				
SQ	SEQUENCE 397 AA; 45764 MW; 43AE8281F714E071 CRC64;				
Query Match					
Best Local Similarity 58.8%; Score 50; DB 2; Length 397;					
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;					
QY	2	NDSPVTEQOATW	15		
DB	169	DDNPVTEVATRW	182		
RESULT 2					
ID	Q5C0B3_CRYPV	PRELIMINARY;	PRT;	1522 AA.	
AC	Q5C0B3				

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DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Possible ABC transporter with AAA domain and 12 transmembrane
DE domains.
GN ORFNames=cgd4_1390;
OS Cryptosporidium parvum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
OC Cryptosporidiidae; Cryptosporidium.
NC NCBI_Taxid=5807;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Iowa type II;
RA PubMed=15044751; DOI=10.1126/science.1094786;
RA Abrahamson M.S., Templeton T.J., Enomoto S., Abrahamte J.E., Zhu G.,
RA Lanco C.A., Deng M., Liu C., Widmer G., Tzipori S., Buck G.A., Xu P.,
RA Bankier A.T., Dear P.H., Kontorov B.A., Spriggs H.F., Iyer L.,
RA Anantharaman V., Aravind L., Kapur V.;
RT "Complete genome sequence of the apicomplexan, Cryptosporidium
RT parvum.";
RL Science 304:441-445(2004).
DR EMBL; AAEE01000009; EAK87614.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016867; F:ATPase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PSS0893; ABC_TRANSPORTER_2; 1.
KW Transmembrane.
SQ SEQUENCE 1522 AA; 176017 MW; 75C04515093B3981 CRC64;

Query Match 58.8%; Score 50; DB 2; Length 1522;
Best Local Similarity 53.3%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HNDSPVTEQOATTW 15
Db 72 HNDKQVPESEISIW 86

RESULT 3
08XXG1_RALSO
ID 08XXG1_RALSO PRELIMINARY; PRT; 735 AA.
AC 08XXG1;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE PROBABLE BIFUNCTIONAL ENZYME: (P)PGPP SYNTHETASE II AND GUANOSINE-
DE 3',5'-BIDIPHOSPHATE 3'-PYROPHOSPHOHYDROLASE (PPGPPASE) PROTEIN
DE (EC 2.7.6.5) (EC 3.1.7.2).
GN Name=ppp1; OrderedLocNames=RSC2153; ORFNames=R801611;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
NC NCBI_Taxid=305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GW11000;
RA MEDLINE=2161879; PubMed=11823852; DOI=10.1038/415497a;
RA Sialoubat M., Genin S., Artiguenave F., Guzy J., Mangnot S.,
RA Ailat M., Billault A., Broctier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schick T.,
RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weisenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646068; CAD15860.1; -; Genomic DNA.
DR GO; GO:0016597; F:amino acid binding; IEA.
DR GO; GO:0008893; F:guanosine-3',5'-bis(diphosphate) 3'-diphosp. .; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.

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DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0015969; F:guanosine tetraphosphate metabolism; IEA.
DR GO; GO:008152; P:metabolism; IEA.
DR InterPro; IPR002912; ACT.
DR InterPro; IPR006674; HD_hydro.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR007685; RelA_Spot.
DR InterPro; IPR004811; Spot_rela.
DR InterPro; IPR004095; TGS.
DR Pfam; PF01842; ACT; 1.
DR Pfam; PF01966; HD; 1.
DR Pfam; PF04607; RelA_Spot; 1.
DR Pfam; PF02824; TGS; 1.
DR SMART; SM00471; HDc; 1.
DR TIGRFAMs; TIGR00691; spot_rela; 1.
KW Complete proteome; Hydrolase; Transferase.
SQ SEQUENCE 735 AA; 81861 MW; 9A6B0051104FD241 CRC64;

Query Match 56.5%; Score 48; DB 2; Length 735;
Best Local Similarity 53.3%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HNDSPVTEQOATTW 15
Db 358 HNDSPVTEQOATTW 372

RESULT 4
07PCB5_GOSAR
ID 07PCB5_GOSAR PRELIMINARY; PRT; 84 AA.
AC 07PCB5;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Putative phytoalexin peptide precursor.
GN Name=PSK1;
OS Gossypium arboreum (Tree cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
NC NCBI_Taxid=29729;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lorbiecke R., Sauter M.M.;
RT "Comparative analysis of PSK peptide growth factor precursor
RT homologs.";
RL Plant Sci. 163:321-332(2002).
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BK000114; DA00278.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR InterPro; IPR009438; PSK.
DR Pfam; PF06404; PSK; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 84 AA; 9242 MW; 6B04F8D05BC36C9B CRC64;

Query Match 55.3%; Score 47; DB 2; Length 84;
Best Local Similarity 61.5%; Pred. No. 2.8;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPVTEQOATT 14
Db 32 NDSPVTEQOATT 44

RESULT 5
094189_CRYNE
ID 094189_CRYNE PRELIMINARY; PRT; 1083 AA.
AC 094189;
DT 01-MAY-1999 (TReMBLrel. 10, Created)

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DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Phosphatidylinositol 3-kinase TOR1 (Fragment).
GN Name=TOR1;
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B3501;
RX MEDLINE=99262981; PubMed=10330150;
RA Cruz M.C., Cavallo L.M., Goriach J.M., Cox G., Perfect J.R.,
RA Cardenas M.E., Heitman J.;
RT "Rapamycin antifungal action is mediated via conserved complexes with
RT FKBP12 and TOR kinase homologs in Cryptococcus neoformans.";
RL Mol. Cell. Biol. 19:4101-4112(1999).
DR EMBL; AF098973; AAD16274.1; -; mRNA.
DR HSSP; P42345; LAUE.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016773; F:phosphotransferase activity, alcohol group . . .; IEA.
DR InterPro; IPR003151; FAT.
DR InterPro; IPR00403; P13/4_kinase_cat.
DR InterPro; IPR01990; TPR-like_helical.
DR Pfam; PF02259; FAT; 1.
DR Pfam; PF00454; P13_P14_kinase; 1.
DR SMART; SM00146; PI3K; 1.
DR PROSITE; PS00915; P13_4_KINASE_1; 1.
DR PROSITE; PS50290; P13_4_KINASE_3; 1.
KW Kinase; Transferase.
FT NON_TER
FT TER
SQ SEQUENCE 1083 AA; 123973 MW; 0C48A1D758353A9 CRC64;

Query Match 55.3%; Score 47; DB 2; Length 1083;
Best Local Similarity 53.3%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQTW 15
DB 202 HADEPARQEMORQTW 216

RESULT 6
ID 094188_CRYNE PRELIMINARY; PRT; 2360 AA.
AC 094188;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Phosphatidylinositol 3-kinase TOR1.
GN Name=TOR1;
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H99;
RX MEDLINE=99262981; PubMed=10330150;
RA Cruz M.C., Cavallo L.M., Goriach J.M., Cox G., Perfect J.R.,
RA Cardenas M.E., Heitman J.;
RT "Rapamycin antifungal action is mediated via conserved complexes with
RT FKBP12 and TOR kinase homologs in Cryptococcus neoformans.";
RL Mol. Cell. Biol. 19:4101-4112(1999).
DR EMBL; AF098972; AAD16273.1; -; Genomic_DNA.
DR HSSP; P42345; LAUE.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0016773; F:phosphotransferase activity, alcohol group . . .; IEA.
DR InterPro; IPR011989; ARM-like.

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DR InterPro; IPR003151; FAT.
DR InterPro; IPR003152; FATC.
DR InterPro; IPR000357; HEATC.
DR InterPro; IPR00403; P13/4_kinase_cat.
DR Pfam; PF02259; FAT; 1.
DR Pfam; PF02260; FATC; 1.
DR Pfam; PF02985; HEAT; 3.
DR Pfam; PF00454; P13_P14_kinase; 1.
DR SMART; SM00146; PI3K; 1.
DR PROSITE; PS00915; P13_4_KINASE_1; 1.
DR PROSITE; PS50290; P13_4_KINASE_3; 1.
KW Kinase
SQ SEQUENCE 2360 AA; 267216 MW; ED4A1059B1AA2B2A CRC64;

Query Match 55.3%; Score 47; DB 2; Length 2360;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQTW 15
DB 1479 HADEPARQEMORQTW 1493

RESULT 7
ID 055R83_CRYNE PRELIMINARY; PRT; 2360 AA.
AC 055R83;
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CNBP1080;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA Wickes B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA01000030; BAU20296.1; -; Genomic_DNA.
DR KW Hypothetical protein.
SQ SEQUENCE 2360 AA; 267302 MW; EB7ABF66AB68ADF CRC64;

Query Match 55.3%; Score 47; DB 2; Length 2360;
Best Local Similarity 53.3%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQTW 15
DB 1479 HADEPARQEMORQTW 1493

RESULT 8
ID 05KEY7_CRYNE PRELIMINARY; PRT; 2360 AA.
AC 05KEY7;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE Phosphatidylinositol 3-kinase TOR1.
GN ORFNames=CNF03740;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=214684;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=JSC21;
 RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Uterback T.,
 RA Van Aken S., Fraser C.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=JSC21;
 RA PubMed=15653466; DOI=10.1126/science.1103773;
 RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
 RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
 RA Boeder I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
 RA D'Souza C.A., Fox D.S., Grindberg V., Fu J., Fukushima M., Haas B.J.,
 RA Huang J.C., Janson G., Jones S.J.M., Koo H.L., Kzysinski M.I.,
 RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
 RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,
 RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
 RA Suh B.B., Tenney A., Uterback T.R., Wickes B.L., Wotman J.R.,
 RA Wye N.H., Kronstad J.W., Lodge J.K., Heltman J., Davis R.W.,
 RA Fraser C.M., Hyman R.W.;
 RT "The genome of the basidiomycetous yeast and human pathogen
 RT *Cryptococcus neoformans*.";
 RL Science 307:1121-1124(2005).
 DR EMBL: AEO17346; AAM44029.1; -, Genomic DNA.
 DR GO: GO:0016301; F:kinase activity; IEA.
 DR GO: GO:0016773; F:phosphotransferase activity, alcohol group . . .; IEA.
 DR InterPro: IPR011989; AAM-like.
 DR InterPro: IPR003151; FAT.
 DR InterPro: IPR003152; PAT.
 DR InterPro: IPR000357; HEAT.
 DR InterPro: IPR000403; P13/4_kinase_cat.
 DR InterPro: IPR011990; TPR-like_helical.
 DR Pfam: PF02259; FAT; 1.
 DR Pfam: PF02260; PATC; 1.
 DR Pfam: PF02985; HEAT; 3.
 DR Pfam: PF00454; P13_P14_kinase; 1.
 DR SMART: SM00146; P13K; 1.
 DR PROSITE: PS00915; P13_4_KINASE_1; 1.
 DR PROSITE: PS50290; P13_4_KINASE_3; 1.
 DR Complete proteome: Kinase.
 SQ SEQUENCE 2360 AA; 267304 MW; EBAABF966A6BADF CRC64;
 QY 1 HNDSPVTEQATW 15
 Db 1479 HADEPAKQWQROT 1493
 Query Match 55.3%; Score 47; DB 2; Length 2360;
 Best Local Similarity 53.3%; Pred. No. 1,le+02;
 Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 RESULT 9
 ID OSVGS4_DROME PRELIMINARY; PRT; 425 AA.
 AC OSVGS4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CG31299-PB, isoform B.
 GN Name=nocutrin; ORNames=CG31299;
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscormorpha;
 OC Ephydroidea; Drosophilidae; *Drosophila*.
 OC NCBI_TaxID=7227;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,

Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Adair J.F., Agbayani A., An H.-J., Andrews-Plamkoch C., Baldwin D.,
 RA Ballaw R.M., Baen A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokerstein P., Brotter P.,
 RA Butts K.C., Buam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostali M., Houston K.A., Howland T.J., Wei M.-H., Ileguam C.,
 RA Jaisai M., Kalush F., Karpem G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshell A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
 RA Battencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;

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RT "Drosophila melanogaster release 4 sequence."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003690; AAF54601.2; -; Genomic DNA.
DR Ensembl; CG31299; Drosophila melanogaster.
DR FlyBase; FBgn0037872; CG31299.
DR FlyBase; FBgn0037872; nocturnin.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
SQ SEQUENCE 425 AA; 47584 MW; AABF2F74541D29F CRC64;

Query Match          54.1%; Score 46; DB 2; Length 425;
Best Local Similarity 53.3%; Pred. No. 25;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HNDSPVTEQOATW 15
    ||| ||| ||| |||
    109 HNDGFVRCPEALTW 123

RESULT 10
Q8MT26 DROME PRELIMINARY; PRT; 449 AA.
AC Q8MT26;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Nocturnin.
GN Name=nocturnin; ORFNames=CG31299;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=11747467;
RA Dupressoir A., Morel A.-P., Barbot W., Loizeau M.-P., Corbo L.,
RA Heidmann T.;
RT "Identification of four families of YCCRA- and Mg2+-dependent
RT endonuclease-related proteins in higher eukaryotes, and
RT characterization of orthologs of YCCRA with a conserved leucine-rich
RT repeat essential for hCAFL/hPO2 binding."
RL BMC Genomics 2:9-9(2001).
DR EMBL; AY043266; AAK85704.1; -; mRNA.
DR Ensembl; CG31299; Drosophila melanogaster.
DR FlyBase; FBgn0037872; CG31299.
DR FlyBase; FBgn0037872; nocturnin.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
SQ SEQUENCE 449 AA; 50275 MW; 1607DF25A418A024 CRC64;

Query Match          54.1%; Score 46; DB 2; Length 449;
Best Local Similarity 53.3%; Pred. No. 27;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HNDSPVTEQOATW 15
    ||| ||| ||| |||
    133 HNDGFVRCPEALTW 147

RESULT 11
Q6AWF6 DROME PRELIMINARY; PRT; 526 AA.
AC Q6AWF6;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE GH03334p.
GN Name=nocturnin;

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OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkeley;
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Man K., Yu C., Rubin G.M., Celinker S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT015292; AAT94521.1; -; mRNA.
DR InterPro; IPR005135; Exo_endo_phos.
DR Pfam; PF03372; Exo_endo_phos; 1.
SQ SEQUENCE 526 AA; 58950 MW; BDE21244AB110FA CRC64;

Query Match          54.1%; Score 46; DB 2; Length 526;
Best Local Similarity 53.3%; Pred. No. 32;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 HNDSPVTEQOATW 15
    ||| ||| ||| |||
    210 HNDGFVRCPEALTW 224

RESULT 12
Q9VGS5 DROME PRELIMINARY; PRT; 621 AA.
AC Q9VGS5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE CG31299-PA, isoform A.
GN Name=nocturnin; ORFNames=CG31299;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Suton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fouts R.K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hooten D., Houston K.A., Howland T.J., Wei M.-H., Ibegun C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kerchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

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RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*,"
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Peclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svireksas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence,"
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svireksas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celinker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective,"
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Battencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review,"
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svireksas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence,"
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AEO03690; AAF54600.2; -, Genomic DNA.
 DR Ensembl: CG31299; Drosophila melanogaster.
 DR FlyBase: FBgn0037872; CG31299.
 DR FlyBase: FBgn0037872; nocturnin.
 DR Interpro: IPR005135; Exo endo phos.
 DR Pfam: PF03372; Exo_endo_phos; 1.
 SQ SEQUENCE 621 AA; 69511 MW; A775AD0BB776FEF1 CRC64;

Query Match 54.1%; Score 46; DB 2; Length 621;
 Best Local Similarity 53.3%; Pred. No. 39;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 HNDSPVTEQQTW 15
 DB 305 HNDGFVRCPEALTW 319

RESULT 13
 OS0K3_ENCCU
 ID OS0K3_ENCCU PRELIMINARY; PRT; 700 AA.

AC OS0K3;
 DT 01-JUN-2002 (TEMBLrel. 21, Created)
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE VCUOLAR ATP SYNTHASE 95KDa SUBUNIT.
 GN OrderedLocusNames=ECU09_1790;
 OS Encephalitozoon cuniculi.
 OC Eukaryota; Fungi; Microsporidia; Unikaryoniidae; Encephalitozoon.
 ON NCBI_TaxID=6035;
 RN [1]
 RP NCLEOTIDE SEQUENCE.
 RC STRAIN=GB-M1;
 RX MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
 RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomaret F.,
 RA Prensler G., Barbe V., Peyreclat E., Brotlier P., Wincker P.,
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weisenbach J., Vives C.P.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 RT Encephalitozoon cuniculi,"
 RL Nature 414:450-453(2001).
 RL EMBL: AL590451; CAD27151.1; -, Genomic DNA.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
 DR GO: GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.
 DR GO: GO:0046361; F:hydrogen-transporting ATP synthase activity; IEA.
 DR GO: GO:0015986; P:ATP synthesis coupled proton transport; IEA.
 DR GO: GO:0015992; P:proton transport; IEA.
 DR Interpro: IPR00711; ATPsyn OSCP.
 DR Interpro: IPR002355; Cu ox copper BS.
 DR Interpro: IPR002490; V_ATPase_sub16.
 DR Pfam: PF01436; V_ATPase_1; 1.
 DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
 KM Complete proteome.
 SQ SEQUENCE 700 AA; 80781 MW; FD79BB62373763D CRC64;

Query Match 53.5%; Score 45.5; DB 2; Length 700;
 Best Local Similarity 45.0%; Pred. No. 54;
 Matches 9; Conservative 2; Mismatches 4; Indels 5; Gaps 1;

QY 1 HNDSPVTEQQTW 15
 DB 233 HNDFAIRKEQKIRHFAWTW 252

RESULT 14
 IPNS STRCT
 ID IPNS STRCT STANDARD; PRT; 321 AA.
 AC Q53932;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Isopenicillin N synthetase (EC 1.21.3.1) (IPNS) (Isopenicillin N
 DE synthase).
 GN Namepbc; Synonym=ipns;
 OS Streptomyces catleya.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycesae; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxID=29303;
 RN [1]
 RP NCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=97350503; PubMed=9206271;
 RA Wang Y., Li R.;
 RT "Cloning and sequencing the isopenicillin N synthetase (IPNS) gene
 RT from Streptomyces catleya,"
 RL Wei Sheng Wu Xue Bao 36:87-92(1996).
 CC -1- FUNCTION: Removes, in the presence of oxygen, 4 hydrogen atoms
 CC from delta-L-(alpha-aminoadipyl)-L-cysteiny-D-valine (ACV) to
 CC form the azetidinone and thiazolidine rings of isopenicillin.
 CC -1- CATALYTIC ACTIVITY: N-((5S)-5-amino-5-carboxypentamoyl)-L-
 CC cysteinyl-D-valine + O(2) = isopenicillin N + 2 H(2)O.
 CC -1- COFACTOR: Iron and ascorbate.
 CC -1- PATHWAY: Biosynthesis of penicillin and cephalosporin.
 CC -1- SIMILARITY: Belongs to the iron/ascorbate-dependent oxidoreductase

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CC family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; D78166; BA011234.1; -; Genomic_DNA.
DR PIR; A58458; A58458.
DR HSSP; P05326; 103E.
DR InterPro; IPR005123; 2OG-Fell_Oase.
DR InterPro; IPR002283; IPN_synth.
DR InterPro; IPR002057; Isopen_N_synth.
DR PANTHER; PTHR10209:SF1; Isopen_N_synth; 1.
DR Pfam; PF03171; 2OG-Fell_Oxy; 1.
DR PRINTS; PR00682; IPNSYNTHASE.
DR PROSITE; PS00185; IPNS_1; 1.
DR PROSITE; PS00186; IPNS_2; 1.
DR Antibiotic biosynthesis; Iron; Metal-binding; Oxidoreductase;
KM Vitamin C.
FT METAL 213 213 Iron (By similarity).
FT METAL 215 215 Iron (By similarity).
FT METAL 269 269 Iron (By similarity).
SQ SEQUENCE 321 AA; 36577 MW; BCC0CFCEFC7C07AF1 CRC64;

Query Match 52.9%; Score 45; DB 1; Length 321;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPVTEQOATW 15
Db 61 NESTTMDQRSTW 74

RESULT 15
Q4WH60 ASPFU PRELIMINARY; PRT; 407 AA.
AC Q4WH60
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE MFS transporter, putative.
GN ORENAMES=AFU708460;
OS Aspergillus fumigatus AF293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=330879;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AF293.
RA Nierman W., Fain A., Anderson M.J., Wortman J., Kim H., Stanley,
RA Arroya J., Bertrian M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins K., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Fooker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Goni K., Griffith-Jones S., Gilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafon A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA Mouyna I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penava M.A., Petrea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renaud H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Rouning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus.";
RL Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.

```

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CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHF01000009; EAL86731.1; -; Genomic DNA.
SQ SEQUENCE 407 AA; 43375 MW; F249C762E0CA8116 CRC64;

Query Match 52.9%; Score 45; DB 2; Length 407;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPVTEQOATW 15
Db 15 NGSPVMAQRSTW 28

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Search completed: December 12, 2005, 20:41:05
Job time : 84.4655 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 20:43:06 ; Search time 112.667 Seconds
(without alignments)
58.497 Million cell updates/sec

Title: US-10-758-165A-3
Perfect score: 74
Sequence: 1 RNNVLIQDQOATTR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 770462

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A.GeneSeq_21:*

- 1: Genesepq1980s:*
- 2: Genesepq1990s:*
- 3: Genesepq2000s:*
- 4: Genesepq2001s:*
- 5: Genesepq2002s:*
- 6: Genesepq2003as:*
- 7: Genesepq2003bs:*
- 8: Genesepq2004s:*
- 9: Genesepq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	15	8	ADRI0603 Horse IGE
2	49	66.2	15	7	ADG64568 Horse Imm
3	41	55.4	15	8	ADRI0601 Dog IGE e
4	40	54.1	15	8	ADRI0607 Pig IGE e
5	37	50.0	15	8	ADRI0602 Cat IGE e
6	32	43.2	15	7	ADRI0602 Cat IGE e
7	32	43.2	15	7	ADRI0602 Cat IGE e
8	29	39.2	12	9	ADRI0602 Cat IGE e
9	29	39.2	12	9	ADRI0602 Cat IGE e
10	29	39.2	12	9	ADRI0602 Cat IGE e
11	29	39.2	12	9	ADRI0602 Cat IGE e
12	29	39.2	12	9	ADRI0602 Cat IGE e
13	29	39.2	12	9	ADRI0602 Cat IGE e
14	29	39.2	12	9	ADRI0602 Cat IGE e
15	29	39.2	12	9	ADRI0602 Cat IGE e
16	29	39.2	12	9	ADRI0602 Cat IGE e
17	29	39.2	12	9	ADRI0602 Cat IGE e
18	29	39.2	12	9	ADRI0602 Cat IGE e
19	29	39.2	12	9	ADRI0602 Cat IGE e
20	29	39.2	12	9	ADRI0602 Cat IGE e
21	29	39.2	12	9	ADRI0602 Cat IGE e
22	29	39.2	12	9	ADRI0602 Cat IGE e
23	29	39.2	12	9	ADRI0602 Cat IGE e
24	29	39.2	12	9	ADRI0602 Cat IGE e

25	27	36.5	15	8	ADN70579 Human 273
26	27	36.5	15	8	ADN71415 Human 273
27	26	35.1	10	8	ADN12489 Scorpion
28	26	35.1	10	8	ADH89500 Scorpion
29	26	35.1	12	9	ADY55643 Hair-bind
30	26	35.1	13	7	ADY43593 CPg2 pept
31	26	35.1	15	5	ADP57763 Human pho
32	25	33.8	9	8	ADN67893 Human 273
33	25	33.8	9	8	ADN67893 Human 273
34	25	33.8	9	8	ADN67893 Human 273
35	25	33.8	9	8	ADN67893 Human 273
36	25	33.8	9	8	ADN67893 Human 273
37	25	33.8	10	8	ADN67893 Human 273
38	25	33.8	10	8	ADN67893 Human 273
39	25	33.8	10	8	ADN67893 Human 273
40	25	33.8	12	4	AAU17678 Novel sig
41	25	33.8	12	4	AAE11146 Chymotryp
42	25	33.8	12	6	ABO27234 Gab5 puta
43	25	33.8	12	7	ADN94386 Novel hum
44	25	33.8	13	2	AAW41492 Peptidy1
45	25	33.8	13	7	ADD23407 Breast ca

ALIGNMENTS

RESULT 1
ADRI0603
ID ADRI0603 standard; peptide, 15 AA.
AC ADRI0603;
XX 21-OCT-2004 (first entry)
DT
XX Horse IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 3.
DE
XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW horse.
XX
XX Equus caballus.
OS
XX
XX WO2004065936-A2.
PN
XX
XX 05-AUG-2004.
PD
XX
XX 15-JAN-2004; 2004WO-US003566.
PF
XX 16-JAN-2003; 2003US-0440472P.
PR
XX (UNNC-) UNIV NORTH CAROLINA STATE.
PA
XX Hammerberg B;
XX WPI; 2004-593545/57.
XX
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
PS
XX Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC (I) is useful for testing an allergen reactivity of an IGE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC horse IGE 5.91 recognition site.

XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDOQATTR 15
 |||||
 Db 1 RNNVLIQTDOQATTR 15

RESULT 2

ADCC45568
 ID ADC64568 standard; peptide; 15 AA.

AC ADC64568;

DT 18-DEC-2003 (first entry)

DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P4.

XX Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.

XX Equus caballus.

OS US2003087314-A1.

PN 08-MAY-2003.

PD 08-NOV-2001; 2001US-00052788.

PF 08-NOV-2001; 2001US-00052788.

PR 08-NOV-2001; 2001US-00052788.

PA (REGC) UNIV CALIFORNIA.

PI Gershwin LJ, Pettigrew HD, Kalina WV;

XX WPI; 2003-765437/72.

PT Immunogenic composition comprising an isolated equine immunoglobulin E
 PT polypeptide that induces production of antibodies which specifically bind
 PT to equine immunoglobulin E.

XX Example 1; Page 8; 14pp; English.

XX The invention relates to an immunogenic composition comprising an
 CC isolated polypeptide having an amino acid sequence that is at least 80%
 CC identical to 6 (SI-86) 15 amino acid peptide sequences derived from
 CC equine immunoglobulin E (the composition induces production of an
 CC antibody that specifically binds to equine immunoglobulin (IgE), the six
 CC polypeptides are not explicitly identified in the specification. Also
 CC included are a composition comprising an antibody that specifically binds
 CC to a polypeptide at least 80% identical to (SI)-(86), an antibody that
 CC specifically binds to equine IGE made by the process of immunising an
 CC animal with a polypeptide at least 80% identical to (SI)-(86), making an
 CC antibody that specifically binds to equine IGE (involving immunising an
 CC animal with a composition further comprising an isolated polypeptide (the
 CC amino acid sequence of the polypeptide is at least 80% identical to (SI)-
 CC (86)), and collecting antiserum from the animal) and a kit for detection
 CC of equine IGE in a biological sample comprising the antibody and means
 CC for detecting specific binding of the antibody to equine IGE. The
 CC antibody is useful for detecting equine IGE protein in a biological
 CC sample (serum) which involves contacting the sample with the antibody/
 CC thus forming an antigen/antibody complex, and detecting the presence or
 CC absence of the antigen/antibody complex. The antibody and antigen are
 CC immobilised on a solid surface. The antibody is labelled such that the
 CC complex can be detected. The complex is detected using a second labelled

CC antibody. The peptides are useful for generating antibodies specific for
 CC IGE which can serve as a diagnostic test for allergy. The present
 CC sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic
 CC peptide from the early portion of the C4 region.

XX
 SQ Sequence 15 AA;

Query Match 66.2%; Score 49; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.071;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IQTDOQATTR 15
 |||||
 Db 1 IQTDOQATTR 10

RESULT 3

ADRI0601
 ID ADRI0601 standard; peptide; 15 AA.

AC ADRI0601;

DT 21-OCT-2004 (first entry)

DE Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;

XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.

OS Canis familiaris.

PN WO2004065936-A2.

PD 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

PA (VINC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

XX WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE.

XX
 SQ Sequence 15 AA;

Query Match 55.4%; Score 41; DB 8; Length 15;
 Best Local Similarity 64.3%; Pred. No. 2;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 RNNVLIQTDOQATT 14
 ||: |||||
 DB 1 RNDSPVRIQTDOQATT 14

RESULT 4

ADRI0607
 ID ADRI0607 standard; peptide; 15 AA.

AC ADRI0607;

DT 21-OCT-2004 (first entry)

DE Pig IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.

KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
 anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 cat.

OS Sus scrofa.

PN WO2004065936-A2.

PD 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

PA (UNNC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

DR WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IGE epitope, useful
 for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC pig IGE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 54.1%; Score 40; DB 8; Length 15;

Best Local Similarity 46.7%; Pred. No. 3.1;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 RNNVLIQTDOQATT 15
 ||: |||||

DB 1 RNDAPVQADRHSTTR 15

RESULT 5

ADRI0602
 ID ADRI0602 standard; peptide; 15 AA.

AC ADRI0602;
 XX 21-OCT-2004 (first entry)
 XX

DE Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.

KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
 anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 cat.

OS Felis catus.

PN WO2004065936-A2.

PD 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

PA (UNNC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

DR WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IGE epitope, useful
 for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC cat IGE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 50.0%; Score 37; DB 8; Length 15;

Best Local Similarity 53.8%; Pred. No. 11;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 RNNVLIQTDOQATT 14
 ||: |||||

DB 2 RNDSPVRIQTDOQATT 14

RESULT 6

ADD44095
 ID ADD44095 standard; peptide; 15 AA.

AC ADD44095;

DT 15-JAN-2004 (first entry)

DE CPG2 peptide #1 able to stimulate human T-cells in vitro.

KW bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;
 immunogenic; T-cell epitope; MHC class II binding ligand;
 immunostimulant; enzyme therapy; immune response;

KM gene directed enzyme prodnrg strategy; vaccine; enzyme; EC 3.4.17.11.
 XX Pseudomonas sp. RS-16.
 XX WO2003045426-A1.
 XX PD 05-JUN-2003.
 XX PF 27-NOV-2002; 2002WO-EP013351.
 XX PR 29-NOV-2001; 2001EP-00128519.
 XX PR 25-JAN-2002; 2002EP-00001778.
 XX PR 13-SEP-2002; 2002EP-00020634.
 XX PA (MERCK) MERCK PATENT GMBH.
 XX PI Hellendoorn K, Baker M, Williams S, Carr FJ;
 XX WPI; 2003-513617/48.
 XX PT New modified bacterial enzyme carboxypeptidase G2 (CPG2) having
 PT substantially non-immunogenic or less immunogenic than any non-modified
 PT CPG2, useful for inducing an immune response in a human host.
 XX PS Claim 3; Page 14; 52pp; English.
 XX CC The invention relates to a novel modified bacterial enzyme
 CC carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2
 CC proteins that are substantially non-immunogenic or less immunogenic than
 CC any non-modified CPG2 having essentially the same biological specificity
 CC when used in vivo, and comprising specific amino acid residues having
 CC alterations compared with the non-modified parochial enzyme. The
 CC alterations cause a reduction or an elimination of one or more of T-cell
 CC epitope sequences, which act in the parental enzyme as MHC class II
 CC binding ligands and stimulate T-cells. The modified CPG2 enzyme and the
 CC CPG2 proteins have immunostimulant activity and may be used in enzyme
 CC therapy. The modified CPG2 enzyme may be used to induce an immune
 CC response in a human host, or as a therapeutic entity such as the gene
 CC directed enzyme prodnrg strategy. The peptide is useful for the
 CC manufacture of a modified CPG2 enzyme having substantially no or less
 CC immunogenicity than any non-modified parental enzyme when used in vivo,
 CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.
 CC This sequence represents a CPG2 enzyme peptide able to stimulate human T-
 CC cells in vitro of the invention.
 XX SQ Sequence 15 AA;
 XX

Query Match 43.2%; Score 32; DB 7; Length 15;
 Best Local Similarity 61.5%; Pred. No. 89;
 Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 RNNVLIQ--TDQQ 11
 |:|||||
 Db 3 RDNVLFQATDEQ 15

RESULT 7
 ADD44240
 ID ADD44240 standard; peptide; 15 AA.
 XX
 AC ADD44240;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Carboxypeptidase G2 (CPG2) enzyme immunogenic peptide #1.
 XX
 KM bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;
 KM immunogenic; T-cell epitope; MHC class II binding ligand;
 KM immunostimulant; enzyme therapy; immune response;
 KM gene directed enzyme prodnrg strategy; vaccine; enzyme; EC 3.4.17.11.
 XX
 OS Pseudomonas sp. RS-16.
 XX

PN WO2003045426-A1.
 XX PD 05-JUN-2003.
 XX PF 27-NOV-2002; 2002WO-EP013351.
 XX PR 29-NOV-2001; 2001EP-00128519.
 XX PR 25-JAN-2002; 2002EP-00001778.
 XX PR 13-SEP-2002; 2002EP-00020634.
 XX PA (MERCK) MERCK PATENT GMBH.
 XX PI Hellendoorn K, Baker M, Williams S, Carr FJ;
 XX WPI; 2003-513617/48.
 XX PT New modified bacterial enzyme carboxypeptidase G2 (CPG2) having
 PT substantially non-immunogenic or less immunogenic than any non-modified
 PT CPG2, useful for inducing an immune response in a human host.
 XX PS Example 2; Fig 1; 52pp; English.
 XX CC The invention relates to a novel modified bacterial enzyme
 CC carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2
 CC proteins that are substantially non-immunogenic or less immunogenic than
 CC any non-modified CPG2 having essentially the same biological specificity
 CC when used in vivo, and comprising specific amino acid residues having
 CC alterations compared with the non-modified parochial enzyme. The
 CC alterations cause a reduction or an elimination of one or more of T-cell
 CC epitope sequences, which act in the parental enzyme as MHC class II
 CC binding ligands and stimulate T-cells. The modified CPG2 enzyme and the
 CC CPG2 proteins have immunostimulant activity and may be used in enzyme
 CC therapy. The modified CPG2 enzyme may be used to induce an immune
 CC response in a human host, or as a therapeutic entity such as the gene
 CC directed enzyme prodnrg strategy. The peptide is useful for the
 CC manufacture of a modified CPG2 enzyme having substantially no or less
 CC immunogenicity than any non-modified parental enzyme when used in vivo,
 CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.
 CC This sequence represents an immunogenic peptide of the CPG2 enzyme of the
 CC invention.
 XX SQ Sequence 15 AA;
 XX

Query Match 43.2%; Score 32; DB 7; Length 15;
 Best Local Similarity 61.5%; Pred. No. 89;
 Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 RNNVLIQ--TDQQ 11
 |:|||||
 Db 3 RDNVLFQATDEQ 15

RESULT 8
 AEC11192
 ID AEC11192 standard; peptide; 12 AA.
 XX
 AC AEC11192;
 XX
 DT 20-OCT-2005 (first entry)
 XX
 DE Pseudomonas aeruginosa phosphoglucoamine mutase peptide.
 XX
 KM protein purification; antibacterial; antimicrobial; infection;
 KM drug screening; phosphoglucoamine mutase.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN US2005181388-A1.
 XX
 PD 18-AUG-2005.
 XX
 PF 04-OCT-2004; 2004US-00958216.
 XX

PR 02-APR-2002; 2002US-0369511P.
 PR 04-APR-2002; 2002US-0369817P.
 PR 04-APR-2002; 2002US-0370102P.
 PR 08-APR-2002; 2002US-0370778P.
 PR 08-APR-2002; 2002US-0370792P.
 PR 08-APR-2002; 2002US-0370820P.
 PR 08-APR-2002; 2002US-0370859P.
 PR 08-APR-2002; 2002US-0370899P.
 PR 08-APR-2002; 2002US-0370915P.
 PR 09-APR-2002; 2002US-0371107P.
 PR 09-APR-2002; 2002US-0371140P.
 PR 09-APR-2002; 2002US-0371185P.
 PR 31-MAY-2002; 2002US-0385089P.
 PR 31-MAY-2002; 2002US-0385426P.
 PR 04-JUN-2002; 2002US-0385751P.
 PR 05-JUN-2002; 2002US-0386018P.
 PR 05-JUN-2002; 2002US-0386367P.
 PR 05-JUN-2002; 2002US-0386549P.
 PR 05-JUN-2002; 2002US-0386553P.
 PR 05-JUN-2002; 2002US-0386566P.
 PR 05-JUN-2002; 2002US-0386577P.
 PR 06-JUN-2002; 2002US-0386283P.
 PR 06-JUN-2002; 2002US-0386390P.
 PR 06-JUN-2002; 2002US-0386430P.
 PR 06-JUN-2002; 2002US-0386430P.
 PR 06-JUN-2002; 2002US-0386601P.
 PR 06-JUN-2002; 2002US-0386826P.
 PR 06-JUN-2002; 2002US-0386869P.
 PR 31-JUL-2002; 2002US-0399972P.
 PR 01-AUG-2002; 2002US-0400348P.
 PR 05-NOV-2002; 2002US-0424053P.
 PR 06-NOV-2002; 2002US-0424380P.
 PR 06-NOV-2002; 2002US-0424395P.
 PR 08-NOV-2002; 2002US-0425086P.
 PR 08-NOV-2002; 2002US-0425200P.
 PR 24-DEC-2002; 2002US-0436243P.
 PR 24-DEC-2002; 2002US-0436288P.
 PR 24-DEC-2002; 2002US-0436345P.
 PR 24-DEC-2002; 2002US-0436349P.
 PR 26-DEC-2002; 2002US-0436566P.
 PR 26-DEC-2002; 2002US-0436567P.
 PR 26-DEC-2002; 2002US-0436568P.
 PR 27-DEC-2002; 2002US-0436675P.
 PR 27-DEC-2002; 2002US-0436708P.
 PR 27-DEC-2002; 2002US-0436734P.
 PR 27-DEC-2002; 2002US-0436804P.
 PR 27-DEC-2002; 2002US-0436834P.
 PR 27-DEC-2002; 2002US-0436842P.
 PR 27-DEC-2002; 2002US-0436861P.
 PR 27-DEC-2002; 2002US-0436885P.
 PR 27-DEC-2002; 2002US-0436889P.
 PR 27-DEC-2002; 2002US-0436893P.
 PR 27-DEC-2002; 2002US-0436900P.
 PR 30-DEC-2002; 2002US-0436947P.
 PR 30-DEC-2002; 2002US-0436971P.
 PR 30-DEC-2002; 2002US-0436987P.
 PR 30-DEC-2002; 2002US-0437013P.
 PR 30-DEC-2002; 2002US-0437038P.
 PR 30-DEC-2002; 2002US-0437141P.
 PR 31-DEC-2002; 2002US-0437281P.
 PR 31-DEC-2002; 2002US-0437527P.
 PR 31-DEC-2002; 2002US-0437620P.
 PR 31-DEC-2002; 2002US-0437638P.
 PR 02-APR-2003; 2003WO-CA000462.
 PR 04-APR-2003; 2003WO-CA000464.
 PR 08-APR-2003; 2003WO-CA000481.
 PR 08-APR-2003; 2003WO-CA000485.

(AFFI-) AFFINUM PHARM INC.

XX Edwards A, Dharmasi A, Vedadi M, Alam MZ, Arrowsmith C, Awrey DE;
 PI Beattie B, Butadzija K, Canadien V, Domagala M, Houston S;
 PI Kanagarajah D, Li Q, Mansoury K, McDonald M, Nethery-Brooks K, Ng I;

PI Ouyang H, Pinder B, Richards D, Tai M, Thalakada R, Vallee F;
 PI Virag C;
 DR WPI; 2005-628189/64.
 PT New composition comprising purified polypeptides from bacteria (e.g.
 PT Escherichia coli), useful for diagnosing, preventing or treating
 PT microbial infections, or in pharmacogenomic or drug screening procedures.
 XX
 PS Example 1; Fig 219; 667pp; English.
 CC The invention relates to a composition (I) comprising purified
 CC polypeptides from bacteria. Also described: (1) a crystallized,
 CC recombinant polypeptide comprising an amino acid sequence of (I), where
 CC the polypeptide is in crystal form; (2) a crystallized complex comprising
 CC the crystallized, recombinant polypeptide and a co-factor or a small
 CC organic molecule, where the complex is in crystal form; and (3) a host
 CC cell comprising a nucleic acid encoding a polypeptide of (I), where a
 CC culture of the host cell produces at least about 1 mg of the polypeptide
 CC per liter of culture and the polypeptide is at least about one-third
 CC soluble as measured by gel electrophoresis. The composition and methods
 CC are useful for diagnosing, preventing or treating diseases, such as
 CC microbial infections. These may also be used in pharmacogenomic or drug
 CC screening procedures. The present sequence represents a pseudomonas
 CC aeruginosa phosphoglucosamine mutase peptide, which is used in an example
 CC from the present invention.
 SQ Sequence 12 AA;

Query Match 39.2%; Score 29; DB 9; Length 12;
 Best Local Similarity 33.3%; Pred. No. 2.4e+02;
 Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 4 VLIOFDQOATTR 15
 DB 1 VMVGEDEASVR 12

RESULT 9
 AAY65622
 ID AAY65622 standard; peptide, 15 AA.
 XX
 AC AAY65622;
 XX

DT 01-FEB-2000 (first entry)
 XX

DE Oestrogen receptor beta ERB binding peptide 17E-beta.
 XX

KM Oestrogen receptor; estrogen; estradiol; oestrogen response element; ERE;
 KM binding; biological activity; fingerprint; molecular biology;
 KM cellular biology; modulation; tamoxifen; breast cancer; ovarian cancer;
 KM menopause; osteoporosis; selective oestrogen receptor modulator;
 KM identification; characterization; classification.
 KM

OS Synthetic.
 OS Homo sapiens.

PN W0954728-A2.
 XX

PD 28-OCT-1999.
 XX

PF 26-MAR-1999; 99WO-US006664.
 XX

PR 23-APR-1998; 98US-0082756P.
 XX

PR 09-SEP-1998; 98US-0099656P.
 XX

PR 08-JAN-1999; 99US-0115345P.
 XX

PA (NOVA-) NOVALON PHARM CORP.

PI Paige LA, Hamilton PT, Fowlkes DM, Buehrer B, Barnett T;
 PI McDonnell DP, Christensen DJ;

DR WPI; 2000-013281/01.

XX Methods for identifying new receptor modulators, especially estrogen
 PT modulators to treat tamoxifen refractory breast cancer.
 XX
 PS Example 2.2; Page 164; 219pp; English.
 CC The present invention describes a method for predicting the biological
 CC activity of new receptor modulating compounds (I) using novel oligomeric
 CC peptides (biokeys) which have differential abilities to bind to 2
 CC different receptor conformations. The method is used to identify new
 CC drugs that are physiological or pharmacological agonists/antagonists and
 CC that target various receptors, which are involved in certain disease
 CC conditions. The system may be used as a primary screening tool to
 CC identify hits, to classify lead compounds from a drug screen to,
 CC characterise selective oestrogen receptor modulators (SERMs) in terms of
 CC agonist and antagonist function and to predict possible clinical effects
 CC of SERMs such as tissue and receptor specificity. The method can also be
 CC applied to the fractionation of mixtures of SERMs to determine which
 CC components are producing agonistic and antagonistic activity. The method
 CC may be used with other receptors (e.g. progesterone, androgen,
 CC glucocorticoid, thyroid, vitamin D, beta-adrenergic, dopamine and
 CC epidermal growth factor, to identify, characterise and classify
 CC modulators of receptor activity. Peptides comprising a LXXLL motif may be
 CC used to modulate the oestrogen receptor in treating e.g. breast and
 CC ovarian cancer and ameliorating the effects of menopause, including
 CC oestroporosis. AAY65439 to AAY65652 represent oestrogen receptor,
 CC estradiol receptor and oestrogen response element binding peptides given
 CC in the exemplification of the present invention. AA235740 to AA235745
 CC represent oligonucleotides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 15 AA;
 Query Match 39.2%; Score 29; DB 3; Length 15;
 Best Local Similarity 46.2%; Pred. No. 3.1e+02;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 3 NVLIQTDQQAATR 15
 Db 3 NLCLLDQEAACSR 15
 RESULT 10
 AAU86359 standard; peptide; 15 AA.
 XX
 AC AAU86359;
 XX
 XX 21-MAY-2002 (first entry)
 DE Oestrogen receptor beta binding peptide 17B-beta.
 XX
 KM Oestrogen receptor; breast cancer; combinatorial peptide library;
 KM receptor modulating compound.
 OS Synthetic.
 XX
 PN WO200204956-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 11-JUL-2001; 2001WO-US021867.
 XX
 PR 12-JUL-2000; 2000US-00614865.
 PR 21-MAY-2001; 2001US-00860688.
 XX
 PA (KARO-) KARO BIO USA INC.
 XX
 PI Fowlkes DM, Barnett TR, Buehrer B;
 XX WPI; 2002-154969/20.
 DR
 XX Identifying receptor-binding peptides comprises screening combinatorial
 PT

PT peptide library presented in form of cells each of which coexpress one
 PT peptide member and receptor with signal producing system for reporting
 PT binding.
 XX
 PS Disclosure; Page 146; 175pp; English.
 XX
 XX The invention relates to identifying a binding peptide which binds a
 CC receptor and which is a member of a combinatorial library of peptides,
 CC comprising screening a combinatorial peptide library presented in the
 CC form of cells which coexpress the receptor or its ligand-binding receptor
 CC moiety and one member of the library, together with a signal producing
 CC system for reporting binding of the peptide to the receptor. Also
 CC included is a method for predicting the receptor-modulating activity of a
 CC compound which modulates the biological activity of a receptor comprising
 CC (a) identifying peptides which bind the receptor by the method above, (b)
 CC using a number of the peptides to predict the receptor-modulating
 CC activity of a compound by (i) providing a panel of identified peptides,
 CC where the members differ in their ability to bind to the receptor
 CC depending on reference conformations known to modulate the biological
 CC activity of the receptor on the binding of each member of the panel is
 CC known and is characterised as a reference fingerprint for each reference
 CC substance, (ii) screening a test substance of unknown activity relative
 CC to the receptor to determine its effect on the binding of each member of
 CC the panel to the receptor, thereby obtaining a test fingerprint for the
 CC test substance, (iii) comparing the test fingerprint to the reference
 CC fingerprints and (iv) predicting the biological activity of the test
 CC substance based on the assumption that its biological activity will be
 CC similar to that of reference substances with similar fingerprints. The
 CC method is useful for identifying a binding peptide which binds a
 CC vertebrate, mammalian, preferably human receptor, an intracellular,
 CC nuclear, oestrogen or androgen receptor. The identified peptides which
 CC bind to the receptor are useful for predicting the receptor-modulating
 CC activity of a compound (e.g. ant/agonists). The receptor-binding library
 CC members are useful in the prediction of the ability of small organic
 CC molecules, suitable for pharmaceutical use (e.g. in the case of oestrogen
 CC receptors, for breast cancer treatment), to interact with the receptor.
 CC The analyte-binding molecules can also be used for in vivo imaging. The
 CC method has several advantages over whole animal-based assay systems in
 CC that the same technology can be applied to a variety of different
 CC receptors, the system can be used for high throughput screening and
 CC compound characterisation, and gives very distinct patterns for agonists
 CC and antagonists of receptor activity using very much less protein. The
 CC present sequence is an oestrogen receptor binding peptide from a
 CC combinatorial peptide library
 XX
 SQ Sequence 15 AA;
 Query Match 39.2%; Score 29; DB 5; Length 15;
 Best Local Similarity 46.2%; Pred. No. 3.1e+02;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 3 NVLIQTDQQAATR 15
 Db 3 NLCLLDQEAACSR 15
 RESULT 11
 ADM79070 standard; peptide; 15 AA.
 ID ADM79070;
 XX
 AC ADM79070;
 XX
 DT 03-JUN-2004 (first entry)
 DE Oestrogen receptor beta binding peptide #57.
 XX
 KM Oestrogen receptor; drug identification; in vivo imaging;
 KM binding peptide; drug identification; in vivo imaging;
 KM oestrogen receptor beta.
 XX
 OS Unidentified.
 XX
 PN US2003224390-A1.

XX 04-DEC-2003.
 PD 17-JAN-2003; 2003US-00346162.
 XX
 PF
 XX 12-JUL-2000; 2000US-00614865.
 PR 21-MAY-2001; 2001US-00860688.
 PR 11-JUL-2001; 2001WO-US021867.
 XX
 PA (KARO-) KARO BIO AB.
 XX
 PI Fowlkes DM, Barnett TR, Buehrer B,
 XX WPI; 2004-060539/06.
 DR
 XX
 PT Identifying a binding peptide that binds a receptor, for use as a
 PT therapeutic or diagnostic agent, comprises screening a combinatorial
 PT peptide library presented in cells co-expressing a peptide, a receptor
 PT and a signal producing system.
 XX
 PS Example; SEQ ID NO 192; 66pp; English.
 XX
 CC The invention relates to a method of identifying a binding peptide which
 CC binds a receptor comprising screening a combinatorial peptide library
 CC presented in cells which co-expresses one member peptide and the
 CC receptor, together with a signal producing system for reporting binding.
 CC The method is useful in identifying drugs which can mediate the
 CC biological activity of a target protein. The receptor-binding library
 CC members may be used as therapeutic or diagnostic reagents, for in vivo
 CC imaging, or to purify target from a fluid, e.g. blood. The present
 CC sequence represents an oestrogen receptor beta binding peptide.
 XX
 SQ Sequence 15 AA;

Query Match 39.2%; Score 29; DB 8; Length 15;
 Best Local Similarity 46.2%; Pred. No. 3.1e+02;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 3 NVLITDQOATTR 15
 |||::|::|::|
 Db 3 NLTCLDQECRSR 15

RESULT 12

ID ADR10604 standard; peptide; 15 AA.
 XX
 AC ADR10604;
 XX
 DT 21-OCT-2004 (first entry)
 XX

DE Sheep IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 4.
 XX

KM Antiasthmatic; Antiallergic; Immunosuppressive; IGF; dog; asthma;
 KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 XX sheep.
 XX

OS Ovis aries.
 XX

PN WO2004065936-A2.
 XX

PD 05-AUG-2004.
 XX

PF 15-JAN-2004; 2004WO-US003566.
 XX

PR 16-JAN-2003; 2003US-0440472P.
 XX

PA (UNNC-) UNIV NORTH CAROLINA STATE.
 XX

PI Hammerberg B;
 XX

XX WPI; 2004-593545/57.
 XX

PT Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.
 XX

PS Example 6; Page 9; 14pp; English.
 XX

CC The present invention relates to a novel monoclonal antibody (1) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (1) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (1) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC sheep IGE 5.91 recognition site.
 XX

SQ Sequence 15 AA;

Query Match 39.2%; Score 29; DB 8; Length 15;
 Best Local Similarity 40.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 RNNVLITDQOATTR 15
 |||::|::|::|
 Db 1 RNKELMREGQHTTQ 15

RESULT 13

AAG95534
 ID AAG95534 standard; peptide; 10 AA.
 XX

AC AAG95534;
 XX

DT 18-SEP-2001 (first entry)
 XX

DE Human complementary peptide, SEQ ID NO: 1728.
 XX

KM Human; complementary peptide; ligand; drug discovery; drug design.
 XX

OS Homo sapiens.
 XX

PN WO200142277-A2.
 XX

PD 14-JUN-2001.
 XX

PF 13-DEC-2000; 2000WO-GB004776.
 XX

PR 13-DEC-1999; 99GB-00029464.
 XX

PA (PROT-) PROTEOM LTD.
 XX

PI Roberts GW, Heal JR;
 XX

DR WPI; 2001-408419/43.
 XX

PT A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.
 XX

PS Example 4; Page 290; 646pp; English.
 XX

CC The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design

CC and development. The present sequence is a complementary peptide provided
CC in the specification
XX
SQ Sequence 10 AA;
Query Match 36.5%; Score 27; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 TDQOATT 14
: ||| |
Db 1 SDQTTT 7
RESULT 14
ADV57215
ID ADV57215 standard; peptide; 11 AA.
XX
AC ADV57215;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 4719.
XX
KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004MO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
PR 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZW.
PA (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
PS Example; SEQ ID NO 4719; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide

CC combo.
XX
SQ Sequence 11 AA;
Query Match 36.5%; Score 27; DB 9; Length 11;
Best Local Similarity 54.5%; Pred. No. 5.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 5 LIOTDQATT 15
: | : ||| |
Db 1 LMHTVEQATLR 11
RESULT 15
ADV54438
ID ADV54438 standard; peptide; 11 AA.
XX
AC ADV54438;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 1935.
XX
KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004MO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
PR 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZW.
PA (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
PS Example; SEQ ID NO 1935; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.

XX	Sequence 11 AA;
SQ	

Query Match 36.5%; Score 27; DB 9; Length 11;
Best Local Similarity 54.5%; Pred. No. 5.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy      5 LIOTDQATTR 15
         | : | | | |
Db      1 LMHTVEQATLR 11
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OM protein - protein search, using SW model

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 186887

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*

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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	33.8	14	2	US-09-236-415-6 Sequence 6, Appli
2	25	33.8	15	1	US-08-221-583-42 Sequence 42, Appl
3	25	33.8	15	4	PCR-US95-04018-42 Sequence 42, Appl
4	24	32.4	11	1	US-08-456-6708-38 Sequence 38, Appl
5	24	32.4	11	2	US-09-372-036-38 Sequence 38, Appl
6	24	32.4	15	1	US-08-403-3788-7 Sequence 7, Appli
7	23	31.1	10	2	US-08-485-324-4 Sequence 4, Appli
8	23	31.1	10	2	US-08-485-324-30 Sequence 30, Appl
9	23	31.1	10	2	US-08-447-506-4 Sequence 4, Appli
10	23	31.1	10	2	US-08-447-506-30 Sequence 30, Appl
11	23	31.1	10	2	US-08-235-437-4 Sequence 4, Appli
12	23	31.1	10	2	US-08-235-437-30 Sequence 30, Appl
13	23	31.1	10	2	US-08-447-515-4 Sequence 4, Appli
14	23	31.1	10	2	US-08-447-515-30 Sequence 30, Appl
15	23	31.1	10	2	US-09-462-645C-29 Sequence 29, Appl
16	23	31.1	10	2	US-09-573-830-4 Sequence 4, Appli
17	23	31.1	10	2	US-09-573-830-30 Sequence 30, Appl
18	23	31.1	12	1	US-08-479-223-8 Sequence 8, Appli
19	23	31.1	12	2	US-09-392-812A-7 Sequence 7, Appli
20	23	31.1	12	4	PCR-US93-00643-8 Sequence 8, Appli
21	23	31.1	14	2	US-10-394-980-55 Sequence 55, Appli
22	23	31.1	15	2	US-09-700-993-6 Sequence 6, Appli
23	22	29.7	5	1	US-08-762-106-19 Sequence 19, Appl
24	22	29.7	5	2	US-09-320-774-19 Sequence 19, Appl
25	22	29.7	6	1	US-08-762-106-17 Sequence 17, Appl
26	22	29.7	6	1	US-08-762-106-18 Sequence 18, Appl
27	22	29.7	6	2	US-09-320-774-17 Sequence 17, Appl

28	22	29.7	6	2	US-09-320-774-18 Sequence 18, Appl
29	22	29.7	8	1	US-08-762-106-15 Sequence 15, Appl
30	22	29.7	8	2	US-09-320-774-15 Sequence 15, Appl
31	22	29.7	9	1	US-08-456-6708-25 Sequence 25, Appl
32	22	29.7	9	1	US-08-762-106-13 Sequence 13, Appl
33	22	29.7	9	1	US-08-762-106-14 Sequence 14, Appl
34	22	29.7	9	2	US-09-320-774-13 Sequence 13, Appl
35	22	29.7	9	2	US-09-320-774-14 Sequence 14, Appl
36	22	29.7	9	2	US-09-372-036-25 Sequence 25, Appl
37	22	29.7	10	2	US-08-981-392-53 Sequence 53, Appl
38	22	29.7	10	2	US-09-908-392-53 Sequence 53, Appl
39	22	29.7	11	2	US-09-194-285-54 Sequence 54, Appl
40	22	29.7	12	2	US-09-517-866-13 Sequence 13, Appl
41	22	29.7	13	1	US-07-718-274A-33 Sequence 33, Appl
42	22	29.7	13	1	US-07-920-519-12 Sequence 12, Appl
43	22	29.7	13	1	US-08-086-410-9 Sequence 9, Appli
44	22	29.7	13	1	US-08-149-106-33 Sequence 33, Appl
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ALIGNMENTS

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; Sequence 6, Application US/09236415
; Patent No. 6309863
; GENERAL INFORMATION:
; APPLICANT: Anderson, Carl W.
; APPLICANT: Appella, Ettore
; APPLICANT: Sakaguchi, Kazuyasu
; TITLE OF INVENTION: METHODS FOR GENERATING PHOSPHORYLATION SITE-SPECIFIC
; TITLE OF INVENTION: IMMUNOLOGICAL REAGENTS
; FILE REFERENCE: U.S. Application 09/236,415
; CURRENT APPLICATION NUMBER: US/09/236,415
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
; OTHER INFORMATION: ANTIGEN
; FEATURE:
; OTHER INFORMATION: Residue Xaa is a phosphoserine mimetic
US-09-236-415-6
Query Match 33.8% Score 25; DB 2; Length 14;
Beat Local Similarity 54.5% Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 NNVLIQTDDQA 12
   |||||
Db 3 NNVLIQTDDQA 13

RESULT 2
US-08-221-583-42
; Sequence 42, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5486595r1s
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25.mdtctmod.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,583
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-221-583-42

Query Match 33.8%; Score 25; DB 1; Length 15;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QDQOATTR 15
Db 4 QVETQATR 12

RESULT 3
PCT-US95-04018-42
Sequence 42, Application PC/TUS9504018
GENERAL INFORMATION:
APPLICANT: Heaven, George A.
APPLICANT: Kruszynski, Marian
APPLICANT: Meriv, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Norris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-42

Query Match 33.8%; Score 25; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QDQOATTR 15
Db 4 QVETQATR 12

RESULT 4
US-08-456-670B-38
Sequence 38, Application US/08456670B
Patent No. 5932415
GENERAL INFORMATION:
APPLICANT: SCHUBERT, PETER
APPLICANT: NEUMANN, SIEGFRIED
APPLICANT: PAMELZIK, MARTINA
APPLICANT: LINXWEILER, WINFRIED
APPLICANT: BURGER, CHRISTA
APPLICANT: HORMANN, GOTTFRIED
APPLICANT: BUBERT, ANDREAS
APPLICANT: GOEBEL, WERNER
APPLICANT: KOHLER, STEFAN
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD., SUITE 1400
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: US
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,670B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,227
FILING DATE: 27-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/075,248
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4239567.4
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 421911.4
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1694D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
TELEX: 64191

; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Listeria innocua
; US-08-456-670B-38

Query Match 32.4%; Score 24; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 9 DQOATTR 15
: ||| :
Db 1 EQOTTk 7

RESULT 5
US-09-372-036-38
; Sequence 38, Application US/09372036
; Patent No. 6951925
; GENERAL INFORMATION:
; APPLICANT: SCHUBERT, PETER
; APPLICANT: NEUMANN, SIEGFRIED
; APPLICANT: PAWELZIK, MARTINA
; APPLICANT: LINKEHEIMER, WINFRIED
; APPLICANT: BURGER, CHRISTA
; APPLICANT: HOFMANN, GOTTFRIED
; APPLICANT: BUBERT, ANDREAS
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KOHLER, STEFAN
; TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING
; TITLE OF INVENTION: LISTERIAS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P. C.
; STREET: 2200 CLARENDON BLVD., SUITE 1400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,036
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/456,670
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,248
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4239567.4
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4219111.4
; FILING DATE: 11-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1694D1
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Listeria innocua
; US-09-372-036-38

Query Match 32.4%; Score 24; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 9 DQOATTR 15
: ||| :
Db 1 EQOTTk 7

RESULT 6
US-08-403-378B-7
; Sequence 7, Application US/08403378B
; Patent No. 5759991
; GENERAL INFORMATION:
; APPLICANT: TOHDOH, NAOKI
; APPLICANT: TOJO, SHIN-ICHIRO
; APPLICANT: KOJIMA, SHIN-ICHI
; APPLICANT: Ueki, YASUYUKI
; APPLICANT: NISHIHARA, TOSHIO
; APPLICANT: FUKUSHIMA, NOBUYUKI
; APPLICANT: IRIE, TSUNEMASA
; APPLICANT: ONO, KEIICHI
; APPLICANT: AGUI, HIDEO
; APPLICANT: OIYKA, KOSEI
; TITLE OF INVENTION: NEUROTROPIC PEPTIDE DERIVATIVES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,378B
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-124668
; FILING DATE: 27-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-080398
; FILING DATE: 30-MAR-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-280590
; FILING DATE: 27-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1-333241
; FILING DATE: 21-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-243003
; FILING DATE: 12-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/758,043
; FILING DATE: 12-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/873,764
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/01214
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIGGART, WADELL A
REGISTRATION NUMBER: 24,861
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: rattus norvegicus
STRAIN: wistar
TISSUE TYPE: hippocampal tissue of brain
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..15
US-08-403-378B-7

Query Match 32.4%; Score 24; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 5.5e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 LIOTDQATR 15

Db 4 LVLTDPAPSR 14

RESULT 7
US-08-485-324-4
Sequence 4, Application US/08485324
Patent No. 6043093
GENERAL INFORMATION:
APPLICANT: Mohlstader, Jacob
TITLE OF INVENTION: SELECTION METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,324
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,437
FILING DATE: 29-APR-1994
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-324-4

Query Match 31.1%; Score 23; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 TDOQAT 14

Db 1 TDOEQTS 7

RESULT 8
US-08-485-324-30
Sequence 30, Application US/08485324
Patent No. 6043093
GENERAL INFORMATION:
APPLICANT: Mohlstader, Jacob
TITLE OF INVENTION: SELECTION METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, & Safford
ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,324
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,437
FILING DATE: 29-APR-1994
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-0712
TELEFAX: (212) 840-3333
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-324-30

Query Match 31.1%; Score 23; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 TDOQAT 14

Db 1 TDOEQTS 7

RESULT 9
US-08-447-506-4
Sequence 4, Application US/08447506

```
Patent No. 6066499
GENERAL INFORMATION:
APPLICANT: Wohlstadter, Jacob
TITLE OF INVENTION: SELECTION METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, & Safford
ADDRESS: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,506
FILING DATE: 23-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,437
FILING DATE: 29-APR-1994
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-447-506-4

Query Match      31.1% Score 23; DB 2; Length 10;
Best Local Similarity 57.1% Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      8 TDQOATT 14
      |||:|:
      1 TDOEOTS 7

Db

RESULT 10
US-08-447-506-30
Sequence 30, Application US/08447506
Patent No. 6066499
GENERAL INFORMATION:
APPLICANT: Wohlstadter, Jacob
TITLE OF INVENTION: SELECTION METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, & Safford
ADDRESS: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/447,506
FILING DATE: 23-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,437
FILING DATE: 29-APR-1994
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-447-506-30

Query Match      31.1% Score 23; DB 2; Length 10;
Best Local Similarity 57.1% Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      8 TDQOATT 14
      |||:|:
      1 TDOEOTS 7

Db

RESULT 11
US-08-235-437-4
Sequence 4, Application US/08235437
Patent No. 6087177
GENERAL INFORMATION:
APPLICANT: Wohlstadter, Jacob
TITLE OF INVENTION: SELECTION METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris, & Safford
ADDRESS: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,437
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-235-437-4

Query Match 31.1%; Score 23; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TDOQATT 14
Db 1 TDOEQTS 7

RESULT 12

US-08-235-437-30

; Sequence 30, Application US/08235437
; Patent No. 6087177
; GENERAL INFORMATION:
; APPLICANT: Wohlstadter, Jacob
; TITLE OF INVENTION: SELECTION METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Curtis, Morris, & Safford
; ADDRESSEE: c/o Barry Evans
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,437
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,412
; FILING DATE: 16-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Barry
; REGISTRATION NUMBER: 22,802
; REFERENCE/DOCKET NUMBER: 370132-2000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-235-437-30

Query Match 31.1%; Score 23; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TDOQATT 14
Db 1 TDOEQTS 7

RESULT 13
US-08-447-515-4
; Sequence 4, Application US/08447515
; Patent No. 6162640
; GENERAL INFORMATION:
; APPLICANT: Wohlstadter, Jacob
; TITLE OF INVENTION: SELECTION METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Curtis, Morris, & Safford

ADDRESSEE: c/o Barry Evans
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,515
FILING DATE: 23-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,437
FILING DATE: 29-APR-1994
APPLICATION NUMBER: US 07/852,412
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370132-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-447-515-4

Query Match 31.1%; Score 23; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TDOQATT 14
Db 1 TDOEQTS 7

RESULT 14

US-08-447-515-30

; Sequence 30, Application US/08447515
; Patent No. 6162640
; GENERAL INFORMATION:
; APPLICANT: Wohlstadter, Jacob
; TITLE OF INVENTION: SELECTION METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Curtis, Morris, & Safford
; ADDRESSEE: c/o Barry Evans
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,515
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,437
; FILING DATE: 29-APR-1994
; APPLICATION NUMBER: US 07/852,412

FILING DATE: 16-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Evans, Barry
 REGISTRATION NUMBER: 22,802
 REFERENCE/DOCKET NUMBER: 370132-2000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-447-515-30

Query Match 31.1%; Score 23; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 5.2e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 TDQOATT 14
 |||:
 Db 1 TDQOETS 7

RESULT 15
 US-09-462-645C-29
 ; Sequence 29, Application US/09462645C
 ; Patent No. 6436561
 ; GENERAL INFORMATION:
 ; APPLICANT: Schroeder, Hartwig
 ; APPLICANT: Hauser, Bernhard
 ; TITLE OF INVENTION: The preparation of biotin
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/462,645C
 ; PRIOR APPLICATION NUMBER: PCT/EP98/04097
 ; PRIOR FILING DATE: 1998-02-07
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: WordPerfect version 6.1
 ; SEQ ID NO 29
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: A. vinelandii
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 7..7_
 ; OTHER INFORMATION: Xaa is unknown. Amino acid sequence is a typical N-terminal
 ; OTHER INFORMATION: sequence of proteins of the Nifs family.
 US-09-462-645C-29

Query Match 31.1%; Score 23; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 5.2e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 LIOTDQOATT 14
 :|||
 Db 1 MIYLDNXYATT 10

Search completed: December 12, 2005, 21:00:46
 Job time : 28 secs

THIS PAGE BEGINS
(USPTO)

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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:30:45 ; Search time 92.6667 Seconds
(without alignments)
67.634 Million cell updates/sec

Title: US-10-758-165A-3
Perfect score: 74
Sequence: 1 RNNVLIQTDOQATTR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 324073

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_A1_Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBSCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10_PUBSCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	US-10-758-165-3	Sequence 3, Appl1
2	49	66.2	15	US-10-052-788-4	Sequence 4, Appl1
3	41	55.4	15	US-10-758-165-1	Sequence 1, Appl1
4	40	54.1	15	US-10-758-165-7	Sequence 2, Appl1
5	37	50.0	15	US-10-758-165-2	Sequence 128, App
6	32	43.2	15	US-10-497-091-128	Sequence 713, App
7	29	39.2	15	US-10-958-216-713	Sequence 192, App
8	29	39.2	15	US-10-346-162-192	Sequence 4, Appl1
9	29	39.2	15	US-10-758-165-4	Sequence 1728, App
10	27	36.5	13	US-10-497-091-14	Sequence 14, Appl1
11	27	36.5	14	US-10-172-425B-17	Sequence 37, App
12	27	36.5	14	US-10-497-091-119	Sequence 129, App
13	27	36.5	12	US-10-935-642-48	Sequence 48, Appl1
14	26	35.1	12	US-11-074-473-48	Sequence 48, Appl1
15	26	35.1	13	US-10-497-091-15	Sequence 15, Appl1
16	26	35.1	12	US-09-764-868-1143	Sequence 1243, App
17	25	33.8	12	US-09-955-999-123	Sequence 123, App
18	25	33.8	14	US-10-221-125-1	Sequence 1, Appl1
19	25	33.8	15	US-10-014-340-796	Sequence 796, App
20	25	33.8	15	US-10-225-567A-1123	Sequence 1123, App
21	25	33.8	15	US-11-004-270-94	Sequence 94, Appl1
22	25	33.8	15	US-11-004-270-94	Sequence 94, Appl1
23	25	33.8	15	US-11-004-270-94	Sequence 94, Appl1
24	24	32.4	9	US-10-117-937-560	Sequence 560, App
25	24	32.4	9	US-11-067-064-560	Sequence 560, App
26	24	32.4	9	US-11-067-159-560	Sequence 560, App
27	24	32.4	10	US-10-117-937-561	Sequence 561, App

28	24	32.4	10	6	US-11-067-064-561	Sequence 561, App
29	24	32.4	10	6	US-11-067-159-561	Sequence 561, App
30	24	32.4	12	4	US-10-097-175-66	Sequence 66, Appl1
31	24	32.4	12	4	US-10-264-309-289	Sequence 289, App
32	24	32.4	12	5	US-10-264-309-289	Sequence 289, App
33	24	32.4	13	3	US-09-791-378-584	Sequence 584, App
34	24	32.4	13	3	US-09-791-378-584	Sequence 584, App
35	24	32.4	13	4	US-10-014-340-568	Sequence 568, App
36	24	32.4	13	4	US-10-014-340-569	Sequence 569, App
37	24	32.4	13	4	US-10-014-338-7	Sequence 7, Appl1
38	24	32.4	13	4	US-10-369-736-31	Sequence 31, Appl1
39	24	32.4	13	4	US-10-112-582-14	Sequence 14, Appl1
40	24	32.4	13	4	US-10-369-738-31	Sequence 31, Appl1
41	24	32.4	13	5	US-10-808-167-706	Sequence 706, App
42	24	32.4	13	5	US-10-807-807-706	Sequence 706, App
43	24	32.4	13	6	US-11-028-058-31	Sequence 31, Appl1
44	24	32.4	14	3	US-09-791-378-135	Sequence 135, App
45	24	32.4	14	3	US-09-791-378-587	Sequence 587, App

ALIGNMENTS

```
RESULT 1
US-10-758-165-3
; Sequence 3, Application US/10758165
; Publication No. US20050196616A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-3

Query Match      100.0%; Score 74; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 2,2e+06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RNNVLIQTDOQATTR 15
      |||||
Db      1 RNNVLIQTDOQATTR 15

RESULT 2
US-10-052-788-4
; Sequence 4, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
; APPLICANT: Gerethwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kallina, Warren V.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; FILE REFERENCE: 023070-121006US
; CURRENT APPLICATION NUMBER: US/10/052,788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence:epitope peptide
OTHER INFORMATION: P4, early portion of C4 of equine IgE epsilon
OTHER INFORMATION: heavy chain
US-10-052-788-4

Query Match 66.2%; Score 49; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IOTDQOATTR 15
|:|:|:|:|:|:|
Db 1 IOTDQOATTR 10

RESULT 3
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammeberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1

Query Match 55.4%; Score 41; DB 5; Length 15;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATT 14
|:|:|:|:|:|:|
Db 1 RNDSPITDQYTTT 14

RESULT 4
US-10-758-165-7
; Sequence 7, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammeberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-7

Query Match 54.1%; Score 40; DB 5; Length 15;
Best Local Similarity 46.7%; Pred. No. 2.9;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATT 15
|:|:|:|:|:|:|
Db 1 RNDAPVQADRHSTR 15

RESULT 5

US-10-758-165-2
; Sequence 2, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammeberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-2

Query Match 50.0%; Score 37; DB 5; Length 15;
Best Local Similarity 53.8%; Pred. No. 10;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 NNVLIQTDOQATT 14
|:|:|:|:|:|:|
Db 2 NDSFRTDOQATT 14

RESULT 6
US-10-497-091-128
; Sequence 128, Application US/10497091
; Publication No. US20050074863A1
; GENERAL INFORMATION:
; APPLICANT: HELLEDOORN, Koen
; APPLICANT: BAKER, Matthew
; APPLICANT: MILLIAMS, Steven
; APPLICANT: CARB, Francis J.
; TITLE OF INVENTION: T-CELL EPTOPES IN CARBOXYPEPTIDASE G2
; FILE REFERENCE: MER-130
; CURRENT APPLICATION NUMBER: US/10/497,091
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: PCT/EP02/13351
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: EP02020634.8
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: EP02001778.6
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EP01128519.4
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 15
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-497-091-128

Query Match 43.2%; Score 32; DB 5; Length 15;
Best Local Similarity 61.5%; Pred. No. 81;
Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 RNNVLIQ-TDQ 11
|:|:|:|:|:|:|
Db 3 RDNVLFQATDEQ 15

RESULT 7
US-10-958-216-713
; Sequence 713, Application US/10958216
; Publication No. US20050181388A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARMSI, AKIL

```

; APPLICANT: VEDADI, MASOUD
; APPLICANT: ALAM, MUHAMMAD ZAHoor
; APPLICANT: ARROWSMITH, CHERYL
; APPLICANT: AMREY, DONALD E.
; APPLICANT: BEATTIE, BRYAN
; APPLICANT: BUHADZICIA, KRISTINA
; APPLICANT: CANADIEN, VERONICA
; APPLICANT: DOMAGALA, MEGAN
; APPLICANT: HOUSTON, SIMON
; APPLICANT: KANAGARAJAH, DHUSHY
; APPLICANT: LI, QIN
; APPLICANT: MANSOURY, KAMRAN
; APPLICANT: McDONALD, MERRY-LYNN
; APPLICANT: NETHERY, KATHLEEN
; APPLICANT: NG, IVY
; APPLICANT: OUYANG, HUI
; APPLICANT: PINDER, BENJAMIN
; APPLICANT: RICHARDS, DAMN
; APPLICANT: TAL, MATTHEW
; APPLICANT: THALAKADA, ROSANNE
; APPLICANT: VALLEE, FRANCOIS
; APPLICANT: VIRAG, CRISTINA
; TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM BACTERIA
; FILE REFERENCE: IFT-205.01
; CURRENT FILING DATE: US/10/958,216
; PRIOR APPLICATION NUMBER: PCT/CA03/00462
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/369,511
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/385,089
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/385,751
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/386,553
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,577
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,367
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,566
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,390
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/386,601
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1132
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 713
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-10-958-216-713

Query Match          39.2% Score 29; DB 5; Length 12;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      4 VLIQTDOQATTR 15
|::|::|::|
DB      1 VMVEGDDEASVR 12

RESULT 8
US-10-346-162-192
; Sequence 192, Application US/10346162
; Publication No. US20030224390A1
; GENERAL INFORMATION:
; APPLICANT: KARO BIO USA, INC.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: BARNETT, Thomas R.
; APPLICANT: BUEHRER, Benjamin
```

```

; TITLE OF INVENTION: METHOD OF IDENTIFYING CONFORMATION-SENSITIVE BINDING PEPTIDES AND
; FILE REFERENCE: THEREOF
; FILE REFERENCE: PAIGE-1H
; CURRENT APPLICATION NUMBER: US/10/346,162
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US 09/614,865
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 09/860,688
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; US-10-346-162-192

Query Match          39.2% Score 29; DB 4; Length 15;
Best Local Similarity 46.2%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      3 NVLIQTDOQATTR 15
|::|::|::|
DB      3 NLCLILDEACSR 15

RESULT 9
US-10-758-165-4
; Sequence 4, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Ovis aries
; US-10-758-165-4

Query Match          39.2% Score 29; DB 5; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1 RNNVLIQTDOQATTR 15
|::|::|::|
DB      1 RNKEIMREGQHTTQ 15

RESULT 10
US-09-572-404B-1728
; Sequence 1728, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 1728
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
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```
FEATURE:
OTHER INFORMATION: sequence located in TPP2 at 1925-1934 and may interact with Sequ
OTHER INFORMATION: 1727 in this patent.
US-09-572-404B-1728
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Query Match      36.5%; Score 27; DB 3; Length 10;
Best Local Similarity 71.4%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY      8 TDQOATT 14
Db      1 SDQOTT 7
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```
RESULT 11
US-10-497-091-14
Sequence 14, Application US/10497091
Publication No. US20050074863A1
GENERAL INFORMATION:
APPLICANT: HELLEDOORN, Koen
APPLICANT: BAKER, Matthew
APPLICANT: WILLIAMS, Steven
APPLICANT: CARR, Francis J.
TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2
FILE REFERENCE: MER-130
CURRENT APPLICATION NUMBER: US/10/497,091
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: PCT/EP02/13351
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: EP02020634.8
PRIOR FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: EP02001778.6
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: EP01128519.4
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 13
TYPE: PRT
ORGANISM: homo sapiens
US-10-497-091-14
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```
Query Match      36.5%; Score 27; DB 5; Length 13;
Best Local Similarity 58.3%; Pred. No. 5.5e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
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QY      2 NNVLIQ--TDQO 11
Db      1 DNVLFOATDQ 12
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RESULT 12
US-10-172-425B-37
Sequence 37, Application US/10172425B
Publication No. US20030147908A1
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Arad, Gila
TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
FILE REFERENCE: A1967-PCT-USA-A-A 066031.0164
CURRENT APPLICATION NUMBER: US/10/172,425B
CURRENT FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: 09/150,947
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/IL97/00438
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119938
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
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LENGTH: 14
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-172-425B-37
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Query Match      36.5%; Score 27; DB 4; Length 14;
Best Local Similarity 44.4%; Pred. No. 6e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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```
QY      6 IOTDOATT 14
Db      1 VOTDKSVT 9
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```
RESULT 13
US-10-497-091-129
Sequence 129, Application US/10497091
Publication No. US20050074863A1
GENERAL INFORMATION:
APPLICANT: HELLEDOORN, Koen
APPLICANT: BAKER, Matthew
APPLICANT: WILLIAMS, Steven
APPLICANT: CARR, Francis J.
TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2
FILE REFERENCE: MER-130
CURRENT APPLICATION NUMBER: US/10/497,091
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: PCT/EP02/13351
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: EP02020634.8
PRIOR FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: EP02001778.6
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: EP01128519.4
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 129
LENGTH: 15
TYPE: PRT
ORGANISM: homo sapiens
US-10-497-091-129
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Query Match      36.5%; Score 27; DB 5; Length 15;
Best Local Similarity 58.3%; Pred. No. 6.5e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
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QY      2 NNVLIQ--TDQO 11
Db      1 DNVLFOATDQ 12
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RESULT 14
US-10-935-642-48
Sequence 48, Application US/10935642
Publication No. US20050050656A1
GENERAL INFORMATION:
APPLICANT: Huang, Xueying
APPLICANT: Wang, Hong
APPLICANT: Wu, Ying
TITLE OF INVENTION: Peptide-Based Conditioners and Colorants for Hair, Skin, and
TITLE OF INVENTION: Nail's
FILE REFERENCE: C12296 US NA
CURRENT APPLICATION NUMBER: US/10/935,642
CURRENT FILING DATE: 2004-09-07
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.2
SEQ ID NO 48
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Hair-binding peptide
```

US-10-935-642-48

Query Match 35.1%; Score 26; DB 5; Length 12;
Best Local Similarity 62.5%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 TDQATTR 15
|||
|:
Db 1 TDMQAPRK 8

RESULT 15

US-11-074-473-48
; Sequence 48, Application US/11074473
; Publication No. US20050226839A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Xueying
; APPLICANT: Wang, Hong
; APPLICANT: Wu, Ying
; TITLE OF INVENTION: Peptide-Based Conditioners and Colorants for Hair, Skin, and
; TITLE OF INVENTION: Nails
; FILE REFERENCE: CL2296 US NA
; CURRENT APPLICATION NUMBER: US/11/074,473
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/10/935,642
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hair-binding peptide
US-11-074-473-48

Query Match 35.1%; Score 26; DB 6; Length 12;
Best Local Similarity 62.5%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 TDQATTR 15
|||
|:
Db 1 TDMQAPRK 8

Search completed: December 12, 2005, 21:05:29
Job time : 92.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: December 12, 2005, 21:00:56 ; Search time 4.66667 Seconds
(without alignments)
17.950 Million cell updates/sec

Title: US-10-758-165A-3
Perfect score: 74
Sequence: 1 RNNVLIQTDOQATTR 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 8641

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_New:*
1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PC1_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	29.7	15	7	US-11-072-170A-21
2	21	28.4	11	6	US-10-467-657-8862
3	21	28.4	13	6	US-10-511-559-802
4	21	28.4	13	6	US-10-511-559-803
5	20	27.0	10	7	US-11-053-076-242
6	20	27.0	10	7	US-11-053-076-247
7	20	27.0	13	6	US-10-511-559-177
8	20	27.0	13	6	US-10-511-559-861
9	20	27.0	13	6	US-10-511-559-862
10	20	27.0	13	6	US-10-511-559-1096
11	20	27.0	13	6	US-10-511-559-1097
12	20	27.0	13	6	US-10-511-559-1098
13	20	27.0	14	6	US-10-939-890-60
14	19	25.7	10	6	US-10-507-662-49
15	19	25.7	12	7	US-11-016-706-5
16	19	25.7	13	6	US-10-511-559-264
17	19	25.7	13	6	US-10-511-559-265
18	19	25.7	13	6	US-10-511-559-266
19	19	25.7	13	6	US-10-511-559-267
20	19	25.7	13	6	US-10-511-559-725
21	19	25.7	13	6	US-10-511-559-863
22	19	25.7	14	6	US-10-467-657-8907
23	18	24.3	7	7	US-11-096-706-192
24	18	24.3	9	6	US-10-491-096-94
25	18	24.3	10	6	US-10-491-096-95

26	18	24.3	12	7	US-11-016-706-26	Sequence 26, Appl
27	18	24.3	13	6	US-10-511-559-199	Sequence 199, App
28	18	24.3	13	6	US-10-511-559-200	Sequence 200, App
29	18	24.3	13	6	US-10-511-559-201	Sequence 201, App
30	18	24.3	13	6	US-10-511-559-202	Sequence 202, App
31	18	24.3	13	6	US-10-511-559-608	Sequence 608, App
32	18	24.3	13	6	US-10-511-559-609	Sequence 609, App
33	18	24.3	13	6	US-10-511-559-610	Sequence 610, App
34	18	24.3	13	6	US-10-511-559-611	Sequence 611, App
35	18	24.3	14	6	US-10-467-657-8804	Sequence 8804, Ap
36	18	24.3	14	6	US-10-524-643-51	Sequence 51, Appl
37	18	24.3	14	7	US-11-054-515-2537	Sequence 2537, Ap
38	18	24.3	14	7	US-11-054-515-2539	Sequence 2539, Ap
39	18	24.3	15	6	US-11-054-515-2622	Sequence 2622, Ap
40	18	24.3	15	6	US-10-467-657-8918	Sequence 8918, Ap
41	17.5	23.6	8	7	US-11-058-727-107	Sequence 107, App
42	17.5	23.6	8	7	US-11-108-389-107	Sequence 107, App
43	17	23.0	4	7	US-11-032-794-58	Sequence 58, Appl
44	17	23.0	6	6	US-10-467-657-9114	Sequence 9114, Ap
45	17	23.0	7	7	US-11-096-706-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-11-072-170A-21
; Sequence 21, Application US/11072170A
; Publication No. US20050260159A1
; GENERAL INFORMATION:
; APPLICANT: Hasty, Karen
; APPLICANT: Postlethwait, Arnold
; APPLICANT: Kanangat, Sivadasan
; TITLE OF INVENTION: Intracellular Interleukin-1 Receptor Antagonist and
; FILE REFERENCE: D6564
; CURRENT APPLICATION NUMBER: US/11/072.170A
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: US 60/550,108
; PRIOR FILING DATE: 2004-03-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Macintosh OS 10
; SEQ ID NO 21
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: IL-1ra peptides
US-11-072-170A-21
Query Match 29.7% Score 22; DB 7; Length 15;
Best Local Similarity 66.7% Pred. No. 62;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Cy 1 RNNVLI 6
Db 4 RNNQLV 9
RESULT 2
US-10-467-657-8862
; Sequence 8862, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467.657
; CURRENT FILING DATE: 2003-08-11

```
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 8862
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8862
```

```
Query Match      28.4%; Score 21; DB 6; Length 11;
Best Local Similarity 57.1%; Pred. No. 66;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 TQDQAT 13
       :|||:
Db      1 KTDRQYT 7
```

```
RESULT 3
US-10-511-559-802
```

```
; Sequence 802, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 802
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-802
```

```
Query Match      28.4%; Score 21; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 81;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 IQTDDQ 11
       :|||:
Db      8 LQSDQE 13
```

```
RESULT 4
US-10-511-559-803
```

```
; Sequence 803, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
```

```
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 803
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-803
```

```
Query Match      28.4%; Score 21; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 81;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 IQTDDQ 11
       :|||:
Db      3 LQSDQE 8
```

```
RESULT 5
US-11-053-076-242
```

```
; Sequence 242, Application US/11053076
; Publication No. US20050255460A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Somoza Diaz-Sarmiento, Chamorro
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008CIP
; CURRENT APPLICATION NUMBER: US/11/053,076
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: PCT/US03/28508
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 242
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-053-076-242
```

```
Query Match      27.0%; Score 20; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      8 TDDQAT 13
       :|||:
Db      1 TSDQAT 6
```

```
RESULT 6
US-11-053-076-247
```



```
; Sequence 247, Application US/11053076
; Publication No. US20050255460A1
; GENERAL INFORMATION:
; APPLICANT: Schweizer, Johannes
; APPLICANT: Lu, Peter S.
; APPLICANT: Somoza Diaz-Sarmiento, Chamorro
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008CIP
; CURRENT APPLICATION NUMBER: US/11/053,076
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: PCT/US03/28508
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 247
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-053-076-247

Query Match      27.0%; Score 20; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-177

Query Match      27.0%; Score 20; DB 6; Length 13;
Best Local Similarity 38.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      3 NVLIQTDDQATTR 15
Db      1 NSIMQDRDASAR 13

RESULT 8
US-10-511-559-861
; Sequence 861, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 861
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-861

Query Match      27.0%; Score 20; DB 6; Length 13;
Best Local Similarity 25.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      8 TDDQAT 13
Db      1 TSDQAT 6

RESULT 7
US-10-511-559-177
; Sequence 177, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
QY      2 NVLIQTDDQAT 13
Db      2 DNIMVTFRQAS 13

RESULT 9
US-10-511-559-862
; Sequence 862, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 862
; LENGTH: 13
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-862
```

```
Query Match          27.0%; Score 20; DB 6; Length 13;
Best Local Similarity 25.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2 NNVLIQDQOQAT 13
      :|::||:
Db      1 DNIVTFRNQAS 12
```

```
RESULT 10
US-10-511-559-1096
; Sequence 1096, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1096
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-1096
```

```
Query Match          27.0%; Score 20; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      6 IQTDQOQATTR 15
      :|::||:
Db      4 LQVDFQKTMK 13
```

```
RESULT 11
US-10-511-559-1097
; Sequence 1097, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1097
; LENGTH: 13
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-1097
```

```
Query Match          27.0%; Score 20; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      6 IQTDQOQATTR 15
      :|::||:
Db      3 LQVDFQKTMK 12
```

```
RESULT 12
US-10-511-559-1098
; Sequence 1098, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1098
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-1098
```

```
Query Match          27.0%; Score 20; DB 6; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      6 IQTDQOQATTR 15
      :|::||:
Db      1 LQVDFQKTMK 10
```

```
RESULT 13
US-10-939-890-60
; Sequence 60, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappa, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondaredidat
; APPLICANT: Shrivastava, Ajay
```

APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617, 70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 60
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Library Isolate
US-10-939-890-60

Query Match 27.0%; Score 20; DB 6; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 IOTDQA 12
|||:
Db 2 ICDRKA 8

RESULT 14
US-10-507-662-49
Sequence 49, Application US/10507662
Publication No. US20050255102A1
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
TITLE OF INVENTION: THE REAGENTS OF THE UNIVERSITY OF CALIFORNIA
FILE REFERENCE: A136PCT
CURRENT APPLICATION NUMBER: US/10/507,662
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: 60/364,991
PRIOR FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 60/426,286
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-507-662-49

Query Match 25.7%; Score 19; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NNVLIO 7
|||:
Db 5 NNDLIE 10

RESULT 15
US-11-016-706-5
Sequence 5, Application US/11016706
Publication No. US2005024434A1
GENERAL INFORMATION:

APPLICANT: CASTILLO, GERARDO
APPLICANT: LAKE, THOMAS P.
APPLICANT: NGUYEN, BETH P.
APPLICANT: SANDERS, VIRGINIA J.
APPLICANT: SNOW, ALAN D.
TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
FILE REFERENCE: PROTEO.P03C13
CURRENT APPLICATION NUMBER: US/11/016,706
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: 09/962,955
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/938,275
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 08/947,057
PRIOR FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 5
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-11-016-706-5

Query Match 25.7%; Score 19; DB 7; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NNVLIO 7
|||:
Db 2 SNVFWQ 7

Search completed: December 12, 2005, 21:17:41
Job time : 5.66667 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 12, 2005, 21:05:42 ; Search time 18 Seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-10-758-165a-3

Perfect score: 74

Sequence: 1 RNNVLIQTDQQTTR 15

Scoring table: BLOSUM62

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	25	33.8	15	2	nitrogenase cofact
2	21	28.4	13	2	Ig kappa chain V-I
3	21	28.4	13	2	Ig kappa chain V-I
4	20	28.4	15	2	Ig heavy chain DJ
5	20	27.0	10	2	cytochrome-c oxida
6	19	25.7	10	2	proteoglycan core
7	19	25.7	13	2	urinary tract ston
8	19	25.7	14	2	synaptonemal-asso
9	18	24.3	9	2	alpha-2-macroglobu
10	18	24.3	11	2	cytochrome-c oxida
11	18	24.3	13	2	epithelial dog all
12	18	24.3	15	2	insulin-like growt
13	18	24.3	15	2	epoxypropan isomer
14	17	23.0	10	2	carcarnine medium/I
15	17	23.0	10	2	T-cell receptor be
16	17	23.0	11	2	proteasome endopep
17	17	23.0	11	4	hypothetical prote
18	17	23.0	12	2	sucrose-6-phosphat
19	17	23.0	13	2	ribosomal protein
20	17	23.0	13	2	proteasome endopep
21	17	23.0	13	2	40K extracellular
22	17	23.0	13	2	deoxynucleotidyltr
23	17	23.0	14	2	Ig heavy chain V r
24	17	23.0	14	2	T-cell receptor be
25	17	23.0	14	2	T-cell receptor de
26	17	23.0	15	2	protein QP20022 -
27	17	23.0	15	2	nitrophorin 4 - Rh
28	17	23.0	15	2	porphobilinogen sy
29	17	23.0	15	2	phospholipase C-be

30	16	21.6	10	2	D54823	olfactory receptor
31	16	21.6	10	2	C54823	olfactory receptor
32	16	21.6	11	2	S70720	trigger factor hom
33	16	21.6	12	2	A33099	163K exoantigen -
34	16	21.6	12	2	S28425	20K protein - rape
35	16	21.6	14	2	B81280	probable proteolys
36	16	21.6	15	2	PQ0681	photosystem I 19.0
37	16	21.6	15	2	PS0452	32K protein 3306 -
38	16	21.6	15	2	PH1631	Ig H chain V-D-J r
39	16	21.6	15	2	AS5096	thymotrophin-releas
40	16	21.6	15	2	A36527	juvenile-hormone e
41	16	21.6	15	2	A35594	calnexin - mouse
42	15	20.3	8	2	S71919	alcohol dehydrogen
43	15	20.3	8	2	T48890	hypothetical prote
44	15	20.3	10	2	PQ0788	NADH2 dehydrogenas
45	15	20.3	11	2	PQ0682	photosystem I 17.5

ALIGNMENTS

RESULT 1

S32677
nitrogenase cofactor synthesis protein nifs - Anabaena variabilis (fragment)
N:Contains: L-cysteine sulfuryltransferase (EC 2.8.1.-)
C:Species: Anabaena variabilis
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S32677
R:Monmerjahn, U.; Boehme, H.
submitted to the EMBL Data Library, December 1992
A:Description: Cloning and expression in E. coli of the Anabaena.
A:Reference number: S32675
A:Accession: S32677
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <MON>
A:Cross-references: UNIPROT:Q44507; UNIPARC:UPI00001301CC; EMBL:X69898; NID:G296503; PID
C:Superfamily: nitrogen fixation protein nifs
C:Keywords: sulfurtransferase

Query Match 33.8%; Score 25; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 LIQTDOQTTR 15
Db 3 VYLDNNATTK 13

RESULT 2

B61458
Ig kappa chain V-I region (BLA) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C:Accession: B61458
R:Brown, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:title: Expression of a public idiotype by human monoclonal IGM directed to myelin-asso
A:Reference number: A61458; MUID:90039128; PMID:2478651
A:Accession: B61458
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BRO>
A:Cross-references: UNIPARC:UPI000017C2SD
C:Keywords: heterotetramer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 IQTDOQTTR 14
Db 2 IQTOSPTT 10

RESULT 3
A61458
Ig kappa chain V-I region (BOU) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C/Accession: A61458; P10156
R/Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mhaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A/Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-assc
A/Reference number: A61458; MUID:90035126; PMID:2478651
A/Accession: A61458
A/Molecule type: protein
A/Residues: 1-13 <BRO>
C/Comment: This protein is one of monoclonal IGM reactive with myeloma-associated glycop
C/Keywords: heterotrimer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 6 IOTDQATT 14
Db 2 IOWTQSPRT 10

RESULT 4
PH1329
Ig heavy chain DJ region (clone C552-104) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1329
R/Masserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:9304761; PMID:1460419
C/Accession: PH1329
A/Molecule type: DNA
A/Residues: 1-15 <MAS>
A/Cross-references: UNIPARC:UPI000017C245
C/Keywords: heterotrimer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNNVLI 6
Db 4 RNEVMI 9

RESULT 5
S43625
cytochrome-c oxidase (EC 1.9.3.1) chain Va, hepatic - rainbow trout (fragment)
C/Species: Oncorhynchus mykiss (rainbow trout)
C/Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C/Accession: S43625
R/Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A/Title: Identification of tissue-specific isoforms for subunits Vb and V1a of cytochr
A/Reference number: S43624; MUID:94237150; PMID:8181469
A/Accession: S43625
A/Molecule type: protein
A/Residues: 1-10 <FRK>
A/Cross-references: UNIPROT:P80328; UNIPARC:UPI0000128131
A/Note: the source is designated as Salmo gairdneri
C/Genetics:
A/Genome: nuclear
C/Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase
Query Match 27.0%; Score 20; DB 2; Length 10;

Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 6 IOTDQ 11
Db 5 VERDEE 10

RESULT 6
A55695
proteoglycan core protein - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 17-Mar-1999
C/Accession: A55695
R/Lark, M.W.; Gordy, J.T.; Weidner, J.R.; Ayala, J.; Kimura, J.H.; Williams, H.R.; Mumfo
J. Biol. Chem. 270, 2550-2556, 1995
A/Title: Cell-mediated catabolism of aggrecan. Evidence that cleavage at the "aggrecanase
A/Reference number: A55695; MUID:9515314; PMID:7852317
A/Accession: A55695
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <LAR>
A/Cross-references: UNIPARC:UPI000017C9A9

Query Match 25.7%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNNVLI 6
Db 2 RNNVIL 7

RESULT 7
H56046
urinary tract stone matrix protein 10, 42K - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C/Accession: H56046
R/Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.
submitted to the Protein Sequence Database, February 1995
A/Description: Isolation, characterization and sequence of stone proteins.
A/Reference number: A56046
A/Accession: H56046
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-13 <BIN>
A/Cross-references: UNIPROT:Q7M4P7; UNIPARC:UPI000017C406

Query Match 25.7%; Score 19; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 2.5e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NNVLITD 9
Db 6 NDLAETD 13

RESULT 8
C44823
synaptosomal-associated protein SNAP-25 peptide 8 - rabbit (fragment)
N/Alternate names: superprotein peptide 8
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C/Accession: C44823
R/Loewy, A.; Liu, W.S.; Balingier, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A/Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A/Reference number: A44823; MUID:92044785; PMID:1941090
A/Accession: C44823
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <LOB>

A:Cross-references: UNIPARC:UPI000017C5E7
A:Experimental source: visual tissue
A>Note: sequence extracted from NCBI backbone (NCBIP:64253)
C:Keywords: membrane trafficking

Query Match 25.7%; Score 19; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 2.7e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 LVLTDDQ 11
| | | | |
DB 2 LVMLDEQ 8

RESULT 9
S6636
alpha-2-macroglobulin isoform 2 - bovine (fragment)
C:Species: Bos primigenius indicus (zebu cattle)
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S6636
R:Dotmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottrup
FEB5 Lett. 372, 93-95, 1995
A:Title: Crystallization and preliminary X-ray analysis of the receptor-binding domain c
A:Reference number: S6634; MUID:96032553; PMID:7556651
A:Accession: S6636
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DB>
A:Cross-references: UNIPROT:Q7M2N7, UNIPARC:UPI000017C480

Query Match 24.3%; Score 18; DB 2; Length 9;
Best Local Similarity 37.5%; Pred. No. 2.8e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 NVLIQTDQ 10
| | | | |
DB 2 NILPKDE 9

RESULT 10
S43626
cytochrome-c oxidase (EC 1.9.3.1) chain Vb-H - trout (fragment)
C:Species: Salmo sp. (trout)
C>Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 02-Jul-1998
C:Accession: S43626
R:Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochr
A:Reference number: S43624; MUID:94237150; PMID:8181469
A:Accession: S43626
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <FRE>
A:Cross-references: UNIPARC:UPI000017BF62
C:Keywords: electron transfer; membrane-associated complex; oxidoreductase; respiratory

Query Match 24.3%; Score 18; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 IQTDQ 11
| | | | |
DB 6 IPTDE 11

RESULT 11
A59491
epithelial dog allergen - Canis familiaris (fragment)
C:Species: Canis familiaris
C>Date: 27-Oct-2003 #sequence_revision 27-Oct-2003 #text_change 27-Oct-2003
C:Accession: A59491
R:Saarelainen, S.; Taitainen, A.; Ryckm-vnen-Nissinen, M.; Autilola, S.; Immonen, A.; MM-
submitted to the Protein Sequence Database, October 2003

A:Description: Diagnosis of dog allergy with recombinant allergens.
A:Reference number: A59491
A:Accession: A59491
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <VIR>
A>Note: IGE-binding protein; allergen

Query Match 24.3%; Score 18; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 NVLIQ 7
| | | | |
DB 3 NVLTQ 7

RESULT 12
PT0205
insulin-like growth factor-binding protein, bone - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 08-Dec-1994
C:Accession: PT0205; A33175
R:Bautista, C.M.; Baylink, D.J.; Mohan, S.
Biochem. Biophys. Res. Commun. 176, 756-763, 1991
A:Title: Isolation of a novel insulin-like growth factor (IGF) binding protein from huma
A:Reference number: PT0205; MUID:9122244; PMID:1709017
A:Accession: PT0205
A:Molecule type: protein
A:Residues: 1-15 <BAU>
A:Cross-references: UNIPARC:UPI000017C275

Query Match 24.3%; Score 18; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 4.5e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 VLIQTDQA 12
| | | | |
DB 5 VVVEPDKA 13

RESULT 13
S72432
epoxypropan isomerase component B - Xanthobacter sp. (strain Py2) (fragment)
C:Species: Xanthobacter sp.
A:Variety: strain Py2
C>Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 07-May-1999
R:Chan Kwo Chion, C.K.N.; Leak, D.J.
Biochem. J. 319, 499-506, 1996
A:Title: Purification and characterization of two components of epoxypropane isomerase/c
A:Reference number: S72431; MUID:97069704; PMID:8912687
A:Accession: S72432
A:Molecule type: protein
A:Residues: 1-15 <CHA>
A:Cross-references: UNIPARC:UPI000017CA9F
A>Note: 3-Met and 13-Leu were also found
C:Complex: homodimer
C:Function:
A:Description: NADP-dependent lipamide reductase
A:Pathway: epoxypropane degradation
A>Note: sensitive to N-ethyl-maleimide and p-chloromercuribenzoate
C:Keywords: PAD

Query Match 24.3%; Score 18; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 4.5e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNVLIQTD 9
| | | | |
DB 7 RNDHLLIXD 15

RESULT 14

A61354
 carnitine medium/long chain acyltransferase (EC 2.3.1.-) - rat (fragment)
 N:Alternate names: endoplasmic reticulum protein ERp61; glucose regulated protein GRP58;
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
 C/Accession: A61354
 R/Murthy, M.S.R.; Pande, S.V.
 Mol. Cell. Biochem. 122, 133-138, 1993
 A>Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the prev
 A/Reference number: A61354; PMID:94049728; PMID:8232244
 A/Accession: A61354
 A>Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-10 <MDR>
 A/Cross-references: UNIPARC:UPI000017C8DE
 C/Keywords: acyltransferase

Query Match

23.0%; Score 17; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 4.4e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 NVLIQTDO 10
 |||||
 Db 2 DVLEITDE 9

RESULT 15

PH0933
 T-cell receptor beta chain V-D-J region (clone 4) - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C/Accession: PH0933
 R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174, 1467-1476, 1991
 A>Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
 A/Reference number: PH0931; PMID:92078857; PMID:1836012
 A/Accession: PH0933
 A/Molecule type: mRNA
 A/Residues: 1-10 <GDU>
 A/Cross-references: UNIPARC:UPI000017C9E5
 A/Experimental source: complete Freund's adjuvant-immunized lymph node
 A/Note: the authors translated the codon CAG for residue 9 as Glu
 C/Keywords: T-cell receptor

Query Match

23.0%; Score 17; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNN 3
 |||||

Db 6 RNN 8

Search completed: December 12, 2005, 21:18:42
 Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 12, 2005, 20:59:31 ; Search time 114 Seconds
(without alignments)
92.833 Million cell updates/sec

Title: US-10-758-165A-3
Perfect score: 74
Sequence: 1 RNNVL1QTDQATTR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 7855

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	33.8	15	1 NIFS1 ANAVA	Q44507 anabaena va
2	24	32.4	15	2 Q98B05 CYNCA	Q98B05 CYNCA card
3	23	31.1	14	2 Q4XS12 PLACH	Q4XS12 plasmodium
4	22	29.7	9	2 P70740 ALCEU	P70740 alcaligenes
5	22	29.7	12	2 Q9WZS4 CANFA	Q9WZS4 canis fam1
6	22	29.7	14	2 Q9TRQ7 BOVIN	Q9TRQ7 bos taurus
7	22	29.7	15	2 Q9TRH1 BOVIN	Q9TRH1 bos taurus
8	21	28.4	10	2 Q6JDM9 CANFA	Q6JDM9 canis fam1
9	21	28.4	13	2 Q7SMV9 HUMAN	Q7SMV9 homo sapien
10	21	28.4	14	2 P83330 STRTR	P83330 streptococc
11	21	28.4	15	2 Q29622 RABIT	Q29622 oryctolagus
12	21	28.4	15	2 Q9TR62 RABIT	Q9TR62 oryctolagus
13	20	27.0	10	1 COX5A ONCMY	P80328 oncomychnu
14	20	27.0	10	2 Q9UJ48 HUMAN	Q9UJ48 homo sapien
15	20	27.0	15	2 Q6WZ21 HUMAN	Q6WZ21 homo sapien
16	20	27.0	15	2 Q5GJH9 COXBU	Q5GJH9 coxiella bu
17	20	27.0	15	2 Q5GJH9 COXBU	Q5GJH9 coxiella bu
18	19	25.7	8	2 Q9S824 TOBAC	Q9S824 nicotiana t
19	19	25.7	10	2 Q76V79 POLYU	Q76V79 polymyaviru
20	19	25.7	10	2 Q53X10 POVBK	Q53X10 polymyaviru
21	19	25.7	10	2 Q53X11 POVBK	Q53X11 polymyaviru
22	19	25.7	10	2 Q53X32 POVBK	Q53X32 polymyaviru
23	19	25.7	10	2 Q53X33 POVBK	Q53X33 polymyaviru
24	19	25.7	11	2 RANP_RANPI	P08951 rana pipien
25	19	25.7	11	2 Q06626 SOLTU	Q06626 solanum tub
26	19	25.7	11	2 Q5EDJ3 LEGPN	Q5EDJ3 legionella
27	19	25.7	13	1 FR12_PEA	P83445 pisum sativ
28	19	25.7	13	2 Q7M4F7 HUMAN	Q7M4F7 homo sapien
29	19	25.7	13	2 Q9SB03 ORYSA	Q9SB03 oryza sativ
30	19	25.7	13	2 Q6RSM3 COXBU	Q6RSM3 coxiella bu
31	19	25.7	14	2 Q9P0W1 HUMAN	Q9P0W1 homo sapien

ALIGNMENTS

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RESULT 1
NIFS1 ANAVA          STANDARD,      PRT,      15 AA.
ID NIFS1 ANAVA
AC Q44507
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cysteine desulfurase 1 (EC 2.8.1.7) (Nitrogenase metalloclusters
DE biosynthesis protein nifs1) (fragment).
GN Name=nifs1; Synonyms=nifs;
OS Anabaena variabilis.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxId=1172;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCC 7937 / ATCC 29413;
RA Monnerjahn U., Boehme H.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
[2]
RP EXPRESSION PATTERN.
RC STRAIN=PCC 7937 / ATCC 29413;
RA MEDLINE=96016168; PubMed=7568132;
RX Thiel T., Lyons B.M., Erker J.C., Ernst A.;
RT "A second nitrogenase in vegetative cells of a heterocyst-forming
RT cyanobacterium.";
CC Proc. Natl. Acad. Sci. U.S.A. 92:9358-9362(1995).
CC -!- FUNCTION: Catalyzes the removal of elemental sulfur atoms from
CC cysteine to produce alanine. Seems to participate in the
CC biosynthesis of the nitrogenase metalloclusters by providing the
CC inorganic sulfur required for the Fe-S core formation (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: L-cysteine + [enzyme]-cysteine = L-alanine +
CC [enzyme]-S-sulfanylcysteine.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- MISCELLANEOUS: Belongs to the Nif1 gene cluster which is expressed
CC in heterocysts under anaerobic and aerobic conditions.
CC -!- SIMILARITY: Belongs to the class-V pyridoxal-phosphate-dependent
CC aminotransferase family. Nifs1/iscs subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X69898; CAA49523.1; -; Genomic_DNA.
CC PIR; S32677; S32677.
CC InterPro; IPR000192; Aminoctrans V.
CC PROSITE; PS00595; AA_TRANSFERR CLASS_5; PARTIAL.
CC Nitrogen fixation; Pyridoxal phosphate; Transferase.
CC NON_TER 15
CC SEQUENCE 15 AA; 1684 MW; 0888P106DE65547D CRC64;

```

Query Match 33.8%; Score 25; DB 1; Length 15;
 Best Local Similarity 45.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 LIOTDOOATR 15
 DB 3 VITYDNNATTK 13

RESULT 2

Q9S8D5_CYNCA PRELIMINARY; PRT; 15 AA.
 AC Q9S8D5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE CARDOSIN A (Fragment).
 OS Cynara cardunculus (Cardoon).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Campanulids; Asterales; Asteraceae; Carduoideae; Cardueae; Cynara.
 NCBI_TaxId=4265;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=96073661; PubMed=8540346;
 RA Faro C., Verissimo P., Lin Y., Tang J., Pires E.
 RT "Cardosin A and B, aspartic proteases from the flowers of cardoon."
 RL Adv. Exp. Med. Biol. 362:373-377(1995).
 SQ SEQUENCE 15 AA; 1555 MW; CC95D9155C97325B CRC64;

Query Match 32.4%; Score 24; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 2.2e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 NVLIQTQOAT 13
 DB 4 SALVATDNQNT 14

RESULT 3

O4XS12_PLACH PRELIMINARY; PRT; 14 AA.
 AC O4XS12;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Oryza sativa L.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 NCBI_TaxId=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karra M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Brittan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jense C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 DR EMBL; CAJ01003511; CAH80130.1; -, Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1781 MW; 989A795983FA9A51 CRC64;

Query Match 31.1%; Score 23; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 3.2e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NNVLIIQ 7
 DB 8 NNVLIFQ 13

RESULT 4

P70740_ALCEU PRELIMINARY; PRT; 9 AA.
 ID P70740;
 AC P70740;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hoxa protein (Fragment).
 GN Name=hoxa;
 OS Alcaligenes eutrophus (Ralstonia eutropha).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Cupriavidus.
 NCBI_TaxId=106590;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=H16;
 RX MEDLINE=94292469; PubMed=8021224;
 RA Lenz O., Schwartz E., Dornedde J., Bittinger M., Friedrich B.
 RT "The Alcaligenes eutrophus H16 hoxa gene participates in hydrogenase
 RT regulation."
 RL J. Bacteriol. 176:4385-4393(1994).
 DR EMBL; X74670; CAAS2736.1; -, Genomic_DNA.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 992 MW; 970BD1ADC6D3A85 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 TDOOAT 13
 DB 2 SDOOAT 7

RESULT 5

O9MZS4_CANFA PRELIMINARY; PRT; 12 AA.
 AC O9MZS4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Growth hormone (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 NCBI_TaxId=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=22319383; PubMed=12431806; DOI=10.1016/S0303-7207(02)00257-5;
 RA Lantigua-van Leeuwen I.S., Timmermans-Sprang E.A., Mol J.A.,
 RT "Cloning and characterization of the 5'-flanking region of the canine
 RT growth hormone gene."
 RL Mol. Cell. Endocrinol. 197:133-141(2002).
 DR EMBL; AF166119; AAF89582.1; -, Genomic_DNA.
 FT NON TER 12
 SQ SEQUENCE 12 AA; 1229 MW; 2B587268ECB45417 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 4.1e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNNVLI 6
 DB 6 RNSVLI 11

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RESULT 6
Q9TRQ7 BOVIN PRELIMINARY; PRT; 14 AA.
ID Q9TRQ7 BOVIN PRELIMINARY; PRT; 14 AA.
AC Q9TRQ7 BOVIN PRELIMINARY; PRT; 14 AA.
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DE 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Calcyclin-associated protein peptide L-8, CAP-50=ANNEXIN
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92317074; PubMed=1618951;
RA Mitutani A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
RA Kobayashi R., Hidaka H.;
RT "CAP-50, a newly identified annexin, localizes in nuclei of cultured
RT fibroblast 3Y1 cells."
RL J. Biol. Chem. 267:13498-13504(1992).
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1446 MW; C8322EB96DD9C6C6 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 4.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TDQQA 12
DB 4 TDQQA 8

RESULT 7
Q9TRH1 BOVIN PRELIMINARY; PRT; 15 AA.
ID Q9TRH1 BOVIN PRELIMINARY; PRT; 15 AA.
AC Q9TRH1 BOVIN PRELIMINARY; PRT; 15 AA.
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DE 01-JUN-2002 (TRENBLREL. 24, Last annotation update)
DE Alkaline phosphodiesterase I (EC 3.1.4.1) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93250579; PubMed=8387370;
RA Maruyama E., Iwamoto A., Takashima S.;
RA Blochem. Mol. Biol. Int. 29:579-586(1993).
RL GO:0004528; F:phosphodiesterase I activity; IEA.
SQ SEQUENCE 15 AA; 1678 MW; BE31498EBA8B7071 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 5.4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 VLQTDQAT 13
DB 2 VLQTDQAT 13

RESULT 8
Q6JDM9 CANFA PRELIMINARY; PRT; 10 AA.
ID Q6JDM9 CANFA PRELIMINARY; PRT; 10 AA.
AC Q6JDM9 CANFA PRELIMINARY; PRT; 10 AA.
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DE 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Mitochondrial H+ transporting ATP synthase F1 (Fragment).

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GN Name=ATP5A1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15233990; DOI=10.1016/j.ygeno.2004.04.001;
RA Housley D.J.E., Ritzert E., Venta P.J.;
RT "Comparative radiation hybrid map of canine chromosome 1 (CFA1)
RT incorporating SNP and indel polymorphisms."
RL Genomics 84:248-264(2004).
DR EMBL: AY514688; AAT44872.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1059 MW; C47457B1A045B042 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 5.2e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 NVLIQTDQ 11
DB 2 NVLIQTDQ 10

RESULT 9
Q75MW9 HUMAN PRELIMINARY; PRT; 13 AA.
ID Q75MW9 HUMAN PRELIMINARY; PRT; 13 AA.
AC Q75MW9;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DE 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein SSBP1 (Fragment).
GN Name=SSBP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.E.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., Delahunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harting R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Stromwater C.,
RA Latreille P., Miller N., Johnson D., Murray J., Moesener J.P.,
RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,
RA Hickmonotham M.T., Eldred S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Purrey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicker P., Bock P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7."
RL Nature 424:157-164(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.

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RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004979; AAS02037.1; -; Genomlc_DNA.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 13 AA; 1565 MW; 9A39BF645040DAB5 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 7e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 NVLIQTQDQ 10
Db 1 NITFLSDQ 8

RESULT 10
P83330 STRTR PRELIMINARY; PRT; 14 AA.
ID P83330 STRTR PRELIMINARY; PRT; 14 AA.
AC P83330 STRTR PRELIMINARY; PRT; 14 AA.
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE M protein, serotype 32 (Fragment).
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=ITGSTR2;
RA Guimont C., Chopard M.A., Galliard J.L., Chamba J.F.;
RT "Comparative study of the protein composition of three strains of
RT Streptococcus thermophilus grown either in M17 medium or in milk.";
RL Lait 0:0-0(2002).
CC -1- FUNCTION: This protein is one of the different antigenic serotypes
CC of protein M. Protein M is closely associated with virulence of
CC the bacterium and can render the organism resistant to
CC phagocytosis (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall (By
CC similarity).
CC -1- SIMILARITY: TO OTHER M PROTEINS.
CC -1- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN
CC THE REGION OF THE MEMBRANE ANCHOR.
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006909; P:phagocytosis; IEA.
KW Antigen; Cell wall; Phagocytosis; Transmembrane; Virulence.
FT NON TER
SQ SEQUENCE 14 AA; 1739 MW; 66339B9F3A3FE24B CRC64;

Query Match 28.4%; Score 21; DB 2; Length 14;
Best Local Similarity 28.6%; Pred. No. 7.7e+03;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NNVLITQDQATTR 15
Db 1 NHOITGNERLTK 14

RESULT 11
Q29622 RABIT PRELIMINARY; PRT; 15 AA.
ID Q29622 RABIT PRELIMINARY; PRT; 15 AA.
AC Q29622 RABIT PRELIMINARY; PRT; 15 AA.
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

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DE Recombination activating protein (Fragment).
GN Name=RAG-2;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RIM/sgm; TISSUE=Thymus;
RX MEDLINE=93354283; Pubmed=8350872; DOI=10.1016/0161-5890(93)90127-W;
RA Puschiotet P., Harindranath N., Mage R.G., McCormack W.T.,
RA Dhanarajan P., Roux K.H.;
RT "Recombination activating genes-1 and -2 of the rabbit: cloning and
RT characterization of germ-line and expressed genes.";
RL MOL. Immunol. 30:1021-1032(1993).
DR EMBL; M99310; AAA03028.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON TER
SQ SEQUENCE 15 AA; 1717 MW; CE095FAD5F7ED42B CRC64;

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RNNVLI 6
Db 9 RNNIAL 14

RESULT 12
Q9TR62 RABIT PRELIMINARY; PRT; 15 AA.
ID Q9TR62 RABIT PRELIMINARY; PRT; 15 AA.
AC Q9TR62 RABIT PRELIMINARY; PRT; 15 AA.
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE Apolipoprotein A-IV (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95329112; Pubmed=7605356; DOI=10.1016/0021-9150(94)05444-N;
RA Mezdour H., Yamamura T., Nomura S., Yamamoto A.;
RT "Genetic but not diet-induced hypercholesterolemia causes low
RT apolipoprotein A-IV level in rabbit sera.";
RL Atherosclerosis 113:171-178(1995).
SQ SEQUENCE 15 AA; 1761 MW; DE115B7351F0ABC CRC64;

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 8.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 IOTDQAT 13
Db 2 VSADQVAT 9

RESULT 13
COX5A ONCMY STANDARD; PRT; 10 AA.
ID COX5A ONCMY STANDARD; PRT; 10 AA.
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cytochrome c oxidase polypeptide Va, mitochondrial (EC 1.9.3.1)

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DE (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.,
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -1- FUNCTION: This is the heme A-containing chain of cytochrome c
CC oxidase, the terminal oxidase in mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR: S43625; S43625.
KW Direct protein sequencing; Heme; Inner membrane; Iron; Membrane;
KW Metal-binding; Mitochondrion; Oxidoreductase.
FT NON_TER
SQ SEQUENCE 10 AA; 1144 MW; C535C5B1AB02C33D CRC64;

Query Match 27.0%; Score 20; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 8.1e+03;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 6 IQTDOQ 11
DB 5 VETDER 10

RESULT 14
O9U48 HUMAN
ID O9U48_HUMAN PRELIMINARY; PRT; 10 AA.
AC O9U48_
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lactophilin-2 (Fragment).
GN Name-LPHN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99153747; PubMed=10030676; DOI=10.1038/sj.onc.1202487;
RA White G.R.M., Varley J.M., Heighway J.,
RT "Isolation and characterisation of a human homologue of the
RT lactophilin gene from a region of 1p31.1 implicated in breast
RT cancer.";
RL Oncogene 17:3513-3519(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20225451; PubMed=10760572; DOI=10.1016/S0167-4781(00)00020-8;
RA White G.R.M., Varley J.M., Heighway J.,
RT "Genomic structure and expression profile of LPHN1, a 7TM gene
RT variably expressed in breast cancer cell lines.";
RL Biochim. Biophys. Acta 1491:75-92(2000).
DR EMBL; AJ244514; CAB60206.1; -; Genomic_DNA.
FT NON_TER 1

```

```

SQ SEQUENCE 10 AA; 1112 MW; 06CC4C2720544724 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 NVLIQ 7
DB 5 NILLQ 9

RESULT 15
O6MZZ1 HUMAN
ID O6MZZ1_HUMAN PRELIMINARY; PRT; 15 AA.
AC O6MZZ1_
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686J2076.
DE Name=DKFZp686J2076;
GN Name=DKFZp686J2076;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human endometrium carcinoma cell line;
RG The German Human CDNA Consortium;
RA Ansgorge W., Krieger S., Regiert T., Ritzmuller C., Schwager B.,
RA Mewes H.W., Weil B., Auld C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640801; CAE45884.1; -, mRNA.
SQ SEQUENCE 15 AA; 1715 MW; 91F5CE0118445CE3 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.3e+04;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 LIQDQ 11
DB 4 LKVDQ 10

```

Search completed: December 12, 2005, 21:17:25
Job time : 116 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2005, 19:37:19 ; Search time 81.3362 Seconds
(without alignments)
81.030 Million cell updates/sec

Title: US-10-758-165A-3
Perfect score: 74
Sequence: 1 RNNVLIQTDDQATTR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	15	ADRI0603	Adri0603 Horse IGE
2	74	100.0	424	AAW50103	AAW50103 Equine IGE
3	74	100.0	424	AAW50104	AAW50104 Equine IGE
4	74	100.0	569	ABP96585	ABP96585 Horse IGE
5	49	66.2	15	ADC64568	ADC64568 Horse Imm
6	43	58.1	417	AE839722	AE839722 L. pneumo
7	43	58.1	452	AE836305	AE836305 L. pneumo
8	43	58.1	580	ABG32001	ABG32001 O. intest
9	43	58.1	580	ADP79623	ADP79623 Giardia i
10	41	55.4	15	ADRI0601	ADRI0601 Dog IGE e
11	41	55.4	312	AAV79995	AAV79995 Dog Immun
12	41	55.4	312	ADN24060	ADN24060 Bacteri
13	41	55.4	417	AAW23067	AAW23067 Canine IGE
14	41	55.4	426	AAW97753	AAW97753 Canine IGE
15	41	55.4	426	ABP96583	ABP96583 Dog IGE h
16	41	55.4	2000	ABR52669	ABR52669 Protein s
17	41	55.4	2000	ADK61774	ADK61774 Disease t
18	40	54.1	15	ADRI0607	ADRI0607 Pig IGE h
19	40	54.1	567	ABP96588	ABP96588 Pig IGE h
20	38	51.4	613	AAW73009	AAW73009 Cobra ven
21	38	51.4	621	AAW73013	AAW73013 Cobra ven
22	38	51.4	703	ABU44458	ABU44458 Protein e
23	38	51.4	814	ABJ26042	ABJ26042 Aspergill
24	37	50.0	15	ADRI0602	ADRI0602 Cat IGE e

25	37	50.0	66	4	AAU62291	AAU62291 Propionib
26	37	50.0	66	6	ABM58810	ABM58810 Propionib
27	37	50.0	223	6	ADJ48583	Adj48583 Oil-aseoc
28	37	50.0	285	2	AAV17498	AAV17498 Zoon prot
29	37	50.0	370	6	ADA34539	Ada34539 Actinob
30	37	50.0	431	8	ADG73237	Adg73237 Cat immun
31	37	50.0	496	6	ABP96580	ABP96580 Cat IGE h
32	37	50.0	496	6	ABU09338	ABU09338 Feline IGE
33	37	50.0	496	6	ABU09336	ABU09336 Feline IGE
34	37	50.0	496	6	ADG73251	Adg73251 Cat parti
35	37	50.0	496	8	ADG73225	Adg73225 Cat parti
36	37	50.0	663	8	ADJ49049	Adj49049 Oil-aseoc
37	37	50.0	1320	4	AAU48101	AAU48101 Propionib
38	37	50.0	1320	6	ADM44620	ADM44620 Propionib
39	36	48.6	21	7	ADM66490	Adm66490 Peptide f
40	36	48.6	75	8	ADV87747	Adv87747 Streptoco
41	36	48.6	75	8	ADV79000	Adv79000 Streptoco
42	36	48.6	143	6	ABJ26246	ABJ26246 Aspergill
43	36	48.6	199	8	ADR94119	Adr94119 Novel S.
44	36	48.6	199	9	AEA57989	Aea57989 Streptoco
45	36	48.6	210	8	ADU47057	Adu47057 Corn Dice

ALIGNMENTS

RESULT 1
ID ADRI0603 standard; peptide: 15 AA.
XX
XX ADRI0603;
AC
XX
XX 21-OCT-2004 (first entry)
DT
XX
XX
DE Horse IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 3.
KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW horse.
XX
XX OS Equus caballus.
XX
XX PN WO2004065936-A2.
XX
XX PD 05-AUG-2004.
XX
XX PF 15-JAN-2004; 2004WO-US003566.
XX
XX PR 16-JAN-2003; 2003US-0440472P.
XX
XX (UNNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hammerberg B;
XX
XX WPI, 2004-593545/57.
XX
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (I) that
XX specifically binds to a mammalian IGE epitope, where the epitope is
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX (I) is useful for testing an allergen reactivity of an IGE sample.
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX and corn allergens. The sample is a biological sample collected from a
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX antibodies recognise epitopes on canine IGE corresponding to amino acid
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IgE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IgE. The present sequence is the
CC horse IgE 5.91 recognition site.

XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIOTDQATTR 15
| | | | | | | | | | | | | | |
Db 1 RNNVLIOTDQATTR 15

RESULT 2

AA50103
ID AAM50103 standard; protein; 424 AA.

AC AAM50103;

DT 02-SEP-2002 (first entry)

DE Equine IgE heavy chain constant region C-epsilon allotype A.

XX Cea; equine; horse; heavy chain; constant region; allotype a; IgE;
KM C-epsilon a; immunoglobulin E; anti-allergic; allergy.

XX
OS Equus caballus.

XX
FH Key Location/Qualifiers

FT Domain 1..97

FT Domain /note= "CH1 domain"

FT Domain 98..205

FT Domain /note= "CH2 domain"

FT Domain 206..312

FT Domain /note= "CH3 domain"

FT Domain 313..424

FT Domain /note= "CH4 domain"

XX
PN WO200250280-A2.

PD 27-JUN-2002.

PF 20-DEC-2001; 2001WO-DE004810.

PR 21-DEC-2000; 2000DE-01064415.

PA (TIER-) TIERAERZTLICHE HOCHSCHULE HANNOVER.

PI Leibold W, Wagner B, Radbruch A;

DR WPI; 2002-508803/54.

DR N-PSDB; ABL61246.

XX
PT DNA sequence encoding part of an equine immunoglobulin G, useful for
PT preparing isotype-specific antibodies for diagnosis and treatment of
PT allergy in horses.

XX
PS Claim 1; Page 31-32; 37pp; German.

XX
CC This invention describes a novel DNA (I) encoding the constant region
CC (CH) of the heavy chain of a horse immunoglobulin E (IgE) allotype. The
CC products of the invention are capable of neutralising IgE activity and
CC have anti-allergic activity. The polynucleotides of the invention are used
CC to produce recombinant IgE (II), and this is used to raise specific
CC monoclonal antibodies (Mab). Both (II) and Mab are useful for diagnosis,
CC particularly of allergy in horses, and Mab can also be used for treatment
CC of allergies. (I) make possible production of isotype-specific
CC antibodies, important for precise evaluation of the immune response. This
CC sequence represents a fragment of the equine IgE heavy chain constant

CC region C-epsilon allotype a (Cea), used in the method of the invention
CC for IgE-isotype recombinant immunoglobulin production

XX
SQ Sequence 424 AA;

Query Match 100.0%; Score 74; DB 5; Length 424;
Best Local Similarity 100.0%; Pred. No. 8.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNNVLIOTDQATTR 15
| | | | | | | | | | | | | | |
Db 356 RNNVLIOTDQATTR 370

RESULT 3

AA50104
ID AAM50104 standard; protein; 424 AA.

AC AAM50104;

DT 02-SEP-2002 (first entry)

DE Equine IgE heavy chain constant region C-epsilon allotype b.

XX Ceb; equine; horse; heavy chain; constant region; allotype b; IgE;
KM C-epsilon b; immunoglobulin E; anti-allergic; allergy.

XX
OS Equus caballus.

XX
FH Key Location/Qualifiers

FT Domain 1..97

FT Domain /note= "CH1 domain"

FT Domain 98..205

FT Domain /note= "CH2 domain"

FT Domain 206..312

FT Domain /note= "CH3 domain"

FT Domain 313..424

FT Domain /note= "CH4 domain"

XX
PN WO200250280-A2.

PD 27-JUN-2002.

PF 20-DEC-2001; 2001WO-DE004810.

PR 21-DEC-2000; 2000DE-01064415.

PA (TIER-) TIERAERZTLICHE HOCHSCHULE HANNOVER.

PI Leibold W, Wagner B, Radbruch A;

DR WPI; 2002-508803/54.

DR N-PSDB; ABL61247.

XX
PT DNA sequence encoding part of an equine immunoglobulin G, useful for
PT preparing isotype-specific antibodies for diagnosis and treatment of
PT allergy in horses.

XX
PS Claim 1; Page 34-36; 37pp; German.

XX
CC This invention describes a novel DNA (I) encoding the constant region
CC (CH) of the heavy chain of a horse immunoglobulin E (IgE) allotype. The
CC products of the invention are capable of neutralising IgE activity and
CC have anti-allergic activity. The polynucleotides of the invention are used
CC to produce recombinant IgE (II), and this is used to raise specific
CC monoclonal antibodies (Mab). Both (II) and Mab are useful for diagnosis,
CC particularly of allergy in horses, and Mab can also be used for treatment
CC of allergies. (I) make possible production of isotype-specific
CC antibodies, important for precise evaluation of the immune response. This
CC sequence represents a fragment of the equine IgE heavy chain constant
CC region C-epsilon allotype b (Ceb), used in the method of the invention
CC for IgE-isotype recombinant immunoglobulin production

SQ Sequence 424 AA;

Query Match 100.0%; Score 74; DB 5; Length 424;
 Best Local Similarity 100.0%; Pred. No. 8,2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATTR 15
 |||||
 Db 356 RNNVLIQTDOQATTR 370

RESULT 4
 ABP96585
 ID ABP96585 standard; protein; 569 AA.

XX AC ABP96585;

XX DT 28-MAY-2003 (first entry)

XX DE Horse IGE heavy chain amino acid sequence SEQ ID NO:30.

XX KM Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
 KM immune response; major histocompatibility complex; MHC; immunogenic;
 KM antiallergic; antiaesthetic; immunosuppressive; vasotropic; cytostatic;
 KM dermatological; antiinflammatory; IGE-mediated condition; food allergy;
 KM atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
 KM atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
 KM urticaria hives.

XX OS Equus caballus.

XX PN MO2003015716-A2.

XX PD 27-FEB-2003.

XX PF 08-AUG-2002; 2002WO-US026986.

XX PR 13-AUG-2001; 2001US-0312120P.

XX PA (IGET-) IGE THERAPEUTICS INC.

XX PI Chen SA, Yang Y, Barankiewicz T, Chen Z;

XX DR WPI; 2003-268242/26.

XX PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
 PT against IGE, by identifying peptide eliciting CTL response to IGE
 PT peptides naturally presented by major histocompatibility complex class I
 PT protein.

XX PS Example 7; Page 157-160; 187pp; English.

XX CC The present invention describes a method (M1) for identifying peptides
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
 CC E (IGE), comprising providing a test peptide (T) suspected of being able
 CC to bind to major histocompatibility complex (MHC) class I molecule, and
 CC evaluating (T) for ability to elicit in a mammal a CTL response to
 CC naturally processed and presented IGE peptides, where a peptide that
 CC induces such a response is identified. Also described are compositions:
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to
 CC elicit in a mammal a CTL response to naturally processed and presented
 CC IGE peptides. C1-3 have antiallergic, antiaesthetic, immunosuppressive,
 CC vasootropic, dermatological, antiinflammatory and cytostatic activities,
 CC and can be used as inducers of a CTL response against IGE, and in
 CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
 CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as
 CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
 CC useful for treating atopic hypersensitivity conditions (such as allergic
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-

CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
 CC hives). The present sequence represents an IGE heavy chain amino acid
 CC sequence, which is given in an example from the present invention
 CC XX

SQ Sequence 569 AA;
 Query Match 100.0%; Score 74; DB 6; Length 569;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATTR 15
 |||||
 Db 501 RNNVLIQTDOQATTR 515

RESULT 5
 ADC64568
 ID ADC64568 standard; peptide; 15 AA.

XX AC ADC64568;

XX DT 18-DEC-2003 (first entry)

XX DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P4.

XX KM Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.

XX OS Equus caballus.

XX PN US2003087314-A1.

XX PD 08-MAY-2003.

XX PF 08-NOV-2001; 2001US-00052788.

XX PR 08-NOV-2001; 2001US-00052788.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Gerhwin LJ, Pettigrew HD, Kalina WV;

XX DR WPI; 2003-765437/72.

XX PT Immunogenic composition comprising an isolated equine immunoglobulin E
 PT polypeptide that induces production of antibodies which specifically bind
 PT to equine immunoglobulin E.

XX PS Example 1; Page 8; 14pp; English.

XX CC The invention relates to an immunogenic composition comprising an
 CC isolated polypeptide having an amino acid sequence that is at least 80%
 CC identical to 6 (S1-S6), 15 amino acid peptide sequences derived from
 CC equine immunoglobulin E (the composition induces production of an
 CC antibody that specifically binds to equine immunoglobulin (Ig)E), the six
 CC polypeptides are not explicitly identified in the specification. Also
 CC included are a composition comprising an antibody that specifically binds
 CC to a polypeptide at least 80% identical to (S1)-(S6), an antibody that
 CC specifically binds to equine IGE made by the process of immunising an
 CC animal with a polypeptide at least 80% identical to (S1)-(S6), making an
 CC antibody that specifically binds to equine IGE (involving immunising an
 CC animal with a composition further comprising an isolated polypeptide (the
 CC amino acid sequence of the polypeptide is at least 80% identical to (S1)-
 CC (S6)), and collecting antiserum from the animal) and a kit for detection
 CC of equine IGE in a biological sample comprising the antibody and means
 CC for detecting specific binding of the antibody to equine IGE. The
 CC antibody is useful for detecting equine IGE protein in a biological
 CC sample (serum) which involves contacting the sample with the antibody,
 CC thus forming an antigen/antibody complex, and detecting the presence or
 CC absence of the antigen/antibody complex. The antibody and antigen are
 CC immobilised on a solid surface. The antibody is labelled such that the
 CC complex can be detected. The complex is detected using a second labelled
 CC antibody. The peptides are useful for generating antibodies specific for
 CC IGE which can serve as a diagnostic test for allergy. The present

CC sequence is a Horse immunoglobulin E, IgE, heavy chain immunogenic
CC peptide from the early portion of the C4 region.
XX
SQ Sequence 15 AA;

Query Match 66.2%; Score 49; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IQTDOQATTR 15
|||
Db 1 IQTDOQATTR 10

RESULT 6
AEB39722
ID AEB39722 standard; protein; 417 AA.
XX

AC AEB39722;

XX 08-SEP-2005 (first entry)

DE L. pneumophila protein SEQ ID NO 4054.

XX detection; infection; Antibacterial; Vaccine.

XX Legionella pneumophila.

XX MO2005049642-A2.

XX 02-JUN-2005.

XX 23-SEP-2004; 2004MO-IB003578.

XX 21-NOV-2003; 2003FR-00013687.

XX (INSP) INST PASTEUR.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (UTLY-) UNIV LYON 1 BERNARD CLAUDE.

PI (CNRS) CNRS CENT NAT RECH SCI.

PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalec C, Glaser P;

PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;

PI Jarraud S;

XX WPI; 2005-388305/40.

XX New genome of Legionella pneumophila Paris strain and derived

PT polypeptides, useful for detection or identification of the strain and

PT for treatment and prevention of infections.

XX Claim 3; SEQ ID NO 4054; 660pp; English.

XX The invention relates to an isolated or purified nucleotide sequences (I)

CC from Legionella pneumophila Paris strain. (II), and their related

CC sequences or fragments, are useful as primers and probes for detection

CC and amplification, including differentiation between the Paris and

CC Philadelphia strains of Legionella pneumophila and to prepare recombinant

CC (hybrid) polypeptides (II). (II) are also useful for preparation of

CC specific antibodies (Ab), also used for detection/identification of

CC Legionella, and some (I), specifically those involved in synthesis of

CC surface proteins, are targets for identification of inhibitors. (II), or

CC vectors that contain (I), are useful as vaccines and immunogenic

CC compositions, for treatment and prevention of infections by L.

CC pneumonia. The present sequence represents the amino acid sequence of a

CC L. pneumophila protein.

XX
XX
SQ Sequence 417 AA;

Query Match 58.1%; Score 43; DB 9; Length 417;
Best Local Similarity 69.2%; Pred. No. 36;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLITQDQOATT 14
|||
Db 63 NNVLITPLEQOQPTT 75

RESULT 7
AEB36305
ID AEB36305 standard; protein; 452 AA.
XX

AC AEB36305;

XX 08-SEP-2005 (first entry)

DE L. pneumophila protein SEQ ID NO 637.

XX detection; infection; Antibacterial; Vaccine.

XX Legionella pneumophila.

XX MO2005049642-A2.

XX 02-JUN-2005.

XX 23-SEP-2004; 2004MO-IB003578.

XX 21-NOV-2003; 2003FR-00013687.

XX (INSP) INST PASTEUR.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (UTLY-) UNIV LYON 1 BERNARD CLAUDE.

PI (CNRS) CNRS CENT NAT RECH SCI.

PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalec C, Glaser P;

PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;

PI Jarraud S;

XX WPI; 2005-388305/40.

XX New genome of Legionella pneumophila Paris strain and derived

PT polypeptides, useful for detection or identification of the strain and

PT for treatment and prevention of infections.

XX Claim 3; SEQ ID NO 637; 660pp; English.

XX The invention relates to an isolated or purified nucleotide sequences (I)

CC from Legionella pneumophila Paris strain. (II), and their related

CC sequences or fragments, are useful as primers and probes for detection

CC and amplification, including differentiation between the Paris and

CC Philadelphia strains of Legionella pneumophila and to prepare recombinant

CC (hybrid) polypeptides (II). (II) are also useful for preparation of

CC specific antibodies (Ab), also used for detection/identification of

CC Legionella, and some (I), specifically those involved in synthesis of

CC surface proteins, are targets for identification of inhibitors. (II), or

CC vectors that contain (I), are useful as vaccines and immunogenic

CC compositions, for treatment and prevention of infections by L.

CC pneumonia. The present sequence represents the amino acid sequence of a

CC L. pneumophila protein.

XX
XX
SQ Sequence 452 AA;

Query Match 58.1%; Score 43; DB 9; Length 452;
Best Local Similarity 69.2%; Pred. No. 39;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLITQDQOATT 14
|||
Db 98 NNVLITPLEQOQPTT 110

RESULT 8
ABG32001
ID ABG32001 standard; protein; 580 AA.

AC	ABG32001,
XX	
DT	06-AUG-2003 (revised)
DT	15-NOV-2002 (first entry)
XX	
DE	Q. intestinalis arginine deiminase gene, QIADIINT.
XX	
KM	Arginine deiminase; cytosolic; ADI; polyethylene glycol; PEG; arginine;
KW	citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;
XX	auxotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.
OS	Giardia intestinalis.
FN	WO200244360-A2.
PD	
XX	06-JUN-2002.
PF	19-SEP-2001; 2001WO-US029184.
PR	28-NOV-2000; 2000US-00723546.
PA	(PHOE-) PHOENIX PHARMACOLOGICS INC.
PI	Clark MA;
DR	WPI; 2002-619003/66.
PT	Compound for treating tumor such as melanoma, hepatoma or sarcoma in a
PT	patient, comprises arginine deiminase covalently bonded by a linking
PT	group such as succinimide to polyethylene glycol.
XX	
PS	Disclosure; Fig 12; 59pp; English.
XX	
CC	The invention discloses a compound comprising arginine deiminase (ADI)
CC	covalently bonded by a linking group to polyethylene glycol (PEG) having
CC	a total weight average molecular weight of about 1000-50000. Also
CC	disclosed is a method for enhancing the circulating half life or the
CC	tumoricidal activity of arginine deiminase by modifying the arginine
CC	deiminase by covalently bonding the arginine deiminase by a linking group
CC	to PEG. Normal cells can synthesize arginine from citrulline in a 2 step
CC	process catalysed by argininosuccinate synthase and argininosuccinate
CC	lyase. In contrast, many cancerous cells do not express argininosuccinate
CC	synthase and are, therefore, auxotrophic for arginine. Arginine deiminase
CC	catalyses the conversion of arginine to citrulline and can be used to
CC	eliminate arginine from the cancerous cells. The compound is useful for
CC	treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or
CC	for treating and inhibiting metatases in a patient. When compared to
CC	native arginine deiminase the compound retains most of its enzymatic
CC	activity, is far less antigenic, has a greatly extended circulating half-
CC	life, and is much more efficacious in the treatment of tumours. The
CC	sequence presented is the Giardia intestinalis arginine deiminase gene,
CC	QIADIINT. (Updated on 06-AUG-2003 to correct OS field.)
XX	
SQ	Sequence 580 AA;
QY	
Query Match	58.1%; Score 43; DB 5; Length 580;
Best Local Similarity	57.1%; Pred. No. 52;
Matches	8; Conservative 2; Mismatches 4; Indels 0; Gaps 0
DB	
168 NNMVFMRDQAITTR	181
QY	2 NNVLIGTDOAATR 15
:	
RESULT 9	
ID	ADP79623
ID	ADP79623 standard; protein; 580 AA.
XX	
AC	ADP79623;
XX	
DT	04-NOV-2004 (first entry)
XX	
DE	Giardia intestinalis arginine deaminase.

XX	Arginine deaminase; cytostatic; virucide; viral replication;
KM	nitric oxide synthesis; tumour; liver function; enzyme.
XX	
OS	Giardia intestinalis.
PN	WO2004046309-A2.
XX	
PD	03-JUN-2004.
XX	
PF	29-SEP-2003; 2003WO-US030770.
XX	
PR	18-NOV-2002; 2002US-0427497P.
XX	
PA	(PHOE-) PHOENIX PHARMACOLOGICS INC.
XX	
PI	Clark MA;
XX	
DR	WPI; 2004-431965/40.
XX	
PT	Inhibiting replication of viruses in individual, involves administering
PR	composition comprising arginine deaminase bonded to polyethylene glycol,
PT	to individual.
XX	
PS	Claim 18; SEQ ID NO 17; 89pp; English.
XX	
CC	The invention relates to inhibiting the replication of one or more
CC	viruses in an individual and involves administering to the individual a
CC	composition comprising an arginine deaminase bonded to polyethylene
CC	glycol. The method is useful for inhibiting replication of one or more
CC	viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,
CC	where the arginine deaminase is derived from Mycoplasma e.g. M. arginini,
CC	M. hominis, M. arthritidis and its combination. It is useful for treating
CC	an individual who is suspected of having been exposed to one or more
CC	viruses, for modulating nitric oxide levels in an individual, or for
CC	selectively inhibiting viral replication in an individual. The method is
CC	also useful for treating a tumour and inhibiting replication of one ore
CC	more viruses in an individual. The tumour is melanoma, sarcoma, or
CC	hepatoma. The tumour is hepatocellular carcinoma. The method is also
CC	useful for improving liver function in an individual. The present
CC	sequence represents a Giardia intestinalis arginine deaminase.
XX	
SO	Sequence 580 AA;
XX	
Query Match	58.1%; Score 43; DB 8; Length 580;
Best Local Similarity	57.1%; Pred. No. 52;
Matches	8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY	2 NNVLIQTDQQTTR 15
	:
DB	168 NNVWFMRDQQTTR 181
XX	
RESULT 10	
ID	ADRI0601 standard; peptide; 15 AA.
XX	
AC	ADRI0601;
XX	
DT	21-OCT-2004 (first entry)
XX	
DE	Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.
XX	
KW	Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
XX	anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
OS	Canis familiaris.
XX	
PN	WO2004065936-A2.
XX	
PD	05-AUG-2004.
XX	
PF	15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.
XX (UYNC-) UNIV NORTH CAROLINA STATE.
XX Hammerberg B;
XX WPI; 2004-593545/57.
XX Novel antibody that specifically binds to mammalian IgE epitope, useful
PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
or treating asthma or anaphylactic shock.
XX Example 6; Page 9; 14pp; English.
XX The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IgE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
CC (I) is useful for testing an allergen reactivity of an IgE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IgE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0603) respectively of the
CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IgE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IgE.
XX Sequence 15 AA;
SQ
Query Match 55.4%; Score 41; DB 8; Length 15;
Best Local Similarity 64.3%; Pred. No. 2;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 RNNVLITQDQOATT 14
||:|||||
Db 1 RNDSPITQDQYTTT 14
RESULT 11
AAV79995
ID AAV79995 standard; protein; 312 AA.
XX
XX AAV79995;
XX
XX 15-MAY-2000 (first entry)
XX
XX Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.
XX
XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KM immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KM antibody; allergy; allergic disease; immunisation; anti-allergic;
KM anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
XX Canis sp.
XX
XX WO967293-A1.
XX
XX PN 29-DEC-1999.
XX
XX PD 21-JUN-1999; 99WO-US013959.
XX
XX PF 20-JUN-1998; 98US-00100287.
XX
XX PR (UNBI-) UNITED BIOMEDICAL INC.
XX
XX PA Wang CY, Walfield AM;
XX
XX PI WPI; 2000-160578/14.
XX
XX DR

PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX for immunization against allergy.
XX Example 1; Page 66-68; 155pp; English.
XX
XX The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
CC a target effector site on the epsilon-heavy chain of IgE, and so
CC preventing triggering and activation of mast cells and basophils and
CC downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe (non-
CC anaphylactogenic) antibodies. AAV79994 to AAV80084 represent amino acid
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 312 AA;
QY 1 RNNVLITQDQOATT 14
||:|||||
Db 255 RNDSPITQDQYTTT 268
RESULT 12
ADN24060
ID ADN24060 standard; protein; 312 AA.
XX
XX ADN24060;
XX
XX 02-DEC-2004 (first entry)
XX
XX Bacterial polypeptide #6713.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KM pathogen tolerance; pest tolerance; plant disease resistance;
KM cell cycle pathway modification; plant growth regulator;
KM homologous recombination; seed oil yield; protein yield; carbohydrate;
KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KM bacterial polypeptide.
XX
XX Bacteria.
XX
XX US2003233675-A1.
XX
XX PN 18-DEC-2003.
XX
XX PD 20-FEB-2003; 2003US-00369493.
XX
XX PF 21-FEB-2002; 2002US-0360039P.
XX
XX PR (CAOY/) CAO Y.
XX
XX PA (HINK/) HINKLE G J.
XX
XX PA (SIAT/) SLATER S C.
XX
XX PA (CHEN/) CHEN X.
XX
XX PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
XX WPI; 2004-061375/06.
XX
XX DR New recombinant DNA construct comprising a promoter positioned to provide
XX
XX PT


```

XX WPI; 1996-277321/28.
DR N-PSDB; AAT29824.
XX
XX New DNA encoding canine IGE and IGA - useful in vaccines, anti-sense
PT therapy, assays, drug screening, etc.
XX
PS Claim 11; Page 29-30; 49pp; English.
XX
XX The canine IGE amino acid sequence (AAR97753) was deduced from an
CC isolated gene (AAT29824) obtd. from a canine liver DNA library. The
CC cloning of the IGE gene allows produ. of large quantities of recombinant
CC IGE using bacterial, yeast, mammalian, insect or viral systems. The IGE
CC can be used in drug development (e.g. small molecule screening, assay
CC development and anti-IGE antibody generation). Fragments of IGE can be
CC used in vaccines or to prevent IGE-mediated hypersensitivity. The new
CC sequence information permits targeted modulation of IGE-mediated immune
CC responses
XX
SQ Sequence 426 AA;
XX
Query Match 55.4%; Score 41; DB 2; Length 426;
Best Local Similarity 64.3%; Pred. No. 85;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATT 14
Db 357 RNDSPITQTDQYTTT 370

RESULT 15
ABP96583
ID ABP96583 standard; protein; 426 AA.
XX
AC ABP96583;
XX
DT 28-MAY-2003 (first entry)
XX
DE Dog IGE heavy chain amino acid sequence SEQ ID NO:28.
XX
XX Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
KM immune response; major histocompatibility complex; MHC; immunogenic;
KM antiallergic; antisthmatic; immunosuppressive; vasotropic; cytostatic;
KM dermatological; antiinflammatory; IGE-mediated condition; food allergy;
KM atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KM atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
KM urticaria hives.
XX
OS Canis familiaris.
XX
XX WO2003015716-A2.
XX
XX 27-FEB-2003.
XX
XX 08-AUG-2002; 2002WO-US026986.
XX
XX 13-AUG-2001; 2001US-0312120P.
XX
XX (IGET-) IGE THERAPEUTICS INC.
XX
XX Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX
XX WPI; 2003-268242/26.
XX
XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL, response
PT against IGE, by identifying peptide eliciting CTL response to IGE
PT peptides naturally presented by major histocompatibility complex class I
PT protein.
XX
XX Example 7; Page 152-154; 187pp; English.
XX
XX The present invention describes a method (M1) for identifying peptides
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin

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```

CC E (IGE), comprising providing a test peptide (T) suspected of being able
CC to bind to major histocompatibility complex (MHC) class I molecule, and
CC evaluating (T) for ability to elicit in a mammal a CTL response to
CC naturally processed and presented IGE peptides, where a peptide that
CC induces such a response is identified. Also described are compositions:
CC (c1) comprising at least one immunogenic peptide (I) identified by (M1);
CC (c2) comprising at least one isolated polynucleotide encoding (I); and
CC (c3) comprising antigen-presenting cells that recognise at least one (I).
CC Where C1-3 are able to bind to at least one MHC class I molecule and to
CC elicit in a mammal a CTL response to naturally processed and presented
CC IGE peptides. C1-3 have antiallergic, antisthmatic, immunosuppressive,
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
CC and can be used as inducers of a CTL response against IGE, and in
CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as
CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic
CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are
CC useful for treating atopic hypersensitivity conditions (such as allergic
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
CC hives). The present sequence represents an IGE heavy chain amino acid
CC sequence, which is given in an example from the present invention
XX
SQ Sequence 426 AA;
XX
Query Match 55.4%; Score 41; DB 6; Length 426;
Best Local Similarity 64.3%; Pred. No. 85;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATT 14
Db 357 RNDSPITQTDQYTTT 370

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OM protein - protein search, using SW model

Run on: December 12, 2005, 19:23:41 ; Search time 20.431 seconds
(without alignments)
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Title: US-10-758-165a-3
Perfect score: 74
Sequence: 1 RNNVLIOYDQOATTR 15

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/PCITIS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	43	58.1	580	US-09-723-546-10	Sequence 10, Appl
2	41	55.4	108	US-09-281-760E-37	Sequence 37, Appl
3	41	55.4	312	US-09-701-623C-2	Sequence 2, Appl
4	41	55.4	426	US-08-336-583-2	Sequence 2, Appl
5	41	55.4	426	PCR-US95-13795-2	Sequence 2, Appl
6	38	51.4	345	US-09-270-767-41480	Sequence 41480, A
7	38	51.4	613	US-09-026-001A-10	Sequence 10, Appl
8	38	51.4	613	US-09-996-620-10	Sequence 10, Appl
9	38	51.4	621	US-09-026-001A-18	Sequence 18, Appl
10	38	51.4	621	US-09-996-620-18	Sequence 18, Appl
11	37	50.0	370	US-09-328-352-5826	Sequence 5826, Ap
12	37	50.0	431	US-09-479-614-14	Sequence 14, Appl
13	37	50.0	496	US-09-479-614-2	Sequence 2, Appl
14	37	50.0	496	US-09-479-614-29	Sequence 29, Appl
15	36	48.6	153	US-09-248-796A-22386	Sequence 22386, A
16	36	48.6	199	US-09-107-433-2754	Sequence 2754, Ap
17	36	48.6	383	US-09-328-352-5969	Sequence 5969, Ap
18	36	48.6	441	US-09-583-110-4400	Sequence 4400, Ap
19	36	48.6	445	US-09-107-433-5039	Sequence 5039, Ap
20	36	48.6	447	US-09-205-258-408	Sequence 408, App
21	36	48.6	447	US-10-004-860-408	Sequence 408, App
22	36	48.6	461	US-09-991-181-301	Sequence 301, App
23	36	48.6	461	US-09-990-444-301	Sequence 301, App
24	36	48.6	461	US-09-997-333-301	Sequence 301, App
25	36	48.6	601	US-09-992-598-301	Sequence 301, App
26	36	48.6	601	US-09-489-039A-8499	Sequence 8499, Ap
27	35	47.3	75	US-09-248-796A-24803	Sequence 24803, A

28	35	47.3	138	2	US-09-540-236-1974	Sequence 1974, Ap
29	35	47.3	213	2	US-09-270-767-46161	Sequence 46161, A
30	35	47.3	286	2	US-09-107-532A-4821	Sequence 4821, A
31	35	47.3	406	2	US-09-134-001C-3544	Sequence 3544, Ap
32	35	47.3	408	2	US-08-630-172-18	Sequence 18, Appl
33	35	47.3	418	2	US-09-375-419-18	Sequence 18, Appl
34	35	47.3	434	2	US-09-198-452A-118	Sequence 118, App
35	35	47.3	434	2	US-09-438-185A-102	Sequence 102, App
36	35	47.3	551	2	US-08-886-886-15	Sequence 15, Appl
37	35	47.3	570	2	US-09-489-039A-12964	Sequence 12964, A
38	35	47.3	650	2	US-09-107-532A-5521	Sequence 5521, Ap
39	35	47.3	695	2	US-09-902-540-10055	Sequence 10055, A
40	35	47.3	1061	2	US-09-489-039A-12740	Sequence 12740, A
41	35	47.3	5024	2	US-09-710-279-2964	Sequence 2964, Ap
42	35	47.3	10182	2	US-09-134-001C-3159	Sequence 3159, Ap
43	34	45.9	92	2	US-09-134-001C-4864	Sequence 4864, Ap
44	34	45.9	135	2	US-09-293-395-2	Sequence 2, Appl
45	34	45.9	135	2	US-09-668-648-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-09-723-546-10
; Sequence 10, Application US/09723546
; Patent No. 6737259
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHOEO059
; CURRENT APPLICATION NUMBER: US/09/723,546
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/023,809
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 10
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Giardia intestinalis
US-09-723-546-10

Query Match      58.1% Score 43; DB 2; Length 580;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 RNNVLIOYDQOATTR 15
      ||: ||| |||
DB      168 NNWVEMRDQOITTR 181

RESULT 2
US-09-281-760E-37
; Sequence 37, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Warner, Brian
; APPLICANT: Francoeur, Greg
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760E
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Canis familiaris
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; LOCATION: (136)..(136)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (413)..(414)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (451)..(451)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
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; FEATURE:
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; LOCATION: (500)..(500)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (530)..(530)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (568)..(568)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (847)..(849)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (853)..(853)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1382)..(1382)
; OTHER INFORMATION: "n" stands for any nucleic acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1832)..(1832)
; OTHER INFORMATION: "n" stands for any nucleic acid
; US-09-281-760E-37

Query Match          55.4%; Score 41; DB 2; Length 108;
Best Local Similarity 64.3%; Pred. No. 4.3;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 RNNVLIGTDOQATT 14
Db      43 RNDSPIGTDQYTTT 56

RESULT 3
US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
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; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IGE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
; US-09-701-623C-2

Query Match          55.4%; Score 41; DB 2; Length 312;
Best Local Similarity 64.3%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 RNNVLIGTDOQATT 14
Db      255 RNDSPIGTDQYTTT 268

RESULT 4
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHRISTINE E. CARTY
; STREET: 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,583
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CARTY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-336-583-2

Query Match          55.4%; Score 41; DB 1; Length 426;
Best Local Similarity 64.3%; Pred. No. 21;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 RNNVLIGTDOQATT 14
Db      357 RNDSPIGTDQYTTT 370

RESULT 5
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PCT-US95-13795-2
 ; Sequence 2, Application PC/TUS9513795
 ; GENERAL INFORMATION:
 ; APPLICANT: HOLLIS, GREGORY F.
 ; APPLICANT: PATEL, MAYUR D.
 ; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: CHRISTINE E. CARTY
 ; STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
 ; CITY: RAHWAY
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07065-0907
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/13795
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CARTY, CHRISTINE E.
 ; REGISTRATION NUMBER: 36,099
 ; REFERENCE/DOCKET NUMBER: 19211Y
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908) 594-6734
 ; TELEFAX: (908) 594-4720
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 426 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-13795-2

Query Match 55.4%; Score 41; DB 4; Length 426;
 Best Local Similarity 64.3%; Pred. No. 21;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTQOATTT 14
 DB 357 RNDSPITQDTQYTTT 370

RESULT 6
 US-09-270-767-41480
 ; Sequence 41480, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7325-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 41480
 ; LENGTH: 345
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; FEATURE:
 ; OTHER INFORMATION: xaa means any amino acid
 US-09-270-767-41480

Query Match 51.4%; Score 38; DB 2; Length 345;
 Best Local Similarity 57.1%; Pred. No. 57;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 NNVLITQDQATTR 15

Db 77 NQKLIRKXQQTTR 90

RESULT 7
 US-09-026-001A-10
 ; Sequence 10, Application US/09026001A
 ; Patent No. 6413760
 ; GENERAL INFORMATION:
 ; APPLICANT: Boodhoo, Amechand
 ; APPLICANT: Seehra, Jasbir
 ; APPLICANT: Shaw, Gray
 ; APPLICANT: Sako, Dianne
 ; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 Cambridgepark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/026,001A
 ; FILING DATE: 18-FEB-1998
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; REFERENCE/DOCKET NUMBER: G15293B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 876-5851
 ; TELEFAX: (617) 876-8224
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 613 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-026-001A-10

Query Match 51.4%; Score 38; DB 2; Length 613;
 Best Local Similarity 53.8%; Pred. No. 1.1e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNNVLIQTQOATTT 13
 DB 261 RNEINVOQSDVQAT 273

RESULT 8
 US-09-996-620-10
 ; Sequence 10, Application US/09996620
 ; Patent No. 6881404
 ; GENERAL INFORMATION:
 ; APPLICANT: Boodhoo, Amechand
 ; APPLICANT: Seehra, Jasbir
 ; APPLICANT: Shaw, Gray
 ; APPLICANT: Sako, Dianne
 ; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
 ; PROTEASE, POLYPEPTIDES ENCODING SAME AND RELATED PROTEASES
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 Cambridgepark Drive

```

; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/996,620
; FILING DATE: 27-Feb. 6881404-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/026,001
; FILING DATE: 18-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15293B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 613 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-996-620-10

Query Match 51.4%; Score 38; DB 2; Length 613;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQAT 13
| : : : :
Db 261 RNEINVSQSDVQAT 273

RESULT 9
US-09-026-001A-18
; Sequence 18, Application US/09026001A
; Patent No. 6413760
; GENERAL INFORMATION:
; APPLICANT: Boonhoo, Amechand
; APPLICANT: Seehra, Jaabir
; APPLICANT: Shaw, Dianne
; APPLICANT: Sako, Dianne
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,001A
; FILING DATE: 18-FEB-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
```

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; REFERENCE/DOCKET NUMBER: G15293B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 621 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-026-001A-18

Query Match 51.4%; Score 38; DB 2; Length 621;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQAT 13
| : : : :
Db 269 RNEINVSQSDVQAT 281

RESULT 10
US-09-996-620-18
; Sequence 18, Application US/09996620
; Patent No. 6881404
; GENERAL INFORMATION:
; APPLICANT: Boonhoo, Amechand
; APPLICANT: Seehra, Jaabir
; APPLICANT: Shaw, Dianne
; APPLICANT: Sako, Dianne
; TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
; TITLE OF INVENTION: THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/996,620
; FILING DATE: 27-Feb. 6881404-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/026,001
; FILING DATE: 18-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15293B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 621 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-996-620-18

Query Match 51.4%; Score 38; DB 2; Length 621;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
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Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDOQATT 13
|:|:|:|:|:|:|
Db 269 RNEINVSQVQATT 281

RESULT 11
US-09-328-352-5826
; Sequence 5826, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5826
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5826

Query Match 50.0%; Score 37; DB 2; Length 370;
Best Local Similarity 42.9%; Pred. No. 95;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RNNVLIQTDOQATT 14
|:|:|:|:|:|:|
Db 175 KNNIYTTDNGSATS 188

RESULT 12
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Fells catus
US-09-479-614-14

Query Match 50.0%; Score 37; DB 2; Length 431;
Best Local Similarity 53.8%; Pred. No. 11e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNVLIQTDOQATT 14
|:|:|:|:|:|:|
Db 363 NDSPVTEQQAATT 375

RESULT 13
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047

; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Fells catus
US-09-479-614-2

Query Match 50.0%; Score 37; DB 2; Length 496;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNVLIQTDOQATT 14
|:|:|:|:|:|:|
Db 428 NDSPVTEQQAATT 440

RESULT 14
US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Fells catus
US-09-479-614-29

Query Match 50.0%; Score 37; DB 2; Length 496;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNVLIQTDOQATT 14
|:|:|:|:|:|:|
Db 428 NDSPVTEQQAATT 440

RESULT 15
US-09-248-796A-22386
; Sequence 22386, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22386
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22386

Query Match 48.6%; Score 36; DB 2; Length 153;
Best Local Similarity 77.8%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 RNNVLIQTD 9
|||
Db 21 RNNYFIQTD 29

Search completed: December 12, 2005, 19:37:05
Job time : 21.431 secs

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OM protein - protein search, using SW model

Run on: December 12, 2005, 19:33:42 ; Search time 66.9828 Seconds
(without alignments)
93.568 Million cell updates/sec

Title: US-10-758-165A-3

Perfect score: 74

Sequence: 1 RNNVLIQTDOQATTR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapexc 0.5

Searched: 1867569 seqs, 417829326 residues 1867569

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA Main:
1: /cgn2_6/ptodata/1/pubppa/US07_PUBSCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppa/US08_PUBSCOMB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US09_PUBSCOMB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US10_PUBSCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US10B_PUBSCOMB.pep.*
6: /cgn2_6/ptodata/1/pubppa/US11_PUBSCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	US-10-758-165-3	Sequence 3, Appli
2	74	100.0	424	US-10-451-078-2	Sequence 2, Appli
3	74	100.0	424	US-10-451-078-4	Sequence 4, Appli
4	74	100.0	569	US-10-214-524-30	Sequence 30, Appli
5	49	66.2	15	US-10-052-788-4	Sequence 4, Appli
6	43	58.1	580	US-10-674-666-17	Sequence 17, Appli
7	43	58.1	580	US-10-757-845-10	Sequence 10, Appli
8	41.5	56.1	854	US-10-732-923-23294	Sequence 23294, A
9	41	55.4	15	US-10-758-165-1	Sequence 1, Appli
10	41	55.4	105	US-10-437-963-129557	Sequence 129557,
11	41	55.4	312	US-10-369-493-6713	Sequence 6713, Ap
12	41	55.4	426	US-10-214-524-28	Sequence 28, Appli
13	41	55.4	917	US-10-437-963-181484	Sequence 181484,
14	40	54.1	15	US-10-758-165-7	Sequence 7, Appli
15	40	54.1	567	US-10-214-524-33	Sequence 33, Appli
16	38	51.4	558	US-10-437-963-185049	Sequence 185049,
17	38	51.4	613	US-09-996-620-10	Sequence 10, Appli
18	38	51.4	613	US-11-066-236-10	Sequence 10, Appli
19	38	51.4	621	US-09-996-620-18	Sequence 18, Appli
20	38	51.4	621	US-11-066-236-18	Sequence 18, Appli
21	38	51.4	703	US-10-282-122A-72382	Sequence 72382, A
22	38	51.4	814	US-10-128-714-8100	Sequence 8100, Ap
23	37	50.0	15	US-10-758-165-2	Sequence 2, Appli
24	37	50.0	67	US-10-437-963-138338	Sequence 138338,
25	37	50.0	223	US-10-389-566-587	Sequence 587, App
26	37	50.0	431	US-09-479-614-14	Sequence 14, Appli
27	37	50.0	431	US-10-409-772-14	Sequence 14, Appli

28	37	50.0	496	3	US-09-479-614-2	Sequence 2, Appli
29	37	50.0	496	3	US-09-479-614-29	Sequence 29, Appli
30	37	50.0	496	4	US-10-214-524-25	Sequence 25, Appli
31	37	50.0	496	4	US-10-409-772-2	Sequence 2, Appli
32	37	50.0	496	4	US-10-409-772-29	Sequence 29, Appli
33	37	50.0	663	4	US-10-389-566-1053	Sequence 1053, Ap
34	37	50.0	663	5	US-10-732-923-9730	Sequence 9730, Ap
35	37	50.0	750	4	US-10-425-115-351098	Sequence 351098,
36	36.5	49.3	272	4	US-10-425-115-233903	Sequence 233903,
37	36	48.6	21	4	US-10-340-288-37	Sequence 37, Appli
38	36	48.6	143	4	US-10-128-714-8304	Sequence 8304, Ap
39	36	48.6	199	4	US-10-425-115-299967	Sequence 299967,
40	36	48.6	199	5	US-10-617-320-2754	Sequence 2754, Ap
41	36	48.6	309	4	US-10-264-237-2751	Sequence 2751, Ap
42	36	48.6	318	4	US-10-128-714-3304	Sequence 3304, Ap
43	36	48.6	333	5	US-10-450-763-45557	Sequence 45557, A
44	36	48.6	348	3	US-09-731-872-247	Sequence 247, App
45	36	48.6	348	3	US-09-876-997-247	Sequence 247, App

ALIGNMENTS

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RESULT 1
US-10-758-165-3
; Sequence 3, Application US/10758165
; Publication No. US20050196616A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-3

Query Match      100.0%; Score 74; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 2,2e+06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RNNVLIQTDOQATTR 15
DB      1 RNNVLIQTDOQATTR 15

RESULT 2
US-10-451-078-2
; Sequence 2, Application US/10451078
; Publication No. US20040115764A1
; GENERAL INFORMATION:
; APPLICANT: Leibold, Wolfgang
; APPLICANT: Bettina, Wagner
; APPLICANT: Radbruch, Andreas
; TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the
; TITLE OF INVENTION: Heavy Chain of an Equine IGE Allotype, Recombinant
; TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding
; TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use
; FILE REFERENCE: 03100177aa
; CURRENT APPLICATION NUMBER: US/10/451,078
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: PCT/DE01/04810
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 100 64 415.5
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 2
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Equus caballus
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (1)..(97)
; OTHER INFORMATION: CH1 domain, IGE allotype a
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (98)..(205)
; OTHER INFORMATION: CH2 domain, IGE allotype a
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (206)..(312)
; OTHER INFORMATION: CH3 domain, IGE allotype a
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (313)..(424)
; OTHER INFORMATION: CH4 domain, IGE allotype a
US-10-451-078-2
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Query Match          100.0%; Score 74; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 9.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RNNVLIQTDOQATTR 15
Db      356 RNNVLIQTDOQATTR 370
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RESULT 3
US-10-451-078-4
; Sequence 4, Application US/10451078
; Publication No. US20040115764A1
; GENERAL INFORMATION:
; APPLICANT: Leibold, Wolfgang
; APPLICANT: Bectina, Wagner
; TITLE OF INVENTION: Deoxyribonucleic Acids which Encode the Constant Region of the
; TITLE OF INVENTION: Heavy Chain of an Equine IGE Allotype, Recombinant
; TITLE OF INVENTION: Immunoglobulins Obtained Using Them, and Corresponding
; TITLE OF INVENTION: Isotype-specific Monoclonal Antibodies and their Use
; FILE REFERENCE: 03100177aa
; CURRENT APPLICATION NUMBER: US/10/451,078
; CURRENT FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: PCT/DE01/04810
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 100 64 415.5
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Equus caballus
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (1)..(97)
; OTHER INFORMATION: CH1 domain, IGE allotype b
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (98)..(205)
; OTHER INFORMATION: CH2 domain, IGE allotype b
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (206)..(312)
; OTHER INFORMATION: CH3 domain, IGE allotype b
; FEATURE:
; NAME/KEY: Domain
; LOCATION: (313)..(424)
; OTHER INFORMATION: CH4 domain, IGE allotype b
US-10-451-078-4
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Query Match          100.0%; Score 74; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 9.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RNNVLIQTDOQATTR 15
Db      356 RNNVLIQTDOQATTR 370
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RESULT 4
US-10-214-524-30
; Sequence 30, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swey-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 30
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Horse (Equus caballus)
US-10-214-524-30
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Query Match          100.0%; Score 74; DB 4; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RNNVLIQTDOQATTR 15
Db      501 RNNVLIQTDOQATTR 515
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RESULT 5
US-10-052-788-4
; Sequence 4, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
; APPLICANT: Gershwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kalina, Warren V.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; TITLE OF INVENTION: Induction of Anti-IGE Antibodies
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052,788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:epitope peptide
; OTHER INFORMATION: P4, early portion of C4 of equine Ige epsilon
; OTHER INFORMATION: heavy chain
US-10-052-788-4
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Query Match          66.2%; Score 49; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      6 IOTDQATTR 15
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Db      1 10TDOQATTR 10
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RESULT 6
US-10-674-666-17
; Sequence 17, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; PRIOR FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 17
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Giardia intestinalis
US-10-674-666-17

Query Match      58.1%; Score 43; DB 4; Length 580;
Best Local Similarity 57.1%; Pred. No. 53;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2  NNVL1QTDQOATTR 15
|||: ||| |||
Db      168  NNWVFMRDQOATTR 181

RESULT 7
US-10-757-843-10
; Sequence 10, Application US/10757843
; Publication No. US20050129706A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHE00059
; CURRENT APPLICATION NUMBER: US/10/757,843
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: US/09/723,546
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/023,809
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Giardia intestinalis
US-10-757-843-10

Query Match      58.1%; Score 43; DB 5; Length 580;
Best Local Similarity 57.1%; Pred. No. 53;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2  NNVL1QTDQOATTR 15
|||: ||| |||
Db      168  NNWVFMRDQOATTR 181

RESULT 8
US-10-732-923-23294
; Sequence 23294, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgettson, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
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; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 23294
; LENGTH: 854
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-732-923-23294

Query Match      56.1%; Score 41.5; DB 5; Length 854;
Best Local Similarity 78.6%; Pred. No. 1.5e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      2  NNVL1Q-TDQOATT 14
| ||| | ||| |
Db      483  NNVL1QKDQOATT 496

RESULT 9
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1

Query Match      55.4%; Score 41; DB 5; Length 15;
Best Local Similarity 64.3%; Pred. No. 1.9;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1  RNNVL1QTDQOATT 14
|||: ||| |||
Db      1  RNDSP1QTDQYTTT 14

RESULT 10
US-10-437-963-129557
; Sequence 129557, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 129557
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31803C.1.pep
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US-10-437-963-129557

Query Match 55.4%; Score 41; DB 4; Length 105;
 Best Local Similarity 46.7%; Pred. No. 18;
 Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNNVLIOTDQOATTR 15
 |||:::|||||
 DB 10 RNNGMVELEQATSR 24

RESULT 11

US-10-369-493-6713
 ; Sequence 6713, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 6713
 ; LENGTH: 312
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-10-369-493-6713

Query Match 55.4%; Score 41; DB 4; Length 312;
 Best Local Similarity 57.1%; Pred. No. 60;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RNNVLIOTDQOATTR 15
 |||:::|||||
 DB 159 DNVLIQKDEENTAR 172

RESULT 12

US-10-214-524-28
 ; Sequence 28, Application US/10214524
 ; Publication No. US20030073142A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Swei-Shen Alex
 ; APPLICANT: Yang, Yong-Min
 ; APPLICANT: Barankiewicz, Theresa J.
 ; APPLICANT: Chen, Zhong
 ; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
 ; FILE REFERENCE: IGE-00101.P.1.1
 ; CURRENT APPLICATION NUMBER: US/10/214,524
 ; CURRENT FILING DATE: 2002-08-08
 ; PRIOR APPLICATION NUMBER: 60/312,120
 ; PRIOR FILING DATE: 2001-08-13
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 28
 ; LENGTH: 426
 ; TYPE: PRT
 ; ORGANISM: Dog (Canis familiaris)
 US-10-214-524-28

Query Match 55.4%; Score 41; DB 4; Length 426;
 Best Local Similarity 64.3%; Pred. No. 86;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIOTDQOATTR 14
 |||:::|||||

DB 357 RNDSPLOTQOYTTT 370

RESULT 13

US-10-437-963-181484
 ; Sequence 181484, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ia Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 181484
 ; LENGTH: 917
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)-(917)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_78753C.1.pep
 US-10-437-963-181484

Query Match 55.4%; Score 41; DB 4; Length 917;
 Best Local Similarity 50.0%; Pred. No. 2e+02;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIOTDQOATTR 14
 |||:::|||||
 DB 143 RNNIMVILDNQMTT 156

RESULT 14

US-10-758-165-7
 ; Sequence 7, Application US/10758165
 ; Publication No. US20050196816A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hammerberg, Bruce
 ; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
 ; FILE REFERENCE: 5051-661
 ; CURRENT APPLICATION NUMBER: US/10/758,165
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: US 60/440,472
 ; PRIOR FILING DATE: 2003-01-16
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 7
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Sus scrofa
 US-10-758-165-7

Query Match 54.1%; Score 40; DB 5; Length 15;
 Best Local Similarity 46.7%; Pred. No. 2.9;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIOTDQOATTR 15
 |||:::|||||
 DB 1 RNDAPVQADRHSTTR 15

RESULT 15

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 12, 2005, 19:34:33 ; Search time 2.4569 Seconds
(without alignments)
34.094 Million cell updates/sec

Title: US-10-758-165A-3

Perfect score: 74
Sequence: 1 RNNVLIQTDOQATTR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	55.4	312	6	US-10-723-207-2
2	38	51.4	1827	7	US-11-057-058-62
3	36	48.6	461	6	US-10-131-826A-454
4	36	48.6	943	6	US-10-467-657-5508
5	35	47.3	5024	6	US-10-793-626-2564
6	34	45.9	310	7	US-10-131-826A-538
7	34	45.9	310	7	US-11-025-834A-13
8	34	45.9	310	7	US-11-025-834A-15
9	34	45.9	362	6	US-10-821-234-1148
10	34	45.9	377	6	US-10-793-626-2526
11	33.5	45.3	522	6	US-10-793-626-456
12	33.5	45.3	522	6	US-10-793-626-2042
13	33	44.6	114	6	US-10-793-626-2252
14	33	44.6	1095	6	US-10-793-626-3154
15	33	44.6	2725	7	US-11-113-424-52
16	32	43.2	409	6	US-10-467-657-5732
17	32	43.2	409	6	US-10-467-657-7450
18	32	43.2	592	6	US-10-467-657-4888
19	32	43.2	2314	7	US-11-097-728-2
20	32	43.2	2353	7	US-11-097-728-6
21	32	43.2	3063	7	US-11-186-284-26
22	31.5	42.6	197	6	US-10-467-657-2812
23	31	41.9	106	7	US-11-008-727-12
24	31	41.9	238	7	US-11-008-727-26
25	31	41.9	270	7	US-11-008-727-24

26	31	41.9	416	6	US-10-793-626-2	Sequence 2, Appli
27	31	41.9	476	7	US-11-008-727-22	Sequence 22, Appl
28	31	41.9	492	6	US-10-793-626-1276	Sequence 1276, Ap
29	31	41.9	509	7	US-11-008-727-16	Sequence 16, Appl
30	31	41.9	531	7	US-11-008-727-18	Sequence 18, Appl
31	31	41.9	543	6	US-10-688-742-78	Sequence 78, Appl
32	31	41.9	703	6	US-10-467-657-7158	Sequence 7158, Ap
33	31	41.9	740	7	US-11-110-837-2	Sequence 2, Appli
34	31	41.9	740	7	US-11-110-837-4	Sequence 4, Appli
35	31	41.9	1189	7	US-11-074-176-134	Sequence 134, App
36	31	41.9	1279	6	US-10-793-626-3188	Sequence 3188, Ap
37	31	41.9	104	6	US-10-467-657-138	Sequence 138, App
38	30	40.5	104	6	US-10-467-657-6972	Sequence 6972, Ap
39	30	40.5	208	6	US-10-878-556A-133	Sequence 133, App
40	30	40.5	226	6	US-10-878-556A-106	Sequence 106, App
41	30	40.5	236	7	US-11-008-727-4	Sequence 4, Appli
42	30	40.5	257	6	US-10-467-652B-73	Sequence 73, Appl
43	30	40.5	263	6	US-10-821-234-1312	Sequence 1312, Ap
44	30	40.5	369	7	US-11-055-822-32	Sequence 32, Appl
45	30	40.5	394	6	US-10-510-386-208	Sequence 208, App

ALIGNMENTS

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RESULT 1
US-10-723-207-2
; Sequence 2, Application US/10723207
; Publication No. US20050250934A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yl
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 1151-4153US2
; CURRENT APPLICATION NUMBER: US/10/723, 207
; PRIOR APPLICATION NUMBER: 2003-11-24
; PRIOR FILING DATE: 2000-12-01
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog IGE
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-10-723-207-2

Query Match          55.4%; Score 41; DB 6; Length 312;
Best Local Similarity 64.3%; Pred. No. 0.53;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 RNNVLIQTDOQATT 14
      |||:|||||
Db      255 RNDSPIDQDYTTT 268

RESULT 2
US-11-057-058-62
; Sequence 62, Application US/11057058
; Publication No. US20050244400A1
; GENERAL INFORMATION:
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; APPLICANT: Lebowitz, Jonathan
; APPLICANT: Mega, John
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
; FILE REFERENCE: SYM-011
; CURRENT APPLICATION NUMBER: US/11/057,058
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: US 60/543,812
; PRIOR FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 1827
; TYPE: PRT
; ORGANISM: Rabbit sp.
; US-11-057-058-62

Query Match      51.4%; Score 38; DB 7; Length 1827;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      2 NNVLIQTDQOATTR 15
      |||:|:|:|
Db      144 NNVLITTESQTRN 157

RESULT 3
; Sequence 454, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P333ORIC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file wrapper or PALM.
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; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 454
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-131-826A-454

Query Match      48.6%; Score 36; DB 6; Length 461;
Best Local Similarity 53.8%; Pred. No. 7.6;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      3 NNVLIQTDQOATTR 15
      |||:|:|:|
Db      175 NNVLITDMQIMVR 187

RESULT 4
; Sequence 5508, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04
; SEQ ID NO 5508
; LENGTH: 943
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-5508

Query Match      48.6%; Score 36; DB 6; Length 943;
Best Local Similarity 46.7%; Pred. No. 18;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      1 RNNVLIQTDQOATTR 15
      |||:|:|:|
Db      886 RNNVHITGELSLX 900

RESULT 5
; Sequence 2964, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P33480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2964
; LENGTH: 5024
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5024)
```

OTHER INFORMATION: variable amino acid
US-10-793-626-2964

Query Match 47.3%; Score 35; DB 6; Length 5024;
Best Local Similarity 46.7%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNNVLIOTDOQATTR 15
: : : : :
Db 3492 QREVMINTNTWATTR 3506

RESULT 6
US-10-131-826A-538

; Sequence 538, Application US/1011826A
; Publication No. US20050245730A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gettleisen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumanabe, Daniel

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C128

CURRENT FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059588

PRIOR FILING DATE: 1997-09-19

Remaining Prior Application data removed - See file Wrapper or PALM.

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 538

LENGTH: 310

TYPE: prt

ORGANISM: Homo sapien

US-10-131-826A-538

Query Match 45.9%; Score 34; DB 6; Length 310;
Best Local Similarity 46.7%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNNVLIOTDOQATTR 15
: : : : :
Db 175 RNDVPLPTDSRANPR 189

Db 175 RNDVPLPTDSRANPR 189

RESULT 7
US-11-025-834A-13

; Sequence 13, Application US/11025834A
; Publication No. US20050266426A1

GENERAL INFORMATION:

APPLICANT: IMHOF, BEAT ALBERT

APPLICANT: AURRAND-LIONS, MICHEL

TITLE OF INVENTION: CONFERENCE REGULATED ADHESION MOLECULES USEFUL IN MODULATING VASC

TITLE OF INVENTION: PERMEABILITY

FILE REFERENCE: 011422-0314432

CURRENT APPLICATION NUMBER: US/11/025, 834A

CURRENT FILING DATE: 2004-12-30

PRIOR APPLICATION NUMBER: 09/524, 531

PRIOR FILING DATE: 2000-03-13

PRIOR APPLICATION NUMBER: EP 99, 200746, 8

PRIOR FILING DATE: 1999-03-11

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13

LENGTH: 310

TYPE: prt

ORGANISM: Mus musculus

US-11-025-834A-13

Query Match 45.9%; Score 34; DB 7; Length 310;
Best Local Similarity 46.7%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNNVLIOTDOQATTR 15
: : : : :
Db 175 RNDVPLPTDSRANPR 189

RESULT 8
US-11-025-834A-15

; Sequence 15, Application US/11025834A
; Publication No. US20050266426A1

GENERAL INFORMATION:

APPLICANT: IMHOF, BEAT ALBERT

APPLICANT: AURRAND-LIONS, MICHEL

TITLE OF INVENTION: CONFERENCE REGULATED ADHESION MOLECULES USEFUL IN MODULATING VASC

TITLE OF INVENTION: PERMEABILITY

FILE REFERENCE: 011422-0314432

CURRENT APPLICATION NUMBER: US/11/025, 834A

CURRENT FILING DATE: 2004-12-30

PRIOR APPLICATION NUMBER: 09/524, 531

PRIOR FILING DATE: 2000-03-13

PRIOR APPLICATION NUMBER: EP 99, 200746, 8

PRIOR FILING DATE: 1999-03-11

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15

LENGTH: 310

TYPE: prt

ORGANISM: Homo sapiens

US-11-025-834A-15

Query Match 45.9%; Score 34; DB 7; Length 310;
Best Local Similarity 46.7%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNNVLIOTDOQATTR 15
: : : : :
Db 175 RNDVPLPTDSRANPR 189

RESULT 9
US-10-821-234-1148

; Sequence 1148, Application US/10821234
; Publication No. US20050255114A1

```

; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_gene Version 1.0
; SEQ ID NO 1148
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1148
```

```
Query Match          45.9%; Score 34; DB 6; Length 362;
Best Local Similarity 46.7%; Pred. No. 14;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      1 RNNVLIOTDQATR 15
Db      227 RNDVPLPTDSRAMR 241
```

```
RESULT 10
US-10-793-626-2926
; Sequence 2926, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2926
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2926
```

```
Query Match          45.9%; Score 34; DB 6; Length 377;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 NNNVLIOTDQ 11
Db      118 NNIVIFSDQ 127
```

```
RESULT 11
US-10-793-626-456
; Sequence 456, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
```

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 456
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-456
```

```
Query Match          45.3%; Score 33.5; DB 6; Length 522;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
```

```
QY      1 RNNVLIOTDQ-QATT 14
Db      394 RRGALISMDCQATS 408
```

```
RESULT 12
US-10-793-626-2042
; Sequence 2042, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2042
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2042
```

```
Query Match          45.3%; Score 33.5; DB 6; Length 522;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;
```

```
QY      1 RNNVLIOTDQ-QATT 14
Db      394 RRGALISMDCQATS 408
```

```
RESULT 13
US-10-793-626-2252
; Sequence 2252, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2252
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2252
```

Query Match 44.6%; Score 33; DB 6; Length 114;
Best Local Similarity 38.5%; Pred. No. 5.4;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 3 NNVLQTDQATR 15
DB 52 NILVTDKTRK 64

RESULT 14
US-10-793-626-3154
; Sequence 3154, Application US/10793626
; Publication No. US2005025478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUJ480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3154
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3154

Query Match 44.6%; Score 33; DB 6; Length 1095;
Best Local Similarity 60.0%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 NNVLQTDQ 11
DB 318 NNALVQAKQ 327

RESULT 15
US-11-113-424-52
; Sequence 52, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangoli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52

; LENGTH: 2725
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-52

Query Match 44.6%; Score 33; DB 7; Length 2725;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 RNNVLQTDQAT 14
DB 1691 RNNVLQTDQAT 1704

Search completed: December 12, 2005, 20:19:48
Job time : 2.4569 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:49 ; Search time 12.6724 Seconds
(without alignments)
113.889 Million cell updates/sec

Title: US-10-758-165A-3

Perfect score: 74

Sequence: 1 RNNVLIQTDOQATTR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_80:.*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	60.8	917	2 P95884	probable sensory h
2	43.5	58.8	285	2 H84219	hypothetical prote
3	43	58.1	580	2 T45064	arginine deiminase
4	41	55.4	312	2 T32446	hypothetical prote
5	41	55.4	312	2 A89460	protein H42K12.1 l
6	41	55.4	2145	2 S61041	glutamate synthase
7	39	52.7	263	2 B85042	hypothetical prote
8	39	52.7	716	2 H84421	probable receptor-
9	38	51.4	138	2 G97191	probable membrane
10	38	51.4	829	2 A12531	hypothetical prote
11	38	51.4	1827	1 A23945	sucrose alpha-gluc
12	37	50.0	128	1 H64842	probable translati
13	37	50.0	128	2 H80785	hypothetical prote
14	37	50.0	128	2 B56445	hypothetical prote
15	36.5	49.3	1017	2 S67804	Lrg1 protein - yea
16	36	48.6	140	2 S72252	hemoglobin, extrac
17	36	48.6	205	2 B88095	protein F395.5 (l
18	36	48.6	407	2 AG2150	serine proteinase
19	36	48.6	412	2 T24441	hypothetical prote
20	36	48.6	433	2 C70163	GTP-binding protei
21	36	48.6	441	2 G98126	histidine protein
22	36	48.6	441	2 B95261	probable sensor h
23	36	48.6	468	2 A53889	protein-tyrosine-p
24	36	48.6	468	2 T43622	targeted effector
25	36	48.6	468	2 S01054	violence protein
26	36	48.6	487	1 S07062	glutamate receptor
27	36	48.6	487	1 S12201	kinase-binding pr
28	36	48.6	962	2 C81060	translation initia
29	36	48.6	967	2 C70831	probable mmp4 pro

30	36	48.6	1157	2 AD1728	ATP-dependent deox
31	36	48.6	1418	2 T15232	hypothetical prote
32	36	48.6	1449	2 T20181	hypothetical prote
33	36	48.6	1464	2 JCS144	murinoglobulin pre
34	36	48.6	1584	2 T20180	hypothetical prote
35	36	48.6	1586	2 T20179	hypothetical prote
36	36	48.6	2021	2 AD2267	serine/threonine k
37	36	47.3	185	2 T14523	hypothetical prote
38	35	47.3	225	2 AC0587	KDP operon transcr
39	35	47.3	225	2 B80719	transcription regu
40	35	47.3	225	2 C85569	hypothetical prote
41	35	47.3	225	2 B64804	transcription regu
42	35	47.3	252	2 T20321	hypothetical prote
43	35	47.3	276	2 B84597	probable disease r
44	35	47.3	345	2 S73498	Mc456 homolog K05
45	35	47.3	386	2 T09019	phosphoprotein pho

ALIGNMENTS

RESULT 1
P95884
Probable sensory histidine kinase protein [Imported] - Sinorhizobium meliloti (strain 1021)
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: P95884
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-Kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: P95884
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-917 <KIR>
A:Cross-references: UNIPROT:Q92WJ7, UNIPARC:UP100000CB4C5; GB:AL591985; PIN:CA6742.1;
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
Hebalt, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.;
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb20356
A:Genome: plasmid

Query Match 60.8%; Score 45; DB 2; Length 917;
Best Local Similarity 57.1%; Pred. NO. 3.6;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQAT 14
DB 188 RNEVVQTEKRTAT 201

RESULT 2
H84219
Hypothetical protein Vng0617h [Imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: H84219
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Iasky, S.
; Leithauser, B.; Keller, K.; Cruz, R.; Danon, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Proc. Natl. Acad. Sci. U.S.A. 97, 12116-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: H84219

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-285 <STO>
A;Cross-references: UNIPROT:Q9HRN4; UNIPARC:UPI00000636A7; GB:AE004437; NID:G10580210; F
C;Genetics:
A;Gene: VNG0617H

Query Match 58.4%; Score 43.5; DB 2; Length 285;
Best Local Similarity 58.4%; Pred. No. 1.8;
Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;
QY 2 NNVLQTDQOATTR 15
DB 212 NNVLQTDSTETLTTR 228

RESULT 3
T45064
arginine deiminase (EC 3.5.3.6) [validated] - Giardia intestinalis
C;Species: Giardia intestinalis
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45064
R;Knodler, L.A.; Sekyere, E.O.; Stewart, T.S.; Schofield, P.J.; Edwards, M.R.
J. Biol. Chem. 273, 4470-4477, 1998
A;Title: Cloning and expression of a prokaryotic enzyme, arginine deiminase, from a pr
A;Reference number: Z22902; MUID:98136144; PMID:9468500
A;Accession: T45064
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-580 <KNO>
A;Cross-references: UNIPROT:Q27657; UNIPARC:UPI000004CCBB; EMBL:U49236; PIDN:AA06116.1
A;Experimental source: strain Portland 1
C;Function:
A;Description: EC 3.5.3.6 [validated, MUID:98136144]
C;Superfamily: Giardia intestinalis arginine deiminase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 580;
Best Local Similarity 57.1%; Pred. No. 5.2;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 NNVLQTDQOATTR 15
DB 168 NNWFMKDQITTR 161

RESULT 4
T32446
hypothetical protein H42K12.1 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 05-Oct-2004
C;Accession: T32446
R;Meggs, L.; Harper, M.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid H42K12.
A;Reference number: Z21169
A;Accession: T32446
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-312 <MAG>
A;Cross-references: UNIPARC:UPI000017A469; EMBL:AF026207; PIDN:AA071265.1; GSPDB:GN00028
C;Experimental source: strain Bristol N2; clone H42K12
C;Genetics:
A;Gene: CESP:H42K12.1
A;Map position: X
A;Intons: 4/2; 40/3; 106/1; 167/1; 196/2; 251/3

Query Match 55.4%; Score 41; DB 2; Length 312;
Best Local Similarity 57.1%; Pred. No. 6.1;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 NNVLQTDQOATTR 15
DB 168 NNWFMKDQITTR 161

DB 159 DNVLQKDEENTAR 172

RESULT 5
A89460
protein H42K12.1 (imported) - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 31-Dec-2004
C;Accession: A89460
R;Anonymous, The C. elegans Sequencing Consortium.
Science 283, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:98069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_eleg
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: A89460
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-312 <STO>
A;Cross-references: UNIPARC:UPI000017A469; GB:chr_X; PIDN:AA071265.1; PID:G2435556; GSPDB
A;Note: Similar to protein kinase
C;Genetics:
A;Gene: H42K12.1
A;Map position: X

Query Match 55.4%; Score 41; DB 2; Length 312;
Best Local Similarity 57.1%; Pred. No. 6.1;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 NNVLQTDQOATTR 15
DB 159 DNVLQKDEENTAR 172

RESULT 6
S61041
glutamate synthase (NADH2) (EC 1.4.1.14) glt1 precursor [similarity] - yeast (Saccharomyc
N;Alternate names: protein D1448; protein YDL171c
C;Species: Saccharomyces cerevisiae
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 12-Jul-2004
C;Accession: S61041; S67723
R;Pohl, T.M.
submitted to the EMBL Data Library, November 1995
A;Reference number: S61041
A;Accession: S61041
A;Molecule type: DNA
A;Residues: 1-2145 <POH>
A;Cross-references: UNIPARC:UPI00001682D6; EMBL:Z67750; NID:G1061256; PIDN:CAA91574.1; P
R;Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67708
A;Accession: S67723
A;Molecule type: DNA
A;Residues: 1-2145 <POH>
A;Cross-references: UNIPARC:UPI00001682D6; EMBL:Z74219; NID:G1431273; PIDN:CAA98745.1; P
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:GLT1
A;Cross-references: SGD:S0002330; MIPS:YDL171c
A;Map position: 4L
C;Superfamily: glutamate synthase (NADH/NADPH), eukaryotic type
C;Keywords: 3fe-4S; metalloprotein; oxidoreductase; transmembrane protein
F;1-53/Domain: propeptide #status predicted <PRO>
F;54-2145/Product: glutamate synthase #status predicted <MAT>
F;1077-1093/Domain: transmembrane #status predicted <TM1>
F;1172-1188/Domain: transmembrane #status predicted <TM2>
F;54/Active site: Cys #status predicted
F;1185,1191,1196/Binding site: 3fe-4S cluster (Cys) (covalent) #status predicted

Query Match 55.4%; Score 41; DB 2; Length 2145;
Best Local Similarity 57.1%; Pred. No. 55;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTDQOATT 14
|||:|||||
Db 1145 RNNVVTQTDGQLRT 1158

RESULT 7

E85042
hypothetical protein AT4g03350 (imported) - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: E85042
R/Anonymous: The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A/Reference number: A85001; MUID:20083488; PMID:10617198
A/Accession: E85042
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-263 <STO>
A/Cross-references: UNIPROT:Q9ZQZ6; UNIPARC:UPI00000A63C9; GB:NC_001268; NID:G7270205; F
C/Genetics:
A/Gene: AT4g03350
A/Map position: 4

Query Match 52.7% Score 39; DB 2; Length 263;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 RNNVLIQTDQOATT 14
|||:|||||
Db 145 RNNVVTQTDGQLRT 158

RESULT 8

H84421
Probable receptor-like protein kinase (imported) - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C/Accession: H84421
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
W.; Koo, H.; Wolfat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: H84421
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-716 <STO>
A/Cross-references: UNIPROT:Q9ZU46; UNIPARC:UPI00000A1C90; GB:AE002093; NID:G4262228; PI
C/Genetics:
A/Gene: Atg901210
A/Map position: 2
C/Superfamily: Receptor-like protein kinase

Query Match 52.7% Score 39; DB 2; Length 716;
Best Local Similarity 53.3%; Pred. No. 38;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 RNNVLIQTDQOATT 15
|||:|||||
Db 568 GSNRIOTDQOQER 582

RESULT 9

G97191
Probable membrane protein (imported) - Clostridium acetobutylicum
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C/Accession: G97191
R/Noelling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, O.; Gibson, R.; Lee,
J.; Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: G97191
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-138 <KUR>
A/Cross-references: UNIPROT:Q97GK0; UNIPARC:UPI00000CA4D0; GB:AE001437; PIDN:AAK80322.1;
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC2366

Query Match 51.4% Score 38; DB 2; Length 138;
Best Local Similarity 53.8%; Pred. No. 9;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 NNVLQSGQASST 14
|||:|||||
Db 42 NNVLQSGQASST 54

RESULT 10

AT2531
hypothetical protein alr7540 (imported) - Nostoc sp. (strain PCC 7120) plasmid pCC7120be
C/Species: Nostoc sp. PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AT2531
R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kunitz, T.; Sasamoto, S.; Matsumbe, A.; Iriyuchi
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AT2531
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-829 <KUR>
A/Cross-references: UNIPROT:Q8ZSH0; UNIPARC:UPI00000CCD69; GB:AP003602; PIDN:BAB7183.1;
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: alr7540
A/Genome: plasmid

Query Match 51.4% Score 38; DB 2; Length 829;
Best Local Similarity 70.0%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NNVLQTDQO 11
|||:|||||
Db 591 NNVLQTDQO 600

RESULT 11

A23945
sucrose alpha-glucosidase (EC 3.2.1.48) / oligo-1,6-glucosidase (EC 3.2.1.10) - rabbit
N/Alternate names: small intestinal sucrase/isomaltase (SI)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 24-May-1996
C/Accession: A23945; B25987; A25163
R/Hunziker, W.; Spiess, W.; Semenza, G.; Lodish, H.F.
Cell 146, 227-234, 1996
A/Title: The sucrase-isomaltase complex: primary structure, membrane-orientation, and ev
A/Reference number: A23945; MUID:86245068; PMID:3755079
A/Accession: A23945
A/Molecule type: mRNA
A/Residues: 1-1827 <HUN>
A/Cross-references: UNIPARC:UPI00001729E8
R/Sjoestrom, H.; Noren, O.; Christensen, L.A.; Wacker, H.; Spiess, M.; Bigler-Meier, B
FEBS Lett. 148, 321-325, 1982
A/Title: N-terminal sequences of pig intestinal sucrase-isomaltase and pro-sucrase-isoma
A/Reference number: A25987; MUID:83105704; PMID:7152027
A/Accession: B25987
A/Molecule type: protein
A/Residues: 2-32, 'XXX', 36-38; 1008, 'N', 1010-1014, 'E' <SU2>

A;Cross-references: UNIPARC:UPI00001729B9; UNIPARC:UPI00001729EA
R;Frank, G.; Brunner, U.; Jauser, H.; Wacker, H.; Semenza, G.; Zuber, H.
FEBS Lett. 96, 183-188, 1978
A;Title: The hydrophobic anchor of small-intestinal sucrase-isomaltase. N-terminal sequ
A;Reference number: A29163; MUID:79086207; PMID:729784
A;Accession: A29163
A;Molecule type: protein
A;Residues: 2,'VNA',6-32,'XXX',36-38 <FRA>
A;Cross-references: UNIPARC:UPI00001729EB
C;Comment: Carbohydrate analysis of the mature enzyme complex indicates both N- and O-1,4
C;Function: <TSM>
A;Description: oligo-1,6-glucosidase catalyzes the hydrolysis of 1,6-alpha-D-glucosidic
A;Pathway: carbohydrate digestion
C;Function: <SUC>
A;Description: sucrase alpha-glucosidase catalyzes the hydrolysis of the 1,2-alpha-D-gluc
C;Superfamily: sucrase/isomaltase; sucrase/isomaltase homology; trefoil homology
C;Keywords: carbohydrate digestion; duplication; glycoprotein; glycosidase; hydrolase; m
F;2-1007/Product: oligo-1,6-glucosidase (isomaltase chain) #status experimental <ISO>
F;13-33/Domain: membrane associated #status predicted <TMM>
F;43-65/Region: serine/threonine-rich
F;63-109/Domain: trefoil homology <TRF1>
F;189-840/Domain: sucrase/isomaltase homology <SIM>
F;931-977/Domain: trefoil homology <TRF2>
F;1008-1827/Product: sucrase alpha-glucosidase (sucrase chain) #status experimental <SUC
F;1062-1734/Domain: sucrase/isomaltase homology <STM2>
F;12/Binding site: carbonyl (Thr) (covalent) #status experimental
F;99,455,559,896,904,1235,1303,1353,1354,1368,1403,1535,1572,1748,1763,1799/Binding
F;1007-1008/Cleavage site: Arg-1le (trypsin) #status predicted

Query Match 51.4%; Score 38; DB 1; Length 1827;
Best Local Similarity 50.0%; Pred. No. 1,7e+02;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 NNVL10TDOQATTR 15
DB 144 NNVLTTESQTANR 157

RESULT 12
H64842
probable translation initiation regulator b1010 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Dec-2004
C;Accession: H64842
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64842
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-128 <BLAT>
A;Cross-references: UNIPROT:P75896; UNIPARC:UPI000013A5E1; GB:AE002022; GB:U00096; NID:9
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: translation initiation inhibitor, TdcF type

Query Match 50.0%; Score 37; DB 1; Length 128;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 NNVL10TDOQATTR 15
DB 40 NNVLFPADDPKQTR 53

RESULT 13
H90785
hypothetical protein Ecg1256 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004

C;Accession: H90785
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A;Reference number: A96229; MUID:21156231; PMID:11258796
A;Accession: H90785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-128 <NAV>
A;Cross-references: UNIPROT:O8XAU5; UNIPARC:UPI00000D067B; GB:BA000007; PIDN:BAB34679.1;
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetic:
A;Gene: Ecg1256
C;Superfamily: translation initiation inhibitor, TdcF type

Query Match 50.0%; Score 37; DB 2; Length 128;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 NNVL10TDOQATTR 15
DB 40 NNVLFPADDPKQTR 53

RESULT 14
F85645
hypothetical protein Z1509 [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C;Accession: F85645
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
Miller, L.; Grobeck, E.U.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: F85645
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-128 <STO>
A;Cross-references: UNIPROT:O8XAU5; UNIPARC:UPI00000D067B; GB:AE005174; NID:G12514367; PJ
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetic:
A;Gene: Z1509
C;Superfamily: translation initiation inhibitor, TdcF type

Query Match 50.0%; Score 37; DB 2; Length 128;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 NNVL10TDOQATTR 15
DB 40 NNVLFPADDPKQTR 53

RESULT 15
S67804
Lrg1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D0764; protein YDL240W
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67804; S43158; S47956
R;Alt-Moerke, J.; Schneider, C.; Moro, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67798
A;Accession: S67804
A;Molecule type: DNA
A;Residues: 1-1017 <ALT>
A;Cross-references: UNIPROT:P35688; UNIPARC:UPI000012E93A; EMBL:Z74288; NID:G1431407; PFI
A;Experimental source: strain S288C
R;Weller, A.; Xu, G.; Wells, R.; Hollenberg, C.P.; Piepersberg, W.
submitted to the EMBL Data Library, March 1994
A;Description: Lrg1 is expressed during sporulation in Saccharomyces cerevisiae and cont

A:Reference number: S43158
A:Accession: S43158
A:Molecule type: DNA
A:Residues: 1-530,'Q','S','767-790','T','792-820','Q','822-837','S','839-848','L','850-89
A:Cross-references: UNIPARC:UPI0000168CBB; EMBL:X78453; NID:9468734; PID:9468735
R:Mueller, L.; Xu, G.; Wells, R.; Hollenberg, C.P.; Pieperberg, W.
Nucleic Acids Res. 22, 3151-3154, 1994
A>Title: LRGI is expressed during sporulation in *Saccharomyces cerevisiae* and contains m
A:Reference number: S47956; MUID:9434479; PMID:8065929
A:Accession: S47956
A:Molecule type: DNA
A:Residues: 28-89:98-136,'M','139-148:157-184:419-474:755-765','S','767-790','T','792-820','Q
A:Cross-references: UNIPARC:UPI000017B2C8; UNIPARC:UPI000017B2C9; UNIPARC:UPI000017B2CA;
C:Genetics:
A:Gene: SGD:LRGI
A:Cross-references: SGD:S0002399; MIPS:YDL240w
A:Map position: 4L
C:Keywords: transmembrane protein
F:28-89/Domain: LIM metal-binding repeat homology <LIM1>
F:98-148/Domain: LIM metal-binding repeat homology <LIM2>
F:157-184/Domain: LIM metal-binding repeat homology <LIM3>
F:348-364/Domain: transmembrane #status predicted <TM1>
F:419-474/Domain: LIM metal-binding repeat homology <LIM4>
F:487-503/Domain: transmembrane #status predicted <TM2>

Query Match 49.3%; Score 36.5; DB 2; Length 1017;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 5; Gaps 1;

OY 3 NVLIQTD----QQATTR 15
|:||||| |:
Db 583 NLVIQTDPPSSSQGVSTR 600

Search completed: December 12, 2005, 20:42:48
Job time : 13.6724 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:41 ; Search time 81.4655 Seconds
(without alignments)
129.907 Million cell updates/sec

Title: US-10-758-165A-3
Perfect score: 74
Sequence: 1 RNNVLIQTDQOATTR 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_tr embl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	63.5	2081	2	Q9LH98 ARATH
2	45	60.8	917	2	Q92WJ7 RHIME
3	44	59.5	649	2	Q54AY3 DICTDI
4	44	59.5	649	2	Q55B16 DICTDI
5	43.5	58.8	285	2	Q9HRN4 HALSA
6	43	58.1	416	2	Q5WV87 LEGPL
7	43	58.1	417	2	Q5X3U5 LEGPL
8	43	58.1	463	2	Q5ZU51 LEGPH
9	43	58.1	505	2	Q7R036 GIALA
10	43	58.1	580	2	Q21657 GIALA
11	41.5	56.1	854	2	Q7ZX14 XENLA
12	41	55.4	106	2	Q8H475 ORYSA
13	41	55.4	247	2	Q6FP28 CANGA
14	41	55.4	260	2	Q4SVF5 TENG
15	41	55.4	540	2	Q4RX65 TENG
16	41	55.4	550	2	Q7XUQ6 ORYSA
17	41	55.4	2141	2	Q6CMK0 KUOLA
18	41	55.4	2144	1	GLT1_YEAST
19	41	55.4	2152	2	Q6FLS3 CANGA
20	41	55.4	2195	2	Q75917 ASHGO
21	41	55.4	4936	2	Q6D5C2 ERWCT
22	40	54.1	135	2	Q5QVQD IDILO
23	40	54.1	136	2	Q9XRP4 AMBME
24	40	54.1	136	2	Q9XRP5 AMBME
25	40	54.1	828	2	Q6W442 PARUM
26	39	52.7	166	2	Q74K19 LACUO
27	39	52.7	263	2	Q9ZQZ6 ARATH
28	39	52.7	359	2	Q5LNB7 SIILO
29	39	52.7	646	2	Q5VLKO NPVSF
30	39	52.7	676	2	Q9C2A6 NEUCR
31	39	52.7	716	2	Q9ZU46 ARATH

32	39	52.7	946	2	Q6JPV5 ACTSU
33	39	52.7	946	2	Q6JPV7 ACTSU
34	39	52.7	948	2	Q84143 ACTPL
35	39	52.7	1401	2	Q54J46 DICTDI
36	39	52.7	1460	2	Q6CVK3 KUOLA
37	38	51.4	138	2	Q97GK0 CIOAB
38	38	51.4	271	2	Q4S7L7 TENG
39	38	51.4	370	2	Q4MOR3 BACCE
40	38	51.4	407	2	Q4FUS6 GCAMM
41	38	51.4	442	2	Q73DS1 BACCI
42	38	51.4	448	2	Q6HNN4 BACCH
43	38	51.4	448	2	Q81141 BACCR
44	38	51.4	448	2	Q63G64 BACC2
45	38	51.4	448	2	Q81VB9 BACAN

ALIGNMENTS

RESULT 1

ID	Q9LH98 ARATH	PRELIMINARY;	PRT;	2081 AA.
AC	Q9LH98;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Arabidopsis thaliana genomic DNA, chromosome 3, BAC clone: T19N8.			
OS	Arabidopsis thaliana (mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
OC	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI_Taxid=3702;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=20363099; PubMed=10907853;			
RA	Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Tabata S.;			
RT	"Structural analysis of Arabidopsis thaliana chromosome 3. II.			
RT	Sequence features of the 4,251,695 bp regions covered by 90 pl, TAC			
RT	and BAC clones."			
RL	DNA Res. 7:217-221(2000).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;			
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AP002057; BAB03174.1; -, Genomic_DNA.			
DR	HSSP; P01096; 1H93.			
DR	InterPro; IPR009605; DUF1216.			
DR	Pfam; PF06746; DUF1216; 2.			
SQ	SEQUENCE 2081 AA; 232852 MW; D3603E1F85EFPF29 CRC64;			
Query Match	63.5%;	Score 47;	DB 2;	Length 2081;
Best Local Similarity	53.3%;	Pred. No. 27;		
Matches	8;	Conservative	4;	Mismatches 3; Indels 0; Gaps 0;
Oy	1 RNNVLIQTDQOATTR 15			
Db	1302 KNEILMQADSQATTG 1316			
RESULT 2				
ID	Q92WJ7 RHIME			
ID	Q92WJ7 RHIME PRELIMINARY;			
AC	Q92WJ7;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Putative sensory histidine kinase protein.			
GN	OrderedLocusNames=RB0342; ORFNames=SMB20356;			
OS	Rhizobium meliloti (Sinorhizobium meliloti).			
OC	Phylum PSYMB.			
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
OC	Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.			
OX	NCBI_Taxid=382;			

[1]
 NCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=1021;
 RX MEDLINE=1336508; PubMed=11461431; DOI=10.1073/pnas.161294698;
 RA Fuan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
 RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
 RA Golding B., Puelier A.;
 RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
 RT fixing endosymbiont *Sinorhizobium meliloti*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 DR EMBL: AL591985; CAC48742.1; -, Genomic_DNA.
 DR PIR: P95884; P95884.
 DR HSP: P52934; IOMP.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR GO: GO:0016301; F:kinase activity; IEA.
 DR GO: GO:0000156; F:two-component response regulator activity; IEA.
 DR GO: GO:0000155; F:two-component sensor molecule activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR GO: GO:0000160; P:two-component signal transduction system (p. . .); IEA.
 DR InterPro: IPR003594; AtPbdn ATPase.
 DR InterPro: IPR005467; His_kinase.
 DR InterPro: IPR003661; His_kinase.
 DR InterPro: IPR003660; His_kin_HAMP.
 DR InterPro: IPR004358; His_kin_like_C.
 DR InterPro: IPR000014; PAS.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam: PF00672; HAMP; 1.
 DR Pfam: PF02518; HATPase_C; 1.
 DR Pfam: PF00512; HisKA; 1.
 DR Pfam: PF00072; Response_reg; 2.
 DR PRINTS: PR00344; BCTRLSENSOR.
 DR Prodom: PD000039; Response_reg; 2.
 DR SMART: SM00304; HAMP; 1.
 DR SMART: SM00387; HATPase_C; 1.
 DR SMART: SM00388; HisKA; 1.
 DR SMART: SM00091; PAS; 1.
 DR SMART: SM00448; REC; 2.
 DR PROSITE: PSS0865; HAMP; 1.
 DR PROSITE: PSS0109; HIS_KIN; 1.
 DR PROSITE: PSS0110; RESPONSE_REGULATOR; 2.
 DR Complete proteome; Kinase; Pfamid.
 KW Complete proteome; Kinase; Pfamid.
 SQ SEQUENCE 917 AA; 100821 MW; 23847f2374CE99A1 CRC64;

Query Match 60.8%; Score 45; DB 2; Length 917;
 Best Local Similarity 57.1%; Pred. No. 25;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOOAT 14
 ||:|||||
 Db 188 RNEVVVTEKTAT 201

RESULT 3
 Q54AY3_DICDI PRELIMINARY; PRT; 649 AA.
 ID Q54AY3_DICDI PRELIMINARY;
 AC Q54AY3;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=DD80215056;
 OS Dictyostelium discoideum (Slime mold).
 OS Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OC NCBI_Taxid=44689;
 RN NCLEOTIDE SEQUENCE.
 RP STRAIN=AX4;
 RC Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
 RA Tunggal B., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
 RA Tunggal B., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,

RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
 RA Louesged H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward J., Winkler T., Tanaka Y.,
 RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Bartell B., Kuapa A.;
 RT "The genome of the social amoeba *Dictyostelium discoideum*.";
 RL Nature 0:0-0(2005).
 CC -i- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AAF101000301; EAL60430.1; -, Genomic_DNA.
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 649 AA; 77580 MW; B366A94429CD53 CRC64;

Query Match 59.5%; Score 44; DB 2; Length 649;
 Best Local Similarity 61.5%; Pred. No. 26;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 NNVLIQTDOOAT 14
 ||:|||||
 Db 611 NNIIITQOQKPT 623

RESULT 4
 Q55B16_DICDI PRELIMINARY; PRT; 649 AA.
 ID Q55B16_DICDI PRELIMINARY;
 AC Q55B16;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=DD80216848;
 OS Dictyostelium discoideum (Slime mold).
 OS Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OC NCBI_Taxid=44689;
 RN NCLEOTIDE SEQUENCE.
 RP STRAIN=AX4;
 RC Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
 RA Sugang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
 RA Tunggal B., Kummerfeld S., Madera N., Kontorlov B.A., Rivero F.,
 RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
 RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
 RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
 RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
 RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
 RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
 RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
 RA Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
 RA Louesged H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
 RA Sugano S., White B., Walker D., Woodward J., Winkler T., Tanaka Y.,
 RA Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Bartell B., Kuapa A.;
 RT "The genome of the social amoeba *Dictyostelium discoideum*.";
 RL Nature 0:0-0(2005).
 CC -i- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AAF101000013; EAL71869.1; -, Genomic_DNA.
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 649 AA; 77580 MW; B366AD152ACDA23 CRC64;

Query Match 59.5%; Score 44; DB 2; Length 649;
 Best Local Similarity 61.5%; Pred. No. 26;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLIOOTDOOQATT 14
 Db 611 NNVLIOOTDOOQPT 623

RESULT 5

Q5WV87_HALSA PRELIMINARY; PRT; 285 AA.
 AC Q5WV87;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Vng0617h.
 GN OrderedLocuNames=VNG0617H;
 OS Halobacterium salinarum (Halobacterium halobium).
 OC Archaeae; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 NCBI_TaxID=2242;

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=NR-1 / ATCC 700922 / JCM 11081;
 MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
 NG W.V., Kennedy S.P., Mahaira G.G., Bergquist B., Pan M.,
 Shukla H.D., Leaky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 Swartell S., Weir D., Hall J., Dahl T.A., Weir R.,
 Lettousier B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 Maddocks D.G., Jablonksi P.E., Krebs M.P., Angvine C.M., Dale H.,
 Isenbarger T.A., Peck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,
 Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
 RT "Genome sequence of Halobacterium species NRC-1."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AF005010; AAG19124.1; -; Genomic_DNA.
 DR PIR; H84219; H84219.
 KW Complete proteome.
 SQ SEQUENCE 285 AA; 29163 MW; 31223D1A949BC1B3 CRC64;

Query Match 58.8%; Score 43.5; DB 2; Length 285;
 Best Local Similarity 58.8%; Pred. No. 12;
 Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 2 NNVLIOOTDOO--ATTR 15
 Db 212 NNVLIOOTDSETELTTR 228

RESULT 6

Q5WV87_LEGPL PRELIMINARY; PRT; 416 AA.
 AC Q5WV87;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocuNames=lp11930;
 OS Legionella pneumophila (strain Lens).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Legionellaceae; Legionella.
 NCBI_TaxID=297245;

NUCLEOTIDE SEQUENCE.

PUBMED=15467720; DOI=10.1038/ng1447;
 RA Casalez C., Rusnlok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
 Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
 Etienne J., Glaeser P., Buchrieser C.;
 RT "Evidence in the Legionella pneumophila genome for exploitation of
 host cell functions and high genome plasticity.";
 RL Nat. Genet. 36:1165-1173(2004).

DR EMBL; CR628337; CAH16170.1; -; Genomic_DNA.
 DR Legiolist; lp11930; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 416 AA; 48861 MW; 0E153EDD3778592E CRC64;

Query Match 58.1%; Score 43; DB 2; Length 416;
 Best Local Similarity 69.2%; Pred. No. 24;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLIOOTDOOQATT 14
 Db 63 NNVLIPLEOQPT 75

RESULT 7

OSX3U5_LEGPA PRELIMINARY; PRT; 417 AA.
 AC OSX3U5;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocuNames=lp11939;
 OS Legionella pneumophila (strain Paris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Legionellaceae; Legionella.
 NCBI_TaxID=297246;

NUCLEOTIDE SEQUENCE.

PUBMED=15467720; DOI=10.1038/ng1447;
 RA Casalez C., Rusnlok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
 Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
 Etienne J., Glaeser P., Buchrieser C.;
 RT "Evidence in the Legionella pneumophila genome for exploitation of
 host cell functions and high genome plasticity.";
 RL Nat. Genet. 36:1165-1173(2004).
 DR EMBL; CR628336; CAH13091.1; -; Genomic_DNA.
 DR Legiolist; lp11939; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 417 AA; 49131 MW; 01F6B5A430C7E2 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 417;
 Best Local Similarity 69.2%; Pred. No. 24;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLIOOTDOOQATT 14
 Db 63 NNVLIPLEOQPT 75

RESULT 8

Q5ZU51_LEGPH PRELIMINARY; PRT; 463 AA.
 AC Q5ZU51;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Ebha protein.
 GN OrderedLocuNames=lp1957;
 OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
 OS ATCC 33152).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Legionellaceae; Legionella.
 NCBI_TaxID=272624;

NUCLEOTIDE SEQUENCE.

PUBMED=15448271; DOI=10.1126/science.1099776;
 RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
 Assemani G., Hill K., Nwara J., Feder M., Rineer J., Greenberg J.J.,
 Stehenko V., Park S.H., Zhao B., Teplickaya E., Edwards J.R.,
 Pampou S., Georgilou A., Chou I.-C., Iannuccilli W., Utz M.B.,
 Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
 Segal G., Qu X., Rzhetsky A., Zhang P., Cavanaugh E., De Jong P.J.,

RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
 RT "The genomic sequence of the accidental pathogen *Legionella*
 RL *pneumophila*."
 DR Science 305:1966-1968(2004).
 KW EMBL: AB017354; AAU28026.1; -; Genomic_DNA.
 SQ Complete proteome.
 Sequence 463 AA; 54449 MW; BE76CBED5D81D264 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 463;
 Best Local Similarity 69.2%; Pred. No. 27;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NNVLIOQTDOQATTR 14
 Db 87 NNVLIPLEQQPTT 99

RESULT 9
 Q7R036_GIALA PRELIMINARY; PRT; 505 AA.

AC Q7R036;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DE GIP_456_18539_20056.
 OS *Giardia lamblia* ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; *Giardia*.
 NCBI_TaxID=184922;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=WB CG;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the *Giardia lamblia* genome."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACB0100038; EAA40651.1; -; Genomic DNA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR003198; Amidino_trans.
 DR Pfam; PF02274; Amidino_transf.1.
 SQ SEQUENCE 505 AA; 55735 MW; 99E2CBF5B56824B0 CRC64;

Query Match 58.1%; Score 43; DB 2; Length 505;
 Best Local Similarity 57.1%; Pred. No. 30;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NNVLIOQTDOQATTR 15
 Db 93 NNWVFMRDQITTR 106

RESULT 10
 Q27657_GIALA PRELIMINARY; PRT; 580 AA.
 AC Q27657;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Arginine deiminase (EC 3.5.3.6).
 OS *Giardia lamblia* (*Giardia intestinalis*).
 OC Eukaryota; Diplomonadida; Hexamitidae; *Giardia*.
 NCBI_TaxID=5741;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Portland 1;
 RA MEDLINE=98136144; PubMed=9468500; DOI=10.1074/jbc.273.8.4470;
 RA Knodler L.A., Sekyere E.O., Stewart T.S., Schofield P.J.,
 RA Edwards M.R.;
 RT "Cloning and expression of a prokaryotic enzyme, arginine deiminase,
 RT from a primitive eukaryote *Giardia intestinalis*."
 RL J. Biol. Chem. 273:4470-4477(1998).

DR EMBL; U49236; AAC06116.1; -; Genomic_DNA.
 DR PIR; T45064; T45064.
 DR GO; GO:0016990; F:arginine deiminase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR003198; Amidino_trans.
 DR Pfam; PF02274; Amidino_transf.1.
 SQ SEQUENCE 580 AA; 64131 MW; 4812F389D0F5357A CRC64;

Query Match 58.1%; Score 43; DB 2; Length 580;
 Best Local Similarity 57.1%; Pred. No. 35;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 NNVLIOQTDOQATTR 15
 Db 168 NNWVFMRDQITTR 161

RESULT 11
 Q7ZX14_XENLA PRELIMINARY; PRT; 854 AA.

AC Q7ZX14;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE MGCS2979 protein.
 OS *Xenopus laevis* (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; *Xenopus*; *Xenopus*.
 NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Embryo;
 RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
 RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*
 RT initiative."
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the AAA ATPase family.
 DR EMBL; BC044980; AAH44980.1; -; mRNA.
 DR HSSP; Q01853; IR7R.
 DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO:0005739; C:mitochondrion; IEA.
 DR GO:0005524; F:ATP binding; IEA.
 DR GO:0007111; F:nucleoside-triphosphatase activity; IEA.
 DR GO:0000166; F:nucleotide binding; IEA.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003559; AAA_ATPase_cent.
 DR InterPro: IPR003960; AAA_sub.
 DR Pfam: PF00004; AAA; 2.
 DR SMART: SM00382; AAA; 2.
 DR PROSITE: PS00674; AAA; 2.
 DR ATP-binding; Nucleotide-binding; Transmembrane.
 SO SEQUENCE 854 AA; 93597 MW; F91339502C41BB3 CRC64;

Query Match 56.1%; Score 41.5; DB 2; Length 854;
 Best Local Similarity 78.6%; Pred. No. 1; 1e-02;
 Matches 11; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 2 NNVLIQ-TDQQT 14
 DB 483 NRVLIQIKDQQT 496

RESULT 12
 O8H475_ORYSA PRELIMINARY; PRT; 106 AA.

AC O8H475;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein P0470D12.115.
 GN Name=P0470D12.115;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 CX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsunoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
 RT clone: P0470D12.1";
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004300; BAC15985.1; -; Genomic_DNA.
 DR Gramene; O8H475; -;
 KW Hypothetical protein.
 SO SEQUENCE 106 AA; 12281 MW; 8016731B1945298F CRC64;

Query Match 55.4%; Score 41; DB 2; Length 106;
 Best Local Similarity 46.7%; Pred. No. 12;
 Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNNVLICDQQT 15
 DB 10 RNNGVMELEQATSR 24

RESULT 13
 O6FP28_CANGA PRELIMINARY; PRT; 247 AA.

AC O6FP28;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Similar to sp|P39721|Saccharomyces cerevisiae YAL049c.
 GN OrderedLocustName=CAGL00071289;
 OS Candida glabrata (Yeast) (Torulopsis glabrata).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 CX NCBI_TaxID=5478;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 2001 / CBS 138;
 RX PubMed=15329592; DOI=10.1038/nature02579;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Nevegliese C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barry S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boirame A., Boyer J., Catolico L., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaitre M., Lesur I., Ma L., Muller H.,
 RA Nicoud J.-M., Nikolaki M., Ozas S., Ozler-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierly A.,
 RA Bouchier C., Caudron B., Scarpelli C., Galliard C., Weissbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004)
 DR EMBL; CR380956; CAG60967.1; -; Genomic_DNA.
 DR GO:0016787; F:hydrolase activity; IEA.
 DR InterPro: IPR02925; DieneIactn_hydro.
 DR Pfam: PF01738; DLH; 1.
 KW Complete proteome.
 SO SEQUENCE 247 AA; 27274 MW; ABE540BB8B628D35 CRC64;

Query Match 55.4%; Score 41; DB 2; Length 247;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 NNVLIQTDQQT 13
 DB 57 NNVLIQTDQQT 68

RESULT 14
 O4SVF5_TETNG PRELIMINARY; PRT; 260 AA.

AC O4SVF5;
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Chromosome 7 SCAR13760, whole genome shotgun sequence.
 GN ORFNames=GSTENG00012005001;
 OS Tetradon nigriviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 CX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Maudel E., Bouteau L., Fischer C., Ozouf-Costez C., Bernot A.,
 RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Bessat C., Segurens B.,
 RA Daesliwa C., Salanoubat M., Levy M., Boudet N., Caselham S.,
 RA Anthouard V., Jubin C., Castel V., Kacinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brotier P., Couanau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Landet V., Schachter V., Queller F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander B.S., Weissbach J., Roest Croliuss H.;
 RT "Genome duplication in the teleost fish Tetraodon nigriviridis reveals
 the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; GAE01013760; CAG95377.1; -; Genomic_DNA.
 DR EMBL; GAE01013760; CAG95377.1; -; Genomic_DNA.
 SO SEQUENCE 260 AA; 28404 MW; 7E3DC627AF6D41A2 CRC64;

Query Match 55.4%; Score 41; DB 2; Length 260;
 Best Local Similarity 70.0%; Pred. No. 34;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NNVLITQTDQ 11
 ||:||||:
 Db 69 NNILAQTDQ 78

RESULT 15

OARX65_TESTNG

ID OARX65_TESTNG PRELIMINARY; PRT; 540 AA.

AC OARX65;

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Chromosome 11 SCAP14979, whole genome shotgun sequence.

GN ORFNames=GSTBNG0027545001;

OS Tetraodon nigroviridis (Green puffer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

OC Tetraodontidae; Tetraodontidae; Tetraodon.

OX NCBI_TaxID=99883;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,

RA Mucelli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

RA Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

RA Desilva C., Salenouat M., Levy M., Boudet N., Castellano S.,

RA Blomont C., Skalli Z., Castello L., Poulain J., De Berardinis V.,

RA Cruaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,

RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,

RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,

RA Wincker P., Lander E.S., Weissenbach J., Roest Croliius H.,

RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals

RT the early vertebrate proto-karyotype."

RL Nature 411:946-957(2004).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RG Genoscope; Whitehead Institute Centre for Genome Research;

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; CAE01014979; CAG07017.1; -; Genomic DNA.

SQ SEQUENCE 540 AA; 61012 MW; BFDPE580B06E83DE CRC64;

Query Match 55.4%; Score 41; DB 2; Length 540;
 Best Local Similarity 60.0%; Pred. No. 79;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNNVLITQTDQATTR 15
 |||||:|:
 Db 54 RNNVRAQLKORANTR 68

Search completed: December 12, 2005, 20:41:07
 Job time : 83.4655 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:20:50 ; Search time 109.333 Seconds
(without alignments)
72.337 Million cell updates/sec

Title: US-10-758-165A-9
Perfect score: 97
Sequence: 1 VDGQKATNIPPTAPGTR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 827869

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : λ Geneseq_21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	18	ADRI0609	Dog IGE e
2	87	89.7	18	ADRI0610	Cat IGE e
3	55	56.7	18	ADRI0612	Sheep IGE
4	37	38.1	15	ADCS6890	Peptide f
5	34	35.1	15	ADCS6890	Horse Imm
6	34	35.1	18	ADRI0611	Horse IGE
7	32.5	33.5	15	ADW78189	Human met
8	32	33.0	9	AAU76520	Anti-Inte
9	32	33.0	9	AAE15818	Human mAb
10	32	33.0	11	ADT40399	Human mAb
11	32	33.0	11	ADT79816	SARS vir
12	32	33.0	11	ADT37929	hSARS vir
13	32	33.0	12	AAW52787	CCR5-bind
14	32	33.0	12	ADV13048	Human pho
15	32	33.0	15	AAV65747	Breast ca
16	32	33.0	15	ADW64911	HLA bindi
17	31	32.0	13	ADBS7003	Strainless
18	31	32.0	14	AAV31329	B. subtil
19	31	32.0	15	ADN64927	HLA bindi
20	31	32.0	18	ADBS4934	Beta-site
21	30	30.9	9	ABJ19961	MHC bindi
22	30	30.9	9	ADD94584	Human STM
23	30	30.9	10	ADD94544	Human STM
24	30	30.9	14	AAAB39162	Human sec

25	30	30.9	14	3	AAAB39163	Human sec
26	30	30.9	16	2	AARS53562	Bitch pol
27	30	30.9	16	8	ADQ90450	RANTES re
28	30	30.9	17	2	AAR95159	bcl-x(L)/
29	29	29.9	9	2	AAW24775	Human Imm
30	29	29.9	9	2	AAW80144	Light cha
31	29	29.9	9	2	AAW80142	Light cha
32	29	29.9	9	2	AAV40427	Amino aci
33	29	29.9	9	5	ABP62411	Human Imm
34	29	29.9	9	6	ABJ26739	VEGF bind
35	29	29.9	9	6	ABR06299	Human can
36	29	29.9	9	8	ADK18234	Mouse VEG
37	29	29.9	9	8	ADV26692	Human 109
38	29	29.9	9	8	ADV29257	Human 109
39	29	29.9	10	6	ABR06391	Human can
40	29	29.9	10	6	ABR06436	Human can
41	29	29.9	10	8	ADQ73723	Cancer re
42	29	29.9	10	8	ADQ72657	Cancer re
43	29	29.9	10	8	ADQ68445	Cancer re
44	29	29.9	10	8	ADQ70207	Cancer re
45	29	29.9	10	8	ADQ69505	Cancer re

ALIGNMENTS

RESULT 1
ADRI0609
ID ADRI0609 standard; peptide, 18 AA.
XX AC ADR10609;
XX DT 21-OCT-2004 (first entry)
XX DE Dog IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.
XX AC Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
XX KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
XX OS Canis familiaris.
XX WO2004065936-A2.
XX PD 05-AUG-2004.
XX PF 15-JAN-2004; 2004WO-US003566.
XX PR 16-JAN-2003; 2003US-0440472P.
XX PA (UNNC-) UNIV NORTH CAROLINA STATE.
XX PI Hammerberg B;
XX DR WPI, 2004-593545/57.
XX PT Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX Example 6; Page 9; 14pp; English.
XX The present invention relates to a novel monoclonal antibody (I) that
XX specifically binds to a mammalian IGE epitope, where the epitope is
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX (I) is useful for testing an allergen reactivity of an IGE sample. The
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX and corn allergens. The sample is a biological sample collected from a
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX antibodies recognise epitopes on canine IGE corresponding to amino acid
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
XX cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and

CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE.
 XX

XX Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.2e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAPG 18
 |||||
 1 VDGQKATNIFPYTAPG 18

RESULT 2

ADRI0610
 ID ADRI0610 standard; peptide; 18 AA.

AC ADRI0610;

XX 21-OCT-2004 (first entry)

DE Cat IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.

KW Antisclerotic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
 KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 XX cat.

OS Felis catus.

PN WO2004065936-A2.

PD 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

PA (UYN-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

XX WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IgE epitope, useful
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IgE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE. The present sequence is the
 CC cat IgE 3.76 recognition site.

XX Sequence 18 AA;

Query Match 89.7%; Score 87; DB 8; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.9e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAPG 16
 |||||
 1 VDGQKATNIFPYTAPG 16

DB

RESULT 3
 ADRI0612
 ID ADRI0612 standard; peptide; 18 AA.

AC ADRI0612;

XX 21-OCT-2004 (first entry)

DE Sheep IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 12.

KW Antisclerotic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
 KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 XX sheep.

OS Ovis aries.

PN WO2004065936-A2.

PD 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

PA (UYN-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

XX WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IgE epitope, useful
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IgE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE. The present sequence is the
 CC sheep IgE 3.76 recognition site.

XX Sequence 18 AA;

Query Match 56.7%; Score 55; DB 8; Length 18;
 Best Local Similarity 66.7%; Pred. No. 0.067;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYTAP 15
 |||||
 1 VDGQEDRNLFSTYAP 15

DB

RESULT 4

ADCS6890
 ID ADCS6890 standard; peptide; 15 AA.

```

XX AC ADC64569;
XX DT 18-DEC-2003 (first entry)
XX PT Peptide fragment Seq ID7 related to human protein 36-41.
XX DE human; protein 36-41; arrhythmia; asthma; dementia.
XX KW Homo sapiens.
XX OS CN382718-A.
XX PD 04-DEC-2002.
XX PF 26-APR-2001; 2001CN-00112751.
XX PR 26-APR-2001; 2001CN-00112751.
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX DR WPI; 2003-269480/27.
XX PT New human macroprotein-36-41, encoding polynucleotide, antagonist and
XX PT recombinant production, useful for treating dementia, arrhythmia, asthma
XX PT and digestive ulcers.
XX PS Example 6; SEQ ID NO 7; 33pp; Chinese.
XX CC This invention relates to a novel protein, human protein 36-41, and the
XX CC DNA sequence encoding it. The protein of the invention may be useful for
XX CC the treatment of diseases such as arrhythmia, asthma and dementia. The
XX CC present sequence is the amino acid sequence of a peptide fragment of
XX CC human protein 36-41 which was used in the exemplification of the
XX CC invention.
XX SQ Sequence 15 AA;

Query Match 38.1%; Score 37; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 58;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGQKATNIPYTP 15
   :||: |||: |
Db 1 MDGKMQPNSPFWQSP 15

RESULT 5
ADC64569
ID ADC64569 standard; peptide; 15 AA.
XX AC ADC64569;
XX DT 18-DEC-2003 (first entry)
XX DE Horse immunoglobulin E, IgE, heavy chain immunogenic peptide P5.
XX KW Horse; immunoglobulin E; IgE; heavy chain; immunogen; allergy.
XX OS Equus caballus.
XX OS US2003087314-A1.
XX PD 08-MAY-2003.
XX PF 08-NOV-2001; 2001US-00052788.
XX PR 08-NOV-2001; 2001US-00052788.
XX PA (REGC ) UNIV CALIFORNIA.
XX PA

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PI Gershwin LJ, Pettigrew HD, Kalina WV;
XX WPI; 2003-765437/72.
XX DR
XX PT Immunogenic composition comprising an isolated equine immunoglobulin E
XX PT polypeptide that induces production of antibodies which specifically bind
XX PT to equine immunoglobulin E.
XX PS Example 1; Page 8; 14pp; English.
XX CC The invention relates to an immunogenic composition comprising an
XX CC isolated polypeptide having an amino acid sequence that is at least 80%
XX CC identical to 6 (S1-S6), 15 amino acid peptide sequences derived from
XX CC equine immunoglobulin E (the composition induces production of an
XX CC antibody that specifically binds to equine immunoglobulin (Ig)E, the six
XX CC polypeptides are not explicitly identified in the specification. Also
XX CC included are a composition comprising an antibody that specifically binds
XX CC to a polypeptide at least 80% identical to (S1)-(S6), an antibody that
XX CC specifically binds to equine IgE made by the process of immunising an
XX CC animal with a polypeptide at least 80% identical to (S1)-(S6), making an
XX CC antibody that specifically binds to equine IgE (involving immunising an
XX CC animal with a composition further comprising an isolated polypeptide (the
XX CC amino acid sequence of the polypeptide is at least 80% identical to (S1)-
XX CC (S6)), and collecting antiserum from the animal) and a kit for detection
XX CC of equine IgE in a biological sample comprising the antibody and means
XX CC for detecting specific binding of the antibody to equine IgE. The
XX CC antibody is useful for detecting equine IgE protein in a biological
XX CC sample (serum) which involves contacting the sample with the antibody,
XX CC thus forming an antigen/antibody complex, and detecting the presence or
XX CC absence of the antigen/antibody complex. The antibody and antigen are
XX CC immobilised on a solid surface. The antibody is labelled such that the
XX CC complex can be detected. The complex is detected using a second labelled
XX CC antibody. The peptides are useful for generating antibodies specific for
XX CC IgE which can serve as a diagnostic test for allergy. The present
XX CC sequence is a Horse immunoglobulin E, IgE, heavy chain immunogenic
XX CC peptide from the middle portion of the C2 region.
XX SQ Sequence 15 AA;

Query Match 35.1%; Score 34; DB 7; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGQKATNIP 11
   :|||: ||
Db 2 IDGQKVDQSP 12

RESULT 6
ADR10611
ID ADR10611 standard; peptide; 18 AA.
XX AC ADR10611;
XX DT 21-OCT-2004 (first entry)
XX DE Horse IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 11.
XX KW Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
XX KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX KW horse.
XX OS Equus caballus.
XX OS WO2004065936-A2.
XX PD 05-AUG-2004.
XX PF 15-JAN-2004; 2004WO-US003566.
XX PR 16-JAN-2003; 2003US-0440472P.
XX PA (UNNC-) UNIV NORTH CAROLINA STATE.
XX PA

```

XX Hammerberg B;
 PI
 XX
 XX WPI; 2004-593545/57.
 DR
 XX
 PT Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.
 PS
 XX Example 6; Page 9; 14pp; English.
 CC The present invention relates to a novel monoclonal antibody (1) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (1) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (1) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC horse IGE 3.76 recognition site.
 CC
 XX
 SQ Sequence 18 AA:
 Query Match 35.1%; Score 34; DB 8; Length 18;
 Best Local Similarity 54.5%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 VDGOKATNIRP 11
 1 IDGKVDGQFP 11
 Db
 RESULT 7
 ADW78189
 ID ADW78189 standard; peptide; 15 AA.
 XX
 AC ADW78189;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE Human metabolic therapy target peptide PAGR.
 XX
 XX Human metabolic therapy target peptide PAGR.
 KW DEF domain; MAP kinase; cytosolic; cardiovascular-gen.; cardiant;
 KW vasotropic; hypotensive; antiarteriosclerotic; antiinflammatory;
 KW antiallergic; immunosuppressive; antibacterial; antisthmatic;
 KW dermatological; antidiabetic; gastrointestinal-gen.; antitumor;
 KW thrombolytic; neuroprotective; ophthalmological; antirheumatic;
 KW antihypertic; uropathic; antipsoriatic; hepatotropic; antianemic;
 KW muscular-gen.; thyromimetic; antithyroid; gynecological; nephrotropic;
 KW hepatocarcinogenic; virucide; anti-HIV; anabolic; hypertensive; anorectic;
 KW endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;
 KW antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.;
 KW antinfertility; cancer; cardiovascular disease; inflammation;
 KW metabolic disorder; neuropathy; sleep disorder.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO2005007090-A2.
 XX
 PD 27-JAN-2005.
 XX
 OS 02-JUL-2004; 2004MO-US021514.
 XX
 PF 03-JUL-2003; 2003US-0484761P.
 XX
 PR
 XX (HARD) HARVARD COLLEGE.
 PA

XX Blenis J, Murphy LO;
 PI
 XX
 XX WPI; 2005-112720/12.
 DR
 XX
 PT Identification of compound for treating e.g. cancer by culturing cells
 PT expressing target protein in the presence of growth factor, cytokine,
 PT tumor promoter or oncogene and assessing binding after contacting with
 PT the compound.
 PS
 XX Claim 14; Page 64; 104pp; English.
 CC The invention relates to a novel method for the identification of a
 CC therapeutic compound. The method involves providing test cells that
 CC express a target protein containing a DEF domain and MAP kinase;
 CC culturing the cells in the presence of growth factor, cytokine, tumor
 CC promoter or oncogene; contacting the cells with a candidate compound; and
 CC assessing the binding of the MAP kinase to the DEF domain relative to the
 CC binding in the absence of the candidate compound. The invention further
 CC comprises a method for the identification of a therapeutic compound;
 CC a method for treatment of cancer, which involves administering a compound
 CC that inhibits the binding of a MAP kinase to the DEF domain of a target
 CC protein; and an antibody that specifically binds to phospho-T-325 C-Ros
 CC (preferably polyclonal or monoclonal). The novel therapeutic compounds
 CC have the following activities: cytosolic, cardiovascular-gen., cardiant,
 CC vasotropic, hypotensive, antiarteriosclerotic, antiinflammatory,
 CC antiallergic, immunosuppressive, antibacterial, antisthmatic,
 CC dermatological, antidiabetic, gastrointestinal-gen., antitumor,
 CC thrombolytic, neuroprotective, ophthalmological, antirheumatic,
 CC antihypertic, uropathic, antipsoriatic, hepatotropic, antianemic, muscular
 CC -gen., thyromimetic, antithyroid, gynecological, nephrotropic,
 CC hepatocarcinogenic, virucide, anti-HIV, anabolic, hypertensive, anorectic,
 CC endocrine-gen., neuroleptic, nootropic, antiparkinsonian, anticonvulsant,
 CC antidepressant, antidiabetic, sedative, hypnotic, CNS-gen., and
 CC antinfertility. The therapeutic compound may be used in the treatment
 CC of: cancer, cardiovascular disorders, inflammatory disorders, metabolic
 CC disorders, neuropathy or a behavioural disorder, and a sleep disorder.
 CC This sequence represents a metabolic therapy target peptide of the
 CC invention.
 CC
 XX
 SQ Sequence 15 AA:
 Query Match 33.5%; Score 32.5; DB 9; Length 15;
 Best Local Similarity 66.7%; Pred. No. 3.3e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
 Oy 5 KATNIRPYTAG 16
 1 KAT--PYTPG 9
 Db
 RESULT 8
 AAU76520
 ID AAU76520 standard; peptide; 9 AA.
 XX
 AC AAU76520;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Anti-interleukin-12 (IL-12) antibody CDR3 light chain.
 XX
 XX Human, antibody; anti-interleukin-12; CDR, light chain; circulatory;
 KW complementarity determining region; neuroprotective; antipsoriatic;
 KW immunostimulant; cytosolic; anti-microbial; psoriasis; infection;
 KW multiple sclerosis; immune disorder; cardiovascular; malignant disease;
 KW neurological disorder.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200212500-A2.
 XX
 PD 14-FEB-2002.
 XX

PF 07-AUG-2001; 2001WO-US024720.
 XX
 PR 07-AUG-2000; 2000US-0223358P.
 PR 29-SEP-2000; 2000US-0236827P.
 PR 01-AUG-2001; 2001US-00920262.
 XX
 PA (CENZ) CENTOCOR INC.
 XX
 PI Giles-Komar J, Knight DM, Peritt D, Scallion B, Shealy D;
 XX
 DR WPI; 2002-257482/30.
 XX
 PT New mammalian anti-IL-12 antibodies, useful for diagnosing or treating IL
 PT -12 related conditions, e.g. psoriasis or multiple sclerosis, as well as
 PT other for treating immune, infectious, malignant or neurological
 PT disorders.
 XX
 PS Claim 41; Page 93; 96pp; English.
 CC
 CC The invention relates to novel isolated mammalian anti-interleukin-12 (IL
 CC -12) antibodies. The antibodies comprise at least one complementarity
 CC determining region (CDR) of a heavy or light chain, a heavy chain or
 CC light chain variable region, or a heavy chain or light chain constant
 CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or
 CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.
 CC The antibodies are also useful for treating immune, cardiovascular,
 CC infectious, malignant or neurological disorders or diseases. The present
 CC sequence represents the amino acid sequence of human anti-Interleukin-12
 CC (IL-12) antibody CDR3 light chain
 XX
 SQ Sequence 9 AA;
 XX
 Query Match 33.0%; Score 32; DB 5; Length 9;
 Best Local Similarity 83.3%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0;
 QY 8 NIPYPT 13
 ||:||||
 4 NIPYPT 9
 Db
 RESULT 9
 AAE15818
 ID AAE15818 standard; peptide; 9 AA.
 XX
 AC AAE15818;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human mAb 12B1 VK complementarity determining region (CDR) #3.
 XX
 KW Human; sialoadhesin factor-3; SAF-3; therapy; cancer; inflammation;
 KW autoimmunity; allergy; asthma; infection; central nervous system; CNS;
 KW rheumatoid arthritis; multiple sclerosis; stem cell mobilisation; AIDS;
 KW haematopoietic development; anaemia; chemoprotective agent; cytostatic;
 KW immunoglobulin; complementarity determining region; CDR; protozoacide;
 KW antiinflammacory; immunosuppressive; anti-HIV; antibacterial; virucide;
 KW fungicide; neuroprotective; light chain variable region; VK; mAb;
 KW monoclonal antibody.
 XX
 XX Homo sapiens.
 OS
 PN WO200190193-A1.
 XX
 PD 29-NOV-2001.
 XX
 PF 24-MAY-2001; 2001WO-US016864.
 XX
 PR 24-MAY-2000; 2000US-00577930.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX

PI Abrahamson JA, Kikly KK;
 XX
 DR WPI; 2002-083094/11.
 XX
 PT Novel monoclonal antibody that binds to human sialoadhesin factor-3 for
 PT treating or preventing cancer, inflammation, autoimmunity, allergy,
 PT asthma, rheumatoid arthritis, multiple sclerosis, AIDS and infections.
 XX
 PS Claim 13; Page 67; 69pp; English.
 CC
 CC The invention relates to monoclonal antibodies that bind to human
 CC sialoadhesin factor-3 (SAF-3). SAF-3 antibody is useful for treating or
 CC preventing cancer, inflammation, autoimmunity, allergy, asthma, central
 CC nervous system (CNS) inflammation, rheumatoid arthritis, multiple
 CC sclerosis, AIDS and bacterial, fungal, protozoan and viral infections
 CC for modulating an immune response in a mammal, where the immune response
 CC is downregulated or enhanced. SAF-3 antibody is useful as diagnostic and
 CC therapeutic reagents, to subcharacterise cell populations during
 CC haematopoietic development, to treat anaemia, as a diagnostic marker to
 CC distinguish between different forms of cancer, to purge bone marrow ex
 CC vivo of cancer cells expressing SAF-3, as a tool to aid in the ex vivo
 CC expansion (proliferation and/or differentiation) of haematopoietic
 CC progenitor cells expressing SAF-3, as a stimulus in vivo for stem cell
 CC mobilisation into the periphery and as an vivo chemoprotective agent.
 CC Protein comprising immunoglobulin complementarity determining region
 CC (CDR) of SAF-3 antibody and its nucleic acid is useful to configure
 CC screening methods for detecting the effect of added compounds on the
 CC production of mRNA and polypeptide in cells. The present sequence is
 CC complementarity determining region of human monoclonal antibody (mAb)
 CC 12B1 light chain variable region (VK), which binds to SAF-3
 XX
 SQ Sequence 9 AA;
 XX
 Query Match 33.0%; Score 32; DB 5; Length 9;
 Best Local Similarity 83.3%; Pred. No. 2e+06; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0;
 QY 8 NIPYPT 13
 ||:||||
 4 NIPYPT 9
 Db
 RESULT 10
 ADT40399
 ID ADT40399 standard; peptide; 11 AA.
 XX
 AC ADT40399;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 DE hSARS virus peptide, SEQ ID 1387.
 XX
 KW Virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.
 KW SARS coronavirus.
 OS
 PN WO2004085650-A1.
 XX
 PD 07-OCT-2004.
 XX
 PF 24-MAR-2004; 2004WO-CN000246.
 XX
 PR 24-MAR-2003; 2003US-0457031P.
 PR 26-MAR-2003; 2003US-0457730P.
 PR 02-APR-2003; 2003US-0459931P.
 PR 03-APR-2003; 2003US-0460357P.
 PR 08-APR-2003; 2003US-0461265P.
 PR 14-APR-2003; 2003US-0462805P.
 PR 23-APR-2003; 2003US-0464886P.
 PR 25-APR-2003; 2003US-0465738P.
 PR 14-MAY-2003; 2003US-04709335P.
 XX
 PA (UYHK-) UNIV HONG KONG.
 XX

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XX Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;
PI Leung FC;
XX WPI; 2004-737326/72.
XX
XX New nucleic acid molecule encoding nucleocapsid- or spike-gene protein of
PT a human Severe Acute Respiratory Syndrome (hSARS) virus, useful for
PT diagnosing and treating SARS.
XX
XX Example; SEQ ID NO 1387; 200pp; English.
XX
XX The present invention relates to novel human Severe Acute Respiratory
CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a
CC hSARS virus having China Center for Type Culture Collection Deposit
CC Accession No. CCTCC-V200303. The present invention also relates to novel
CC nucleic acid molecules (I; ADT41483 or ADT41485) encoding a nucleocapsid-
CC (N) or spike (S)-gene protein of a hSARS virus. Also disclosed are
CC methods for detecting the presence of a N- or S-gene of the hSARS virus
CC or of the protein in a biological sample and identifying a subject
CC infected with the hSARS virus. The hSARS virus, nucleic acid and protein
CC sequences are useful as vaccines for diagnosing or treating SARS. They
CC are also useful in clinical and scientific research applications. The
CC hSARS virus genome (ADT39027) was obtained and the amino acid sequences
CC of all three reading frames were deduced from the complementary strand.
CC ADT40120 is the full-length protein encoded by the first reading frame of
CC the complementary strand and ADT40121-ADT40601 are the peptides from the
CC first reading frame protein. ADT40602 is the full-length protein encoded
CC by the second reading frame of the complementary strand and ADT40603-
CC ADT40976 are the peptides from the second reading frame protein. ADT40977
CC is the full-length protein encoded by the third reading frame of the
CC complementary strand and ADT40978-ADT41482 are the peptides from the
CC third reading frame protein.
XX
XX Sequence 11 AA;
SQ
Query Match 33.0%; Score 32; DB 8; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 GQKATNIFPYT 13
DB 1 GQSQSNILPQT 11
RESULT 11
ADT379816
ID ADS79816 standard; protein; 11 AA.
XX
XX ADS79816;
XX
XX 30-DEC-2004 (first entry)
XX
XX SARS virus complementary DNA strand reading frame 1 protein #279.
XX
XX virucide; vaccine; detection; severe acute respiratory syndrome;
XX real-time quantitative polymerase chain reaction; SARS.
XX
XX SARS coronavirus.
XX
XX WO2004085455-A1.
XX
XX 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-CN000247.
XX
XX 24-MAR-2003; 2003US-0457031P.
XX
XX 26-MAR-2003; 2003US-0457730P.
XX
XX 02-APR-2003; 2003US-0459931P.
XX
XX 03-APR-2003; 2003US-0460357P.
XX
XX 08-APR-2003; 2003US-0461265P.
XX
XX 14-APR-2003; 2003US-0462805P.
XX
XX 23-APR-2003; 2003US-0464886P.
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PR 05-MAY-2003; 2003US-0468139P.
PR 16-MAY-2003; 2003US-0471200P.
XX
XX (UYHK-) UNIV HONG KONG.
XX
XX Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;
PI WPI; 2004-737326/72.
XX
XX New isolated nucleic acid molecule useful for detecting, treating,
PT ameliorating, or preventing the virus causing severe acute respiratory
PT syndrome in humans using a real-time quantitative polymerase chain
PT reaction assay.
XX
XX Example; SEQ ID NO 1387; 183pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule consisting
CC essentially of, and/or hybridizes under stringent conditions to a fully
CC defined nucleotide sequence of 16-25 base pairs (bp), SEQ ID NO: 2471-
CC 2476, or its complement. The methods and compositions of the present
CC invention are useful for the detection of the virus causing Severe Acute
CC Respiratory Syndrome (SARS) in humans using a real-time quantitative
CC polymerase chain reaction (PCR) assay. They can also be used in treating,
CC ameliorating, managing or preventing SARS. This sequence corresponds to a
CC partial SARS protein sequence from the complementary reading frame 1.
XX
XX Sequence 11 AA;
SQ
Query Match 33.0%; Score 32; DB 8; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 GQKATNIFPYT 13
DB 1 GQSQSNILPQT 11
RESULT 12
ADT37929
ID ADT37929 standard; peptide; 11 AA.
XX
XX ADT37929;
XX
XX 30-DEC-2004 (first entry)
XX
XX hSARS virus peptide, SEQ ID 1387.
XX
XX virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.
XX
XX SARS coronavirus.
XX
XX WO2004085633-A1.
XX
XX 07-OCT-2004.
XX
XX 24-MAR-2004; 2004WO-CN000248.
XX
XX 24-MAR-2003; 2003US-0457031P.
XX
XX 26-MAR-2003; 2003US-0457730P.
XX
XX 02-APR-2003; 2003US-0459931P.
XX
XX 03-APR-2003; 2003US-0460357P.
XX
XX 08-APR-2003; 2003US-0461265P.
XX
XX 14-APR-2003; 2003US-0462805P.
XX
XX 23-APR-2003; 2003US-0464886P.
XX
XX (UYHK-) UNIV HONG KONG.
XX
XX Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;
PI Leung FC;
XX
XX WPI; 2004-728736/71.
XX
XX New isolated human severe acute respiratory syndrome (hSARS) virus,
```

CC	The invention relates to a method for identifying a binding compound for
CC	CC chemokine receptor 5 (CCR5). The method involves screening a library
CC	of test molecules (particularly peptides) with immobilised CCR5, and then
CC	identifying those molecules which bind. The invention also relates to
CC	CCR5-binding molecules identified using the method of the invention,
CC	a method for identifying consensus motifs for CCR5-binding peptides, a
CC	transfer vector encoding tagged CCR5, a computer-aided methods for
CC	determining the relative binding affinity of a test molecule to CCR5 and
CC	a computer aided drug screening assay that utilises the three-dimensional
CC	structure of CCR5. Compounds identified using the methods of the
CC	invention are useful for treating or preventing HIV (human
CC	immunodeficiency virus) infection or AIDS (acquired immunodeficiency
CC	syndrome) in a patient. The methods of the invention may also be used to
CC	identify agonists or antagonists of the interaction of CCR5 with its
CC	natural ligand, and to determine a binding motif for CCR5. Sequences
CC	AAM52784-AAM52805 and AAM52814 represent specifically claimed CCR5-
CC	binding peptides identified using methods of the invention
XX	
SQ	Sequence 12 AA;
Query Match	33.0%; Score 32; DB 5; Length 12;
Best Local Similarity	62.5%; Pred. No. 3.1e+02;
Matches	5; Conservative 2; Mismatches 1; Indels 0; Gaps 0
OY	10 PPTAPGT 17 : :: DB 4 YPYSAPT 11
RESULT 14	
ADV13048	
ID	ADV13048 standard; peptide; 12 AA.
XX	
AC	ADV13048;
XX	
DT	10-MAR-2005 (first entry)
XX	
DE	Human phosphorylated peptide from phosphoprotein #986.
XX	
KM	Alzheimers disease; neuroprotective; nootropic; degeneration; tumor;
KW	neoplasm; neurological disease; phosphorylation; protein sequencing;
XX	phosphoprotein.
OS	Homo sapiens.
XX	
PM	WO2004108948-A2.
PD	
XX	16-DEC-2004.
XX	
Pf	04-JUN-2004; 2004WO-US017613.
XX	
PR	04-JUN-2003; 2003US-0476010P.
XX	
PA	(HARD) HARVARD COLLEGE.
XX	
PI	Gysi SP;
XX	
DR	WPI; 2005-031720/03.
XX	
PT	Characterizing phosphorylated polypeptides in a sample comprises
PT	digesting the polypeptides with a protease thus generating test peptides,
PT	and collecting a fraction of test peptides that enriched for positively
PT	charged peptides.
XX	
PS	Claim 16; Page 79; 123pp; English.
XX	
CC	The invention relates to characterizing phosphorylated polypeptides in a
CC	sample comprising digesting the polypeptides with a protease thus
CC	generating test peptides, and collecting a fraction of test peptides thab
CC	enriched for positively charged peptides. Also included are a method
CC	(comprising determining the presence, absence or level of one ore more
CC	phosphorylated peptides as identified above in cells having a cell state

CC and determining the degree of correlation between the presence, absence
 CC or level of phosphorylated polypeptide with the cell state), an isolated
 CC peptide of 5-50 amino acids comprising an amino acid sequence that is a
 CC subsequence of any of the protein sequences given in the specification
 CC (and which comprise a phosphorylation site within the subsequence), an
 CC isolated polypeptide selected from any of the polypeptides listed in the
 CC specification and is modified at a modification site, an isolated peptide
 CC comprising a mass spectral peak signature, a method for identifying a
 CC treatment that modulates phosphorylation of an amino acid in a target
 CC polypeptide, a method for generating a peptide standard, a pair of
 CC peptide standards comprising the peptide obtained (where the peptide is
 CC phosphorylated and a corresponding peptide comprising an identical amino
 CC acid sequence but which is not phosphorylated), a system (comprising a
 CC computer memory comprising data files storing information relating to the
 CC identifying characteristics of positively charged peptides, and a data
 CC analysis module capable of executing instructions for organizing and/or
 CC searching the data files), a computer program product (comprising data
 CC relating to the identifying characteristics of positively charged
 CC peptides and comprising instructions for organizing and/or searching the
 CC data), and a method for identifying N-terminal peptides in a sample. The
 CC method is useful for characterizing phosphorylated polypeptides in a
 CC sample. The present sequence is a peptide derived from a human phosphoprotein,
 CC containing a phosphorylation site, identified by the method of the
 CC invention.

CC Sequence 12 AA;

Query Match 33.0%; Score 32; DB 9; Length 12;
 Best Local Similarity 85.7%; Pred. No. 3.1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAPGR 17
 | | | | |
 Db 3 PATAPGR 9

RESULT 15

AAV65747
 ID AAV65747 standard; peptide; 15 AA.

AC AAV65747;

DT 10-FEB-2000 (first entry)

DE Breast cancer susceptibility (BRCA 2) mutant peptide 31.

KW Human; frameshift mutant; T cell response; tumour; treatment; cancer;
 muten.

OS Homo sapiens.

OS Synthetic.

PN WO958552-A2.

PD 18-NOV-1999.

PF 03-MAY-1999; 99WO-N0000143.

PR 08-MAY-1998; 98NO-00002097.

PA (NHVD) NORSK HYDRO AS.

PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;

DR WPI; 2000-039064/03.

PT New peptides derived from genes with frameshift mutations, used to
 develop products for the treatment and prophylaxis of cancers.

PS Claim 13; Page 25; 166pp; English.

CC Peptides AAV65684-Y66142 are fragments of mutant proteins arising from a
 CC frameshift mutation in a gene from a cancer cell. The peptides are

CC characterised in that they: (i) are at least 8 amino acids long and a
 CC fragment of a mutant protein arising from a frameshift mutation in a gene
 CC of a cancer cell; (ii) consist of at least one amino acid of the mutant
 CC part of a protein sequence encoded by the gene; (iii) comprise 0-10 amino
 CC acid from the carboxyl terminus of the normal part of the protein
 CC sequence preceding the amino terminus of the mutant sequence and may
 CC further extend to the carboxyl terminus of the mutant part of the protein
 CC as determined by a new stop codon generated by the frameshift mutation;
 CC and (iv) induce, either in their full lengths or after processing by an
 CC antigen presenting cell (APC), T cell responses. The genes that the
 CC peptides are derived from, are characterised as susceptible to frameshift
 CC mutation by having a mono nucleoside base repeat sequence of at least 5
 CC residues, or a di-nucleoside base repeat sequence of at least 4 di-
 CC nucleoside base units. The peptides are created by the addition or
 CC deletion of 1 or 2 nucleoside base residues from the repeat sequence. The
 CC novel peptides can elicit T cell responses and toxicity against tumours
 CC and cancer cells carrying genes with frameshift mutations. The novel
 CC peptides and DNA sequences can be used for the preparation of a
 CC composition for the treatment or prophylaxis of cancer

CC Sequence 15 AA;

Query Match 33.0%; Score 32; DB 3; Length 15;
 Best Local Similarity 54.5%; Pred. No. 4e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGQKATNIFP 11
 | : | | : | |
 Db 4 VEDQKTLVFP 14

Search completed: December 12, 2005, 21:52:02
 Job time : 11.333 secs

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OM protein - protein search, using SW model

Run on: December 12, 2005, 21:05:57 ; Search time 27 Seconds
(without alignments)
55.117 Million cell updates/sec

Title: US-10-758-165A-9

Perfect score: 97
Sequence: 1 VDCGKATNIPYTAQTK 18

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 208455

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	33.0	9	2	US-09-920-262A-6
2	32	33.0	15	2	US-09-674-973A-64
3	30	30.9	9	2	US-09-865-548A-126
4	30	30.9	17	1	US-08-333-555-22
5	30	30.9	17	1	US-08-661-479-22
6	29	29.9	9	2	US-09-042-353-366
7	29	29.9	9	2	US-08-758-417A-214
8	29	29.9	11	2	US-09-307-265A-14
9	29	29.9	15	2	US-08-278-774-20
10	29	29.9	15	2	US-09-526-195-9
11	29	29.9	16	2	US-08-957-130-19
12	29	29.9	18	2	US-09-856-920-1
13	28	28.9	10	2	US-09-641-803-18
14	28	28.9	10	2	US-09-641-802-18
15	28	28.9	10	2	US-09-641-801-18
16	28	28.9	10	2	US-10-281-652-18
17	28	28.9	15	1	US-08-080-073-26
18	27	27.8	8	2	US-08-981-392-83
19	27	27.8	8	2	US-09-908-322-83
20	27	27.8	9	1	US-08-346-333-41
21	27	27.8	4	4	PCT-US91-07506-41
22	27	27.8	11	1	US-07-958-903A-5
23	27	27.8	11	1	US-08-462-018-5
24	27	27.8	11	1	US-08-823-245-5
25	27	27.8	11	1	US-07-963-329A-69
26	27	27.8	11	2	US-09-318-001-5
27	27	27.8	11	2	US-09-064-159-5

28	27	27.8	11	2	US-09-809-517A-21	Sequence 21, Appl
29	27	27.8	11	4	PCT-US92-09443A-69	Sequence 69, Appl
30	27	27.8	13	1	US-07-958-903A-8	Sequence 8, Appl
31	27	27.8	13	1	US-08-462-018-8	Sequence 8, Appl
32	27	27.8	13	1	US-08-823-245-8	Sequence 8, Appl
33	27	27.8	13	2	US-07-963-329A-58	Sequence 58, Appl
34	27	27.8	13	2	US-09-318-001-8	Sequence 8, Appl
35	27	27.8	13	2	US-09-064-159-8	Sequence 8, Appl
36	27	27.8	13	4	PCT-US92-09443A-58	Sequence 8, Appl
37	27	27.8	17	1	US-08-325-553-9	Sequence 9, Appl
38	27	27.8	17	1	US-08-394-152A-9	Sequence 9, Appl
39	27	27.8	17	1	US-08-705-477E-9	Sequence 9, Appl
40	27	27.8	17	2	US-08-466-381C-9	Sequence 9, Appl
41	27	27.8	18	1	US-09-017-205-48	Sequence 48, Appl
42	27	27.8	18	1	US-09-017-205-49	Sequence 49, Appl
43	26	26.8	5	2	US-09-788-006-9	Sequence 9, Appl
44	26	26.8	9	2	US-09-197-854-59	Sequence 59, Appl
45	26	26.8	9	2	US-09-511-939-96	Sequence 96, Appl

ALIGNMENTS

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RESULT 1
US-09-920-262A-6
; Sequence 6, Application US/09920262A
; Patent No. 6902734
; GENERAL INFORMATION:
; APPLICANT: Shealy, David
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Pettit, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-6
Query Match      33.0% Score 32; DB 2; Length 9;
Beet Local Similarity 83.3% Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      8 NIPYPT 13
      |||||
Db      4 NIPYPT 9
RESULT 2
US-09-674-973A-64
; Sequence 64, Application US/09674973A
; Patent No. 6759046
; GENERAL INFORMATION:
; APPLICANT: No. 6759046sk Hyato ASA
; TITLE OF INVENTION: Peptidases
; FILE REFERENCE: 26625-296
; CURRENT APPLICATION NUMBER: US/09/674,973A
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
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ORGANISM: Homo sapiens
US-09-674-973A-64

Query Match 33.0%; Score 32; DB 2; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDQKATNFP 11
| | | | |
| | | | |
DB 4 VEDOKTLVFP 14

RESULT 3
US-09-865-548A-126
Sequence 126, Application US/09865548A

PATENT No. 6867283
GENERAL INFORMATION:
APPLICANT: Barnea, Eilon
APPLICANT: Beer, Ilan
APPLICANT: Ziv, Tamay
APPLICANT: Admon, Arle
TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
FILE REFERENCE: 01/22080
CURRENT APPLICATION NUMBER: US/09/865,548A
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: US 60/290,958
PRIOR FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 204
SOFTWARE: PatentIn version 3.1
SEQ ID NO 126
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-865-548A-126

Query Match 30.9%; Score 30; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NIPFY 12
| | | | |
| | | | |
DB 1 NIPFY 5

RESULT 4
US-08-333-565-22
Sequence 22, Application US/08333565

PATENT No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-333-565-22

Query Match 30.9%; Score 30; DB 1; Length 17;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTPAG 16
| | | | |
| | | | |
DB 3 PYTPAG 8

RESULT 5
US-08-661-479-22
Sequence 22, Application US/08661479

PATENT No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-661-479-22

Query Match 30.9%; Score 30; DB 1; Length 17;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTPAG 16

Db 3 PYLAPG 8

RESULT 6
US-09-042-353-366
Sequence 366, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 366:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-042-353-366
Query Match 29.9% Score 29; DB 2; Length 9;
Best Local Similarity 83.3% Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 8 NIPFYT 13
Db 4 NSFPYT 9
RESULT 7
US-08-758-417A-214
Sequence 214, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/165,699
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/352,322
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993

APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-08-758-417A-214

Query Match 29.9%; Score 29; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIFPYT 13
| | | | |
Db 4 NSFPYT 9

RESULT 8
US-09-307-265A-14
Sequence 14, Application US/09307265A
Patent No. 6225456
GENERAL INFORMATION:
APPLICANT: Gu, Trent
APPLICANT: Orita, Satoshi
APPLICANT: Han, Min
TITLE OF INVENTION: RAS SUPPRESSOR SUR-5
FILE REFERENCE: UTC-03732
CURRENT APPLICATION NUMBER: US/09/307,265A
CURRENT FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 14
LENGTH: 11
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-307-265A-14

Query Match 29.9%; Score 29; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 PYTAPGK 18
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Db 1 PYTSSGK 8

RESULT 9
US-08-278-774-20
Sequence 20, Application US/08278774
Patent No. 6653450
GENERAL INFORMATION:
APPLICANT: Berg, Richard A
APPLICANT: Toman, David P
APPLICANT: Wallace, Donald
TITLE OF INVENTION: MUTATED RECOMBINANT COLLAGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: COLLAGEN CORPORATION
STREET: 2500 Faber Place
CITY: Palo Alto

STATE: California
COUNTRY: USA
ZIP: 94303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,774
FILING DATE: 22-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ralayko, Kati L
REGISTRATION NUMBER: 36,644
REFERENCE/DOCKET NUMBER: 94-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-4642
TELEFAX: (415) 354-4752
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-278-774-20

Query Match 29.9%; Score 29; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGKATNIPY 12
: : : : :
Db 2 IGGEKAGFAPY 13

RESULT 10
US-09-526-195-9
Sequence 9, Application US/09526195
Patent No. 6698478
GENERAL INFORMATION:
APPLICANT: Hancock, Gerald E.
APPLICANT: Tebbey, Paul W.
TITLE OF INVENTION: ENHANCED IMMUNE RESPONSE TO ATTACHMENT
FILE REFERENCE: 1646.1030-004
CURRENT APPLICATION NUMBER: US/09/526,195
CURRENT FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/084,863
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: PCT/US98/19656
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: US 60/059,684
PRIOR FILING DATE: 1997-09-19
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-09-526-195-9

Query Match 29.9%; Score 29; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 7 TNIFPYAPGK 18
| | | | |
Db 1 TTIlastPGVK 12


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RESULT 15
US-09-641-801-18
; Sequence 18: Application US/09641801
; Patent No. 6903068
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: GEORGIADIS, Jerry
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOG
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 265, 00230101
; CURRENT APPLICATION NUMBER: US/09/641,801
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,311
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-801-18

Query Match      28.9%; Score 28; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      9 IFPYTAP 15
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Db      1 VYPPTGP 7
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Search completed: December 12, 2005, 21:20:08
Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 12, 2005, 21:20:19 ; Search time 95 Seconds
(without alignments)
79.168 Million cell updates/sec

Title: US-10-758-165a-9

Perfect score: 97
Sequence: 1 VDGQKATNIPFYTAAGTK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 356231

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep.*
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4: /cgn2_6/ptodata/1/pubpaa/US10_PUBSCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	US-10-758-165-9	Sequence 9, Appli
2	87	89.7	18	US-10-758-165-10	Sequence 10, Appl
3	55	56.7	18	US-10-758-165-12	Sequence 12, Appl
4	37	38.1	15	US-10-856-118-34	Sequence 34, Appl
5	34	35.1	15	US-10-052-788-5	Sequence 5, Appli
6	34	35.1	18	US-10-758-165-11	Sequence 11, Appl
7	32	33.0	9	US-09-920-262A-6	Sequence 6, Appli
8	32	33.0	9	US-10-912-994-6	Sequence 6, Appli
9	32	33.0	9	US-10-975-883-6	Sequence 6, Appli
10	32	33.0	9	US-10-975-740A-6	Sequence 6, Appli
11	32	33.0	9	US-10-975-708-6	Sequence 6, Appli
12	32	33.0	11	US-10-808-187-1387	Sequence 1387, Ap
13	32	33.0	11	US-10-807-807-1387	Sequence 1387, Ap
14	32	33.0	12	US-09-813-653-26	Sequence 26, Appl
15	32	33.0	12	US-10-862-195-1037	Sequence 1037, Ap
16	32	33.0	13	US-10-776-224-64	Sequence 64, Appl
17	31	32.0	13	US-10-300-694A-64	Sequence 64, Appl
18	31	32.0	14	US-09-229-751A-16	Sequence 16, Appl
19	31	32.0	18	US-10-685-896-81	Sequence 81, Appl
20	30	30.9	9	US-09-865-548A-126	Sequence 126, App
21	30	30.9	9	US-10-705-459-126	Sequence 126, App
22	30	30.9	18	US-10-195-730-360	Sequence 360, App
23	30	30.9	18	US-10-799-747-360	Sequence 360, App
24	30	30.9	18	US-10-979-183-360	Sequence 360, App
25	29	29.9	9	US-10-482-630-40	Sequence 40, Appl
26	29	29.9	12	US-10-894-672-39	Sequence 39, Appl
27	29	29.9	12	US-10-996-316-39	Sequence 39, Appl

28	29	29.9	15	US-10-783-455-9	Sequence 9, Appli
29	29	29.9	15	US-10-720-831-20	Sequence 20, Appl
30	29	29.9	17	US-09-992-896-51	Sequence 51, Appl
31	29	29.9	17	US-10-306-631-76	Sequence 76, Appl
32	29	29.9	18	US-10-846-548A-1	Sequence 1, Appli
33	28	28.9	9	US-10-160-506-34	Sequence 34, Appl
34	28	28.9	9	US-10-449-379-34	Sequence 34, Appl
35	28	28.9	9	US-10-688-015-34	Sequence 34, Appl
36	28	28.9	9	US-10-160-505-34	Sequence 34, Appl
37	28	28.9	9	US-10-482-284A-186	Sequence 186, App
38	28	28.9	10	US-10-281-652-18	Sequence 18, Appl
39	28	28.9	10	US-10-691-157-18	Sequence 18, Appl
40	28	28.9	10	US-10-691-330-18	Sequence 18, Appl
41	28	28.9	12	US-10-903-529-3	Sequence 3, Appli
42	28	28.9	12	US-10-903-529-25	Sequence 25, Appl
43	28	28.9	12	US-10-937-042-3	Sequence 3, Appli
44	28	28.9	14	US-09-880-748-2653	Sequence 2653, Ap
45	28	28.9	14	US-10-293-418-2653	Sequence 2653, Ap

ALIGNMENTS

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RESULT 1
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hamnerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-9
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Query Match 100.0%; Score 97; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 9, 1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VDGQKATNIPFYTAAGTK 18
|||
DB 1 VDGQKATNIPFYTAAGTK 18
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RESULT 2
US-10-758-165-10
; Sequence 10, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hamnerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-10
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Query Match 89.7%; Score 87; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPG 16
Db 1 VDGOKATNIFPYTAPG 16

RESULT 3

US-10-758-165-12
; Sequence 12, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammetberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-12

Query Match 56.7%; Score 55; DB 5; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.071;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAP 15
Db 1 VDGQEDNLPSTYAP 15

RESULT 4

US-10-856-118-34
; Sequence 34, Application US/10856118
; Publication No. US20050025747A1
; GENERAL INFORMATION:
; APPLICANT: Laidlaw, Stephen
; APPLICANT: Skinner, Mike
; APPLICANT: Hall, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Anderson, Richard
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 3742.1000-000
; CURRENT APPLICATION NUMBER: US/10/856,118
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: PCT/GB02/005411
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: GB0128733.3
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/334,649
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flanking sequence
US-10-856-118-34

Query Match 38.1%; Score 37; DB 5; Length 15;
Best Local Similarity 55.6%; Pred. No. 52;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 TNIFPYTAP 15
|:|:|:|:|

Db 2 TNVYPDVP 10

RESULT 5
US-10-052-788-5
; Sequence 5, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
; APPLICANT: Gershwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kalina, Warren V.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052,788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:epitope peptide
; OTHER INFORMATION: p5, middle portion of C2 of equine IgE epsilon
; OTHER INFORMATION: heavy chain
US-10-052-788-5

Query Match 35.1%; Score 34; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGOKATNIPP 11
:|:|:|:|:|
Db 2 IDGQKVDQEP 12

RESULT 6

US-10-758-165-11
; Sequence 11, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammetberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-11

Query Match 35.1%; Score 34; DB 5; Length 18;
Best Local Similarity 54.5%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGOKATNIPP 11
:|:|:|:|:|
Db 1 IDGQKVDQEP 11

RESULT 7

US-09-920-262A-6
; Sequence 6, Application US/09920262A
; Publication No. US20030124123A1
; GENERAL INFORMATION:
; APPLICANT: Shealy, David

```
; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Gilles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-6
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Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      8 NIPYPT 13
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Db      4 NIPYPT 9
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RESULT 8
US-10-912-994-6
; Sequence 6, Application US/10912994
; Publication No. US2005002937A1
; GENERAL INFORMATION:
; APPLICANT: Gilles-Komar, Jill
; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248DIV1
; CURRENT APPLICATION NUMBER: US/10/912,994
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-912-994-6
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```
Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```
RESULT 9
US-10-975-883-6
; Sequence 6, Application US/10975883
; Publication No. US20050112127A1
; GENERAL INFORMATION:
; APPLICANT: Gilles-Komar, Jill
; APPLICANT: Knight, David
```

```
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND USES
; FILE REFERENCE: CEN0248DIV04
; CURRENT APPLICATION NUMBER: US/10/975,883
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-883-6
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```
Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```
RESULT 10
US-10-975-740A-6
; Sequence 6, Application US/10975740A
; Publication No. US20050196838A1
; GENERAL INFORMATION:
; APPLICANT: Gilles-Komar, Jill
; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND NUCLEIC ACIDS
; FILE REFERENCE: CEN0248DIV03
; CURRENT APPLICATION NUMBER: US/10/975,740A
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-740A-6
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Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```
RESULT 11
US-10-975-708-6
; Sequence 6, Application US/10975708
; Publication No. US20050214293A1
; GENERAL INFORMATION:
; APPLICANT: Gilles-Komar, Jill
```

```

; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND COMPOSITIONS
; FILE REFERENCE: GEN0248DIV02
; CURRENT APPLICATION NUMBER: US/10/975,708
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-708-6
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```
Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
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RESULT 12
US-10-808-187-1387
; Sequence 1387, Application US/10808187
; Publication No. US200500909A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-1387
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```

Query Match          33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      3 GOKATNIFPYT 13
      ||:||||
Db      1 GQSQSNILPOT 11
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RESULT 13
US-10-807-807-1387
; Sequence 1387, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEONG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; TITLE OF INVENTION: CAUSING SEVERE ACUTE RESPIRATORY SYNDROME (SARS)
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-1387
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Query Match          33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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```
QY      3 GOKATNIFPYT 13
      ||:||||
Db      1 GQSQSNILPOT 11
```

```

RESULT 14
US-09-813-653-26
; Sequence 26, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
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; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence identified through phage display for CCR5 binding
US-09-613-653-26

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Query Match          33.0%; Score 32; DB 3; Length 12;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      10 PPYAPGT 17
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Db       4 YPISAPRT 11

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RESULT 15
US-10-862-195-1037
; Sequence 1037, Application US/10862195
; Publication No. US20050164324A1
; GENERAL INFORMATION:
; APPLICANT: GYGI, STEVEN P.
; TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
; FILE REFERENCE: 58890(70207)
; CURRENT APPLICATION NUMBER: US/10/862,195
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/476,010
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 2245
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1037
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: See specification as filed for preferred embodiments
; OTHER INFORMATION: and description of phosphorylation sites
US-10-862-195-1037

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Query Match          33.0%; Score 32; DB 5; Length 12;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      11 PYTAPGT 17
        |||||
Db       3 PATAAPT 9

```

Search completed: December 12, 2005, 21:29:23
Job time : 96 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:17:33 ; Search time 3 Seconds
(without alignments)
33.507 Million cell updates/sec

Title: US-10-758-165A-9
Perfect score: 97
Sequence: 1 VDCGKATNIPFYTAPTK 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues

Total number of hits satisfying chosen parameters: 9754

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:
1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubpaa/FC1_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28.9	14	7	US-11-054-515-2653	Sequence 2653, Ap
2	27.8	14	7	US-11-054-515-2682	Sequence 2682, Ap
3	25.8	9	7	US-11-009-939-10	Sequence 10, Appl
4	25.8	9	7	US-11-009-939-40	Sequence 40, Appl
5	25.8	18	6	US-10-828-033-36	Sequence 36, Appl
6	24.7	16	6	US-10-999-866-57	Sequence 57, Appl
7	24.7	16	6	US-10-507-275-17	Sequence 17, Appl
8	23.5	14	7	US-11-054-515-2617	Sequence 2617, Ap
9	23.7	9	6	US-10-952-535A-28	Sequence 28, Appl
10	23.7	9	6	US-10-952-535A-43	Sequence 43, Appl
11	23.7	9	7	US-11-010-748A-334	Sequence 334, App
12	23.7	9	7	US-11-010-748A-346	Sequence 346, App
13	23.7	9	7	US-11-158-848-41	Sequence 41, Appl
14	23.7	9	7	US-11-178-639-3	Sequence 3, Appl
15	23.7	9	7	US-11-137-671-4	Sequence 4, Appl
16	23.7	10	6	US-10-933-025-19	Sequence 19, Appl
17	23.7	10	7	US-11-093-274-16	Sequence 16, Appl
18	23.7	10	7	US-11-137-671-3	Sequence 3, Appl
19	23.7	11	7	US-11-137-671-2	Sequence 2, Appl
20	23.7	12	6	US-10-632-150-82	Sequence 82, Appl
21	23.7	12	6	US-10-507-662-9	Sequence 9, Appl
22	23.7	12	6	US-10-952-535A-33	Sequence 33, Appl
23	23.7	12	6	US-11-069-858-1	Sequence 1, Appl
24	23.7	12	7	US-11-073-457-82	Sequence 82, Appl
25	23.7	12	7	US-11-137-671-1	Sequence 1, Appl

26	23	23.7	13	6	US-10-511-559-719	Sequence 719, App
27	23	23.7	13	7	US-11-054-669-97	Sequence 97, Appl
28	23	23.7	13	7	US-11-089-551A-8	Sequence 8, Appl
29	23	23.7	14	7	US-11-054-515-2374	Sequence 2374, Ap
30	23	23.7	14	7	US-11-054-515-2474	Sequence 2474, Ap
31	23	23.7	14	7	US-11-054-515-2655	Sequence 2655, Ap
32	23	23.7	14	7	US-11-054-515-2656	Sequence 2656, Ap
33	23	23.7	14	7	US-11-054-515-2657	Sequence 2657, Ap
34	23	23.7	14	7	US-11-054-515-2658	Sequence 2658, Ap
35	23	23.7	14	7	US-11-054-515-2670	Sequence 2670, Ap
36	23	23.7	14	7	US-11-054-515-2673	Sequence 2673, Ap
37	23	23.7	14	7	US-11-054-515-2676	Sequence 2676, Ap
38	23	23.7	14	7	US-11-054-515-2679	Sequence 2679, Ap
39	23	23.7	14	7	US-11-054-515-2710	Sequence 2710, Ap
40	23	23.7	14	7	US-11-054-515-2719	Sequence 2719, Ap
41	23	23.7	15	6	US-10-952-535A-32	Sequence 32, Appl
42	23	23.7	15	7	US-11-058-735-1	Sequence 1, Appl
43	23	23.7	15	7	US-11-058-735-7	Sequence 7, Appl
44	23	23.7	17	7	US-11-058-735-28	Sequence 28, Appl
45	22.5	23.2	14	7	US-11-054-515-2361	Sequence 2361, Ap

ALIGNMENTS

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RESULT 1
US-11-054-515-2653
Sequence 2653, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23p3
CURRENT APPLICATION NUMBER: US/11/054,515
PRIOR FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2653
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-2653
Query Match 28.9%; Score 28; DB 7; Length 14;
Beet Local Similarity 57.1%; Pred. No. 19;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 9 IFPYRAP 15
DB 6 LFPYMP 12
RESULT 2
```

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US-11-054-515-2682
; Sequence 2682, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2682
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2682

Query Match      27.8%; Score 27; DB 7; Length 14;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      9 IFPYT 13
Db      6 LFPT 10

RESULT 3
US-11-009-939-10
; Sequence 10, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-10

Query Match      25.8%; Score 25; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      10 FPYT 13
Db      6 FPYT 9

RESULT 4
US-11-009-939-40
; Sequence 40, Application US/11009939
; Publication No. US20050265998A1
; GENERAL INFORMATION:
; APPLICANT: Elson, Greg Christopher Andrew
; TITLE OF INVENTION: Neutralizing Antibodies and Methods of Use Thereof
; FILE REFERENCE: 23135-402
; CURRENT APPLICATION NUMBER: US/11/009,939
; CURRENT FILING DATE: 2005-12-10
; PRIOR APPLICATION NUMBER: 60/528,811
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,812
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/528,962
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-009-939-40

Query Match      25.8%; Score 25; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 NFPYT 13
Db      4 NTFPWT 9

RESULT 5
US-10-828-033-36
; Sequence 36, Application US/10828033
; Publication No. US20050250206A1
; GENERAL INFORMATION:
; APPLICANT: Paul B. Fisher and Ruoguan Shen
; TITLE OF INVENTION: DEVELOPMENT OF DNA PROBES AND IMMUNOLOGICAL REAGENTS
; TITLE OF INVENTION: SPECIFIC FOR CELL
; FILE REFERENCE: 0667/37590-C-PCT-US
; CURRENT APPLICATION NUMBER: US/10/828,033
; CURRENT FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: US/08/875,553
; PRIOR FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human
US-10-828-033-36

Query Match      25.8%; Score 25; DB 6; Length 18;
Best Local Similarity 55.6%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      3 GOKATNFP 11
Db      10 GQEAVFYFP 18

RESULT 6
US-10-999-866-57
; Sequence 57, Application US/10999866
```

Publication No. US20050266004A1
GENERAL INFORMATION:
APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann
TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AND
FILE REFERENCE: CEN5042NP
CURRENT APPLICATION NUMBER: US/10/999,866
CURRENT FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: 60/527,794
PRIOR FILING DATE: 2003-12-08
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.3
SEQ ID NO 57
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(8)
OTHER INFORMATION: LC CDR3
US-10-999-866-57

Query Match 24.7% Score 24; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 NIPPT 13
Db 3 NTPPT 8

RESULT 7
US-10-507-275-17
Sequence 17, Application US/10507275
Publication No. US20050250166A1
GENERAL INFORMATION:
APPLICANT: Masai, Hisao
APPLICANT: Tamai, Katsuyuki
APPLICANT: Medical and Biological Laboratories Co., Ltd.
APPLICANT: Japan Science and Technology Agency
APPLICANT: Ginkgo Biomedical Research Institute Co., Ltd.
TITLE OF INVENTION: Cdc7-ASK Kinase Complex, Substrates of the Kinase Complex,
TITLE OF INVENTION: Specific Antibodies to the Substrates, and Screening Methods
TITLE OF INVENTION: Using the Same to Screen for Compounds Comprising Cdc7-ASK
FILE REFERENCE: 082368-001100US
CURRENT APPLICATION NUMBER: US/10/507,275
CURRENT FILING DATE: 2004-09-09
PRIOR APPLICATION NUMBER: JP 2002-067702
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: WO PCT/JP03/02918
PRIOR FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: an artificially
US-10-507-275-17

Query Match 24.7% Score 24; DB 6; Length 16;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 9 IFPYTAP 15
Db 1 MYPYDVP 7

RESULT 8
US-11-054-515-2617

Sequence 2617, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2617
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-2617

Query Match 24.2% Score 23.5; DB 7; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Oy 9 IFPYTAPCT 17
Db 6 LFPT-APLT 13

RESULT 9
US-10-952-535A-28
Sequence 28, Application US/1095535A
Publication No. US20050255113A1
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Messer, Anne
APPLICANT: Lecerc, Jean-Michel
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
FILE REFERENCE: INR-004CP
CURRENT APPLICATION NUMBER: US/10/952,535A
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: 60/146,047
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-952-535A-28

Query Match 23.7% Score 23; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 10 PPYTAP 15
: || |
Db 1 YPYDVP 6

RESULT 10
US-10-952-535A-43
; Sequence 43, Application US/10952535A
; Publication No. US20050255113A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Messer, Anne
; APPLICANT: Lecere, Jean-Michel
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
; TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
; FILE REFERENCE: INR-004CP
; CURRENT APPLICATION NUMBER: US/10/952,535A
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/146,047
; PRIOR FILING DATE: 1999-07-27
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-10-952-535A-43

Query Match 23.7%; Score 23; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PPYTAP 15
: || |
Db 1 YPYDVP 6

RESULT 11
US-11-010-748A-334
; Sequence 334, Application US/11010748A
; Publication No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOHL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 334
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 328
US-11-010-748A-334

Query Match 23.7%; Score 23; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KATNIPPY 12
: ||||
Db 1 KIOEIPFF 8

RESULT 12
US-11-010-748A-346
; Sequence 346, Application US/11010748A
; Publication No. US2005024421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOHL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 346
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 328
US-11-010-748A-346

Query Match 23.7%; Score 23; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KATNIPPY 12
: ||||
Db 1 KIOEIPFF 8

RESULT 13
US-11-158-848-41
; Sequence 41, Application US/11158848
; Publication No. US20050249703A1
; GENERAL INFORMATION:
; APPLICANT: Anne Dam Jensen
; TITLE OF INVENTION: Interferon gamma polypeptide variants
; FILE REFERENCE: 231u8410 - INFg variants
; CURRENT APPLICATION NUMBER: US/11/158,848
; CURRENT FILING DATE: 2005-06-22
; PRIOR APPLICATION NUMBER: US/10/116,273
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Tag
US-11-158-848-41

Query Match 23.7%; Score 23; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PPYTAP 15
: || |
Db 1 YPYDVP 6

RESULT 14

US-11-178-639-3
; Sequence 3, Application US/11178639
; Publication No. US20050250824A1
; GENERAL INFORMATION:
; APPLICANT: ONO Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A carboxylic acid derivative and a pharmaceutical
; TITLE OF INVENTION: composition containing the derivative as active
; TITLE OF INVENTION: ingredient
; FILE REFERENCE: Q60772
; CURRENT APPLICATION NUMBER: US/11/178,639
; CURRENT FILING DATE: 2005-07-12
; PRIOR APPLICATION NUMBER: US/09/623,913
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: JP 10-058444
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: JP 10-087560
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Influenza virus
; FEATURE:
; OTHER INFORMATION: hemagglutinin epitope
US-11-178-639-3

Query Match 23.7%; Score 23; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PPYTPAP 15
: || |
Db 1 YPYDVP 6

RESULT 15
US-11-137-671-4
; Sequence 4, Application US/11137671
; Publication No. US20050268350A1
; GENERAL INFORMATION:
; APPLICANT: Kirschbaum, Bernd
; Berglund, Erick
; Melstereimel, Michael
; Polites, Greg
; TITLE OF INVENTION: PURIFICATION OF HIGHER ORDER TRANSCRIPTION
; COMPLEXES FROM TRANSGENIC
; NON-HUMAN ANIMALS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HELLER, EHRMAN, WHITE & MCANULIFFE
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/137,671
; FILING DATE: 25-May-2005
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/849,243
; FILING DATE: 07-May-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 38005-0148
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)912-2000

TELEFAX: (202)912-2020
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-137-671-4

Query Match 23.7%; Score 23; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PPYTPAP 15
: || |
Db 1 YPYDVP 6

Search completed: December 12, 2005, 21:20:42
Job time : 3 secs

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OM protein - protein search, using SW model

Run on: December 12, 2005, 21:18:48 ; Search time 10.6667 Seconds
(without alignments)
162.366 Million cell updates/sec

Title: US-10-758-165a-9

Perfect score: 97

Sequence: 1 VDGQKATNIPFYAPGTK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_80:.*
2: pir1:.*
3: pir2:.*
4: pir3:.*
5: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	
1	28	28.9	15	2	153284	T-cell receptor be
2	27	27.8	15	2	PA00099	phenotypic variati
3	27	27.8	17	2	H49048	T-cell receptor be
4	27	27.8	18	2	A59137	protein P11 - gold
5	26	26.8	18	2	A61577	24k serine protein
6	25	25.8	15	2	D28587	T-cell receptor be
7	25	25.8	15	2	D28587	T-cell receptor be
8	25	25.8	16	2	B28587	T-cell receptor be
9	25	25.8	16	2	F53284	T-cell receptor be
10	24	24.7	14	2	B58502	36k kidney stone p
11	24	24.7	15	2	PH1318	Ig heavy chain D
12	24	24.7	17	2	S18534	hypothetical prote
13	24	24.7	18	2	A25941	Ig heavy chain J-H
14	23	23.7	12	2	C20907	Ig kappa-1 chain J
15	23	23.7	13	2	S23640	Ig kappa chain J s
16	23	23.7	13	2	C53275	Ig kappa-1 chain J
17	23	23.7	15	2	B45115	peptidylprolyl iso
18	23	23.7	16	2	S03532	Ig heavy chain J r
19	23	23.7	16	2	PS0383	Ig heavy chain J r
20	23	23.7	16	2	S38292	30k allergen - rye
21	23	23.7	18	2	P00072	T-cell receptor be
22	23	23.7	18	2	S20322	gluten - wheat
23	23	23.7	18	2	C56046	urinary tract ston
24	22	22.7	12	2	P00786	NADH2 dehydrogenas
25	22	22.7	13	2	S01904	H+-transporting tw
26	22	22.7	14	2	PH1306	Ig heavy chain D
27	22	22.7	15	2	PA0056	protein QF200002 -
28	22	22.7	15	2	PA0087	cytochrome c2 - fu
29	22	22.7	17	2	C84063	hypothetical prote

30	21	21.6	10	2	S71948	matrix metalloprot
31	21	21.6	10	2	A39745	endo-glucosylceram
32	21	21.6	12	2	A53524	ubiquinol-cytochro
33	21	21.6	14	2	PL0142	carbon-monoxide de
34	21	21.6	14	2	S59495	formate dehydrogen
35	21	21.6	15	2	B61457	alpha-glucosidase
36	21	21.6	15	2	S36893	ribosomal protein
37	21	21.6	16	2	E53284	T-cell receptor be
38	21	21.6	17	2	S50901	chlorophyll a/b-b1
39	21	21.6	18	2	S57518	T cell receptor be
40	21	21.6	18	2	S70612	alpha-macroglobuli
41	20	20.6	9	2	D48186	ATPase, RI subunit
42	20	20.6	9	2	S10784	enamelin 1 - bovin
43	20	20.6	13	2	B58533	CD61 homolog - cha
44	20	20.6	14	2	S22336	lipoxigenase (EC 1
45	20	20.6	14	2	G44957	photosystem II oxy

ALIGNMENTS

RESULT 1

T-cell receptor beta 2 chain J region, Ubeta2.7 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C:Accession: I53284

R:Harindranth, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A:Title: Evolutionarily conserved organization and sequences of germline diversity and J

A:Reference number: A53284; MUID:91342695; PMID:1678859

A:Accession: I53284

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <HAR>

A:Cross-references: UNIPARC:UPI0000115418; GB:S60737; NID:9233916; PIDN:AA19525.1; PID:

A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIPI:60747)

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 28.9%; Score 28; DB 2; Length 15;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTAAGTK 18
| | | | |
DB 5 YFAGTK 11

RESULT 2

phenotypic variation protein - fungus (Fusarium sporotrichoides) (fragment)

C:Species: Fusarium sporotrichoides

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: PA0099

R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich

A:Reference number: PA0051

A:Accession: PA0099

A:Molecule type: protein

A:Residues: 1-15 <CHO>

A:Cross-references: UNIPROT:Q7M4Y7; UNIPARC:UPI0000178405

Query Match

Best Local Similarity 27.8%; Score 27; DB 2; Length 15;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PFYAPGTK 17
| | | | |
DB 7 FKYSASGT 14

RESULT 3

H49048
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C/Accession: H49048
R/Stoud, M.; Kleidsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
Eur. J. Immunol. 22, 2413-2418, 1992
A/Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile
A/Accession: H49048; MUID:92387250; PMID:1187614
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-17 <STO>
A/Cross-references: UNIPARC:UPI0000176DF0
A/Experimental source: patient SS, IL-2R+ synovial T-cells
A/Note: sequence extracted from NCBI backbone (NCBIP:113270)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 27.8%; Score 27; DB 2; Length 17;
Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 ATNIFPYT 13
DB 8 AWTFFPYT 15

RESULT 4
A59137
Protein Pil - golden needle mushroom (fragment)
C/Species: Flammulina velutipes (golden needle mushroom)
C/Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C/Accession: A59137
R/Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
Submitted to the Protein Sequence Database, November 1999
A/Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr
A/Reference number: A59137
A/Accession: A59137
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-18 <SAK>
A/Cross-references: UNIPROT:Q7M4M6; UNIPARC:UPI000017CB27

Query Match 27.8%; Score 27; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 11 PYTAP 15
DB 2 PYTSP 6

RESULT 5
A61577
24K serine proteinase (EC 3.4.21.-) - Streptomyces fradiae (fragment)
C/Species: Streptomyces fradiae
C/Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C/Accession: A61577
R/Sinha, U.; Wolz, S.A.; Lad, P.J.
Int. J. Biochem. 23, 979-984, 1991
A/Title: Two new extracellular serine proteases from Streptomyces fradiae.
A/Reference number: A61577; MUID:9215439; PMID:11786859
A/Accession: A61577
A/Molecule type: protein
A/Residues: 1-18 <STN>
A/Cross-references: UNIPROT:Q7M198; UNIPARC:UPI000017AE13
C/Keywords: extracellular protein; hydrolase; serine proteinase

Query Match 26.8%; Score 26; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 5.7e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGKATNIFPY 12
DB 2 VGGTRAAQERFPW 13

RESULT 6
D28587
T-cell receptor beta-2 chain J-B2.5 segment - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C/Accession: D28587
R/Toyonaga, B.; Yoshikai, Y.; Vadász, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A/Title: Organization and sequences of the diversity, joining, and constant region genes
A/Reference number: A94081; MUID:86094276; PMID:3866244
A/Accession: D28587
A/Molecule type: DNA
A/Residues: 1-15 <TOY>
A/Cross-references: UNIPARC:UPI0000113CTC; GB:M14159; NID:g338852; PIDN:AAA60679.1; PID:5
C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 12 YTAGTK 18
DB 5 YFGRGTR 11

RESULT 7
F28587
T-cell receptor beta-2 chain J-B2.7 segment - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C/Accession: F28587
R/Toyonaga, B.; Yoshikai, Y.; Vadász, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A/Title: Organization and sequences of the diversity, joining, and constant region genes
A/Reference number: A94081; MUID:86094276; PMID:3866244
A/Accession: F28587
A/Molecule type: DNA
A/Residues: 1-15 <TOY>
A/Cross-references: UNIPARC:UPI0000113CTE; GB:M14159; NID:g338852; PIDN:AAA60681.1; PID:5
C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 12 YTAGTK 18
DB 5 YFGRGTR 11

RESULT 8
B28587
T-cell receptor beta-2 chain J-B2.3 segment - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C/Accession: B28587
R/Toyonaga, B.; Yoshikai, Y.; Vadász, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A/Title: Organization and sequences of the diversity, joining, and constant region genes
A/Reference number: A94081; MUID:86094276; PMID:3866244
A/Accession: B28587
A/Molecule type: DNA
A/Residues: 1-16 <TOY>
A/Cross-references: UNIPARC:UPI00002FDD6; GB:M14159; NID:g338852; PIDN:AAA60677.1; PID:5
C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 7.4e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 12 YTPAGTK 18
| | | | |
Db 6 YFGPCTR 12

RESULT 9

F53284
T-cell receptor beta 2 chain J region, Jbeta2.3 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: F53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A:Title: Evolutionarily conserved organization and sequences of germline diversity and J
A:Reference number: A53284; MUID:91342695; PMID:1678859
A:Accession: F53284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <HAR>
A:Cross-references: UNIPARC:UPI0000115415; GB:S60737; NID:9233916; PIDN:AA19522.1; PID:
A:Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIPI:60744)
C:Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 7.4e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTPAGTK 18
| | | | |
Db 6 YFGPCTR 12

RESULT 10

B58502
36K kidney stone protein - unidentified bacterium (fragment)
C:Species: unidentified bacterium
C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C:Accession: B58502
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: B58502
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <BIN>
A:Cross-references: UNIPARC:UPI000017A6D0
A:Experimental source: human kidney stone containing Ca ox.monoh dihyd, 1% struvite, CaF
A:Note: tentative identification of 8-Tyr and 9-Thr

Query Match 24.7%; Score 24; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 9.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIFPYT 13
| | | | |
Db 4 NIFGTT 9

RESULT 11

PH1318
Ig heavy chain DJ region (clone C527-121) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1318
R:Masserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1318
A:Molecule type: DNA

A:Residues: 1-15 <MAS>
A:Cross-references: UNIPARC:UPI000017C244
C:Keywords: heterotetramer; immunoglobulin

Query Match 24.7%; Score 24; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 7 TNIFPYTAGT 17
| | | | |
Db 5 TGFPYMGQGT 15

RESULT 12

S18534
hypothetical protein 7 (eryg 3' region) - Saccharopolyspora erythraea (fragment)
C:Species: Saccharopolyspora erythraea
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-Apr-1994
C:Accession: S18534
R:Haydock, S.F.; Dowson, J.A.; Dhillon, N.; Roberts, G.A.; Cortes, J.; Leadlay, P.F.
Mol. Gen. Genet. 230, 120-128, 1991
A:Title: Cloning and sequence analysis of genes involved in erythromycin biosynthesis in
methylintransferases.
A:Reference number: S18530; MUID:92079886; PMID:1840640
A:Accession: S18534
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-17 <HAY>
A:Cross-references: UNIPARC:UPI000017AD81; EMBL:X60379
A:Note: the authors translated the codon CTG for residue 12 as Gly

Query Match 24.7%; Score 24; DB 2; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 IFPYTAG 16
| | | | |
Db 1 IFPAVASC 8

RESULT 13

A25941
Ig heavy chain J-H1 region - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Jun-1998 #sequence_revision 05-Jun-1998 #text_change 23-Jul-1999
C:Accession: A25941; JH0666
R:Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A:Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody
A:Reference number: A25941; MUID:86287397; PMID:3016742
A:Accession: A25941
A:Molecule type: DNA
A:Residues: 1-18 <BRU>
A:Cross-references: UNIPARC:UPI0000114C27; GB:M13798; NID:9204707; PIDN:AAA1371.1; PID:
R:Lang, P.; Mochkat, R.
Gene 102, 261-264, 1991
A:Title: Immunoglobulin heavy-chain joining genes in the rat: comparison with mouse and
A:Reference number: JH0666; MUID:91340162; PMID:1908401
A:Accession: JH0666
A:Molecule type: DNA
A:Residues: 1-18 <LAN>
A:Cross-references: UNIPARC:UPI0000114C27; EMBL:X56791
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 24.7%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 PPTAPGT 17
| | | | |
Db 5 FDFWGPGR 12

RESULT 14

C20907
 Ig kappa-1 chain J3 region - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 16-Aug-1996
 C/Accession: C20907
 R/Emorine, L.; Max, E.E.
 Nucleic Acids Res. 11, 8877-8890, 1983
 A/Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple
 A/Reference number: A20907; MUID:64169523; PMID:6324107
 A/Accession: C20907
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-12 <EMO>
 A/Cross-references: UNIPARC:UPI000017C5CF
 C/Keywords: heterotetramer; immunoglobulin

Query Match 23.7%; Score 23; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PGTK 18
 ||||
 Db 5 PGTK 8

RESULT 15

S23640
 Ig kappa chain J segment (J-kappa-3) - human
 C/Species: Homo sapiens (man)
 C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
 C/Accession: S23640
 R/Huber, C.; Klobeck, H.G.; Zachau, H.G.
 Eur. J. Immunol. 22, 1561-1565, 1992
 A/Title: Ongoing V(kappa)-J(kappa) recombination after formation of a productive V(kappa)
 A/Reference number: S23637; MUID:92289816; PMID:1601042
 A/Accession: S23640
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-13 <HUB>
 A/Cross-references: UNIPARC:UPI0000116784; EMBL:X63370
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
 C/Keywords: heterotetramer; immunoglobulin

Query Match 23.7%; Score 23; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PGTK 18
 ||||
 Db 5 PGTK 8

Search completed: December 12, 2005, 21:24:31
 Job time : 10.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 21:17:48 ; Search time 61.6667 Seconds
(without alignments)
205.938 Million cell updates/sec

Title: US-10-758-165A-9
Perfect score: 97
Sequence: 1 VDGKATNIPFYAPGTK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 11298

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	35.1	17	046473_FELCA	046473 felis silve
2	32	33.0	8	070Y88_GLAMI	070Y88 platostoma
3	28.5	29.4	18	09TWL4_LUCCU	09TWL4 lucilia cup
4	27.5	28.4	16	08L1Y7_PLEBO	08L1Y7 plectonema
5	27	27.8	15	07M4Y7_FUSSE	07M4Y7 fusarium sp
6	27	27.8	18	07M4W6_FLAVE	07M4W6 flamulina
7	26	26.8	15	07S007_NEUCR	07S007 neurospora
8	26	26.8	18	07M198_STRFR	07M198 streptomyces
9	25	25.8	15	09UR63_EMENT	09UR63 emericella
10	24	24.7	14	07I4T5_9CRYP	07I4T5 rhodomonas
11	24	24.7	15	06S142_STRPY	06S142 streptococcus
12	24	24.7	17	06S1Y26_HORSE	06S1Y26 equus caball
13	23	23.7	8	05ZEY7_HUMAN	05ZEY7 homo sapien
14	23	23.7	10	09ZIB1_CLODI	09ZIB1 clostridium
15	23	23.7	14	P78359_HUMAN	P78359 homo sapien
16	23	23.7	14	P82435_TOBAC	P82435 nicotiana gl
17	23	23.7	15	05D4R7_9CYAN	05D4R7 oscillatoria
18	23	23.7	15	08SHM7_9PASS	08SHM7 secale cere
19	23	23.7	16	07M263_SECE	07M263 secale cere
20	23	23.7	16	08L1Y8_9CYAN	08L1Y8 oscillatoria
21	23	23.7	16	089560_HMYR	089560 human herpe
22	23	23.7	16	05R3U1_XENLA	05R3U1 xenopus lae
23	23	23.7	17	09PRU8_CHICK	09PRU8 gallus galli
24	23	23.7	18	07M4Q7_HUMAN	07M4Q7 homo sapien
25	23	23.7	18	07M1G0_WHEAT	07M1G0 triticum ae
26	22	22.7	8	059AB6_HUMAN	059AB6 homo sapien
27	22	22.7	10	071VN2_MOUSE	071VN2 mus musculu
28	22	22.7	12	07M2G3_VICFA	07M2G3 victoria faba
29	22	22.7	14	070Y94_GLAMI	070Y94 ocimum grat
30	22	22.7	15	07M4Z7_FUSSE	07M4Z7 fusarium sp
31	22	22.7	15	09TRE5_BOVIN	09TRE5 bos taurus

32	22	22.7	15	2	09TRN8_PIG	09TRN8 sus scrofa
33	22	22.7	16	2	070Y93_GLAMI	070Y93 platostoma
34	22	22.7	17	2	09K7Q4_BACHD	09K7Q4 bacillus ha
35	22	22.7	18	2	09TWL5_LUCCU	09TWL5 lucilia cup
36	22	22.7	18	2	09TRB6_PIG	09TRB6 sus scrofa
37	22	22.7	18	2	070Y99_GLAMI	070Y99 basilicum p
38	21.5	22.2	17	1	COG2_CARNA	P81609 carcinus ma
39	21.5	22.2	17	2	079E46_COXBU	079E46 coxiella bu
40	21	21.6	9	2	030790_BRWAM	030790 erwinia amy
41	21	21.6	9	2	065711_BEV	065711 beine virus
42	21	21.6	10	2	075SW3_ECOLI	075SW3 escherichia
43	21	21.6	10	2	07MOK7_RHOSO	07MOK7 rhodococcus
44	21	21.6	10	2	09QVE9_SMURI	09QVE9 mus sp. pro
45	21	21.6	11	2	08KTN1_CANTP	08KTN1 candidatus

ALIGNMENTS

```

RESULT 1
046473_FELCA PRELIMINARY; PRT; 17 AA.
ID 046473_FELCA PRELIMINARY; PRT; 17 AA.
AC 046473;
DT 01-JUN-1998 (TRENBLREL. 06, Created)
DT 01-JUN-1998 (TRENBLREL. 06, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Lactase dehydrogenase A (Fragment).
GN Name-LDHA;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=domesticus;
RX MEDLINE=97141918; PubMed=8988168;
RA Lyons L.A., Laughlin T.F., Copeland N.G., Jenkins N.A., Womack J.E.,
O'Brien S.J.;
RT "Comparative anchor tagged sequences (CATS) for integrative mapping of
RT mammalian genomes.";
RL Nat. Genet. 15:47-56(1997).
DR EMBL; AF012095; AAC00072.2; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2018 MM; E47943B2E187C1FC CRC64;
Query Match 35.1%; Score 34; DB 2; Length 17;
Best Local Similarity 46.2%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 3 GOKATNIPFYAP 15
Db 3 GORNVNIFKFIIP 15
ID 070Y88_GLAMI PRELIMINARY; PRT; 8 AA.
AC 070Y88;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN Name=rp16;
OS Platostoma fimbriatum.
OC Chlorofila.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Lamiales; Nepentoidae; Ocimeae; Platostoma.
OX NCBI_TaxID=204168;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
 RA Paton A., Springle D.A., Stude S., Otleno D., Grayer R., Harley M.M.,
 RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
 RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
 based on three plastid DNA regions";
 RL Mol. Phylogenet. Evol. 31:277-299(2004).
 DR EMBL, AJ505368; CAD45489.1; -, Genomic_DNA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 789 MW; 86786772D1BB4772 CRC64;

Query Match 33.0%; Score 32; DB 2; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2.2e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAPG 16
 Db 2 PYTVP 7

RESULT 3

Q9TWA4_LUCCU
 ID Q9TWA4_LUCCU PRELIMINARY; PRT; 18 AA.
 AC Q9TWA4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE 25 kDa chymotrypsin-like enzyme (Fragment)
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Lucilia.
 OX NCBI_Taxid=7375;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95219141; PubMed=7704304;
 RA Casu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Ridding G.A.,
 RA Tellam R.L.;
 RT "Excretory/secretory chymotrypsin from *Lucilia cuprina*: purification,
 RT enzymatic specificity and amino acid sequence deduced from mRNA.";
 RL Insect Mol. Biol. 3:201-211(1994).
 SQ SEQUENCE 18 AA; 1922 MW; 352EB0729B126511 CRC64;

Query Match 29.4%; Score 28.5; DB 2; Length 18;
 Best Local Similarity 58.3%; Pred. No. 1.9e+03;
 Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 2 DQKAT-NIRPY 12
 Db 3 NQGEATVGQFPY 14

RESULT 4

Q8LIY7_PLEBO
 ID Q8LIY7_PLEBO PRELIMINARY; PRT; 16 AA.
 AC Q8LIY7;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Proteolysis-inducing tag (Fragment).
 OS *Plectonema boryanum*.
 OC Bacteria; Cyanobacteria; Oscillatoriales; Leptolyngbya.
 OX NCBI_Taxid=1184;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=UTEX 485;
 RX MEDLINE=21970088; PubMed=11972342; DOI=10.1093/nar/30.9.2025;
 RA Williams K.P.;
 RT "Descent of a split RNA."
 RL Nucleic Acids Res. 30:2025-2030(2002).
 DR EMBL, AY082652; AA003311.1; -, Genomic_DNA.

FT NON_TER 1
 SQ SEQUENCE 16 AA; 1640 MW; 60FE5985B9B00982 CRC64;
 Query Match 28.4%; Score 27.5; DB 2; Length 16;
 Best Local Similarity 53.8%; Pred. No. 2.5e+03;
 Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 6 ATNIPY---TAP 15
 Db 1 ANNIVFPARKTAP 13

RESULT 5

Q7M4Y7_FUSSP
 ID Q7M4Y7_FUSSP PRELIMINARY; PRT; 15 AA.
 AC Q7M4Y7;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Phenotypic variation protein (Fragment).
 OS *Fusarium sporotrichioides*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; *Fusarium*.
 OX NCBI_Taxid=5514;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Chow I.P., Fukaya N., Sugiyura Y., Ueno Y., Tabuchi K., Tsugita A.;
 RL Submitted (OCT-1994) to the PIR data bank.
 DR PIR; PA0099; PA0099.
 FT NON_TER 1
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1648 MW; 4CAFAF966995807 CRC64;

Query Match 27.8%; Score 27; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 2.8e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PPTAPGT 17
 Db 7 FKYSASGT 14

RESULT 6

Q7M4W6_FLAVE
 ID Q7M4W6_FLAVE PRELIMINARY; PRT; 18 AA.
 AC Q7M4W6;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Protein P11 (Fragment).
 OS *Flammulina velutipes*.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Tricholomataceae; *Flammulina*.
 OX NCBI_Taxid=38945;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Sakamoto Y., Ando A., Tamai Y., Miura K.;
 RL Submitted (NOV-1999) to the PIR data bank.
 DR PIR; A59137; A59137.
 FT NON_TER 1
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1956 MW; FB0434B0AF005AEC CRC64;

Query Match 27.8%; Score 27; DB 2; Length 18;
 Best Local Similarity 80.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PYTAP 15
 Db 2 PYTSP 6

RESULT 7

```

Q7S007_NEUCR PRELIMINARY; PRT; 15 AA.
ID Q7S007
AC Q7S007
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU09752.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
ON NCB1_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Gajagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-Y., Smitnov S., Purcell S., Rehman B.,
RA Elvine T., Engels R., Wang S., Nielsen C.B., Butler J., Endritzki M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Seitzemikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Koche G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kanwaseelis M., Mauceli E., Bielke C., Rudd S., Fishman D.,
RA Krysstofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Selter S., Dunlap J., Radford A., Aramayo R.,
RA Nerviig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000580; EAA28619.1; -; Genomic DNA.
SQ SEQUENCE 15 AA; 1832 MW; 012D0180A8C7089D CRC64;

Query Match 26.8%; Score 26; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIPPYT 13
Db 2 NVFEXT 7

RESULT 8
Q7M198_STRFR PRELIMINARY; PRT; 18 AA.
ID Q7M198
AC Q7M198;
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE 24k serine proteinase (EC 3.4.21.-) (Fragment).
OS Streptomyces fradiae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
ON NCB1_TaxID=1906;
RN [1]
RP PROTEIN SEQUENCE.
RC MEDLINE=92155439; PubMed=178659; DOI=10.1016/0020-711X(91)90133-8;
RA Silha U., Moitz S.A., Lad P.J.;
RT "Two new extracellular serine proteases from Streptomyces fradiae.";
RL Int. J. Biochem. 23:979-984(1991).
DR PIR; A61577; A61577.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2004 MW; 6D6DA167845934A5 CRC64;

Query Match 26.8%; Score 26; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 5e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 1 VDQKATNIPY 12
Db 2 VGTTRAAQEPFW 13

RESULT 9
Q9UR63_EMENI PRELIMINARY; PRT; 15 AA.
ID Q9UR63
AC Q9UR63;
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE Beta-D-FRUCTOFURANOSIDE FRUCTOHYDROLASE 60 kDa high molecular weight
DE isoform (EC 3.2.1.26) (Fragment).
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
ON NCB1_TaxID=162425;
RN [1]
RP PROTEIN SEQUENCE.
RC MEDLINE=96409246; PubMed=8814228; DOI=10.1016/0167-4838(96)00073-8;
RA Chen J.S., Saxton J., Hemming F.W., Peberdy J.F.;
RT "Purification and partial characterization of the high and low
RT molecular weight form (S- and F-form) of invertase secreted by
RT Aspergillus nidulans.";
RL Biochim. Biophys. Acta 1296:207-218(1996).
DR GO; GO:0004564; F-beta-fructofuranosidase activity; IEA.
SQ SEQUENCE 15 AA; 1588 MW; 2C992B42211366BB CRC64;

Query Match 25.8%; Score 25; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAP 15
Db 10 PYTSP 14

RESULT 10
Q714T5_9CRYP PRELIMINARY; PRT; 14 AA.
ID Q714T5
AC Q714T5;
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE tmRNA processing tag (Fragment).
OS Name=ssrA;
GN Name=ssrA;
OS Rhodomonas salina.
OC Chloroplast.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
ON NCB1_TaxID=52970;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CCMP1319;
RC PubMed=14681369; DOI=10.1093/nar/gkh102;
RA Guenneau de Novoa P., Williams K.P.;
RT "The tmRNA website: reductive evolution of tmRNA in plastids and other
RT endosymbionts.";
RL Nucleic Acids Res. 32:D104-D108(2004).
DR EMBL; AF550355; AAQ12671.1; -; Genomic DNA.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1528 MW; D995F9B3698210B9 CRC64;

Query Match 24.7%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 8.3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 ATNIPPYT 13
Db 1 ANNVIFPS 8

RESULT 11

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069142_STRPY
 ID 069142_STRPY PRELIMINARY; PRT; 15 AA.
 AC 069142;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Protein SIC (Fragment).
 GN Name=SIC;
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=API;
 RX MEDLINE=98298075; PubMed=9632622;
 RA Berge A., Rasmussen M., Bjorck L.;
 RT "Identification of an insertion sequence located in a region encoding
 RT virulence factors of Streptococcus pyogenes.";
 RL Infect. Immun. 66:3449-3453 (1998).
 DR EMBL; AF064540; AAC38769.1; -; Genomic_DNA.
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1552 MW; 87655FEF847401FF CRC64;

Query Match 24.7%; Score 24; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 8.9e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 NIPPYTAGT 17
 : : | | | |
 Db 6 SVTPPTSAT 15

RESULT 12
 ID 065Y26_HORSE PRELIMINARY; PRT; 17 AA.
 AC 065Y26;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Asparagine-linked glycosylation 8 homolog (Fragment).
 GN Name=ALG8;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hasegawa T., Sato F., Tozaki T., Hirota K.;
 RT "Fine mapping of equine chromosomes corresponding to HSA11.";
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB167785; BAD44704.1; -; Genomic_DNA.
 FT NON_TER 1
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1907 MW; 24AB4757508FF8FC CRC64;

Query Match 24.7%; Score 24; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 1e+04;
 Matches 5; Conservative 3; Mismatches 0; Indels 2; Gaps 1;

QY 8 NIFP--YTPA 15
 : : | | | |
 Db 6 SLFPLFLTPA 15

RESULT 13
 ID 05ZEY7_HUMAN PRELIMINARY; PRT; 8 AA.
 AC 05ZEY7;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Taxol resistance associated gene 3 (Fragment).

GN Name=CSAG2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Dominguez O., Lombardía L.;
 RT "DNA probes built and sequenced for microarray hybridisations.";
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ844639; CAH59758.2; -; mRNA.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 742 MW; 9975B87321A86772 CRC64;

Query Match 23.7%; Score 23; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PGTK 18
 : : | | | |
 Db 2 PGTK 5

RESULT 14
 ID 09ZIB1_CLODI PRELIMINARY; PRT; 10 AA.
 AC 09ZIB1;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE Toxin B (Fragment).
 GN Name=ToxB;
 OS Clostridium difficile.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1496;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=8864;
 RA Dodson A.P., Borriello S.P.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF035716; AAD02038.1; -; Genomic_DNA.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1120 MW; 913DA042C736DDC1 CRC64;

Query Match 23.7%; Score 23; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PYTA 14
 : : | | | |
 Db 1 PYTA 4

RESULT 15
 ID P78359_HUMAN PRELIMINARY; PRT; 14 AA.
 AC P78359;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NF-kappa-B transcription factor p65 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Unbiblical vein;
 RA Remacle J.E., Byrs R., Pype S., Nelles L., Huybrecock D.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U88316; AAB48487.1; -; mRNA.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1662 MW; 5E30458F8262F357 CRC64;

Query Match 23.7%; Score 23; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 IFPYTAP 15
||| : |
Db 8 IFPQSQP 14

Search completed: December 12, 2005, 21:23:54
Job time : 63.6667 secs

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CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IgE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IgE.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGOKATNIFPYTAPGTK 18
1 VDGOKATNIFPYTAPGTK 18
Db

RESULT 2
AAV79995
ID AAV79995 standard; protein; 312 AA.
XX
AC AAV79995;
XX
DT 15-MAY-2000 (first entry)
XX

DE Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.
XX

KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KW antibody; allergy; allergic disease; immunisation; anti-allergic;
KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX

OS Canis sp.
XX

PN WO967293-A1.
XX

PD 29-DEC-1999.
XX

PF 21-JUN-1999; 99WO-US013959.
XX

PR 20-JUN-1998; 98US-00100287.
XX

PA (UNBI-) UNITED BIOMEDICAL INC.
XX

PI Wang CY, Walfield AM;
XX

XX WPI; 2000-160578/14.
XX

PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy.
XX

PS Example 1; Page 66-68; 155pp; English.
XX

XX The present invention describes immunoglobulin E (IgE)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
CC a target effector site on the epsilon-heavy chain of IgE, and so
CC preventing triggering and activation of mast cells and basophils and
CC downregulation of IgE synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against IgE-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe (non-
CC anaphylactogenic) antibodies. AAV79994 to AAV80084 represent amino acid
CC sequences used in the exemplification of the present invention
XX

SO Sequence 312 AA;

Query Match 100.0%; Score 97; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VDGOKATNIFPYTAPGTK 18
1 VDGOKATNIFPYTAPGTK 18
Db 48 VDGOKATNIFPYTAPGTK 65

RESULT 3
AAW23067
ID AAW23067 standard; protein; 417 AA.
XX

AC AAW23067;
XX

DT 30-JUN-2005 (revised)
XX

DT 16-JUN-2005 (revised)
XX

DT 19-FEB-1998 (first entry)
XX

DE Canine IgE heavy chain constant region (exon 1-4 product).
XX
XX IgE; immunoglobulin; antibody; heavy chain constant region; allergy;
KW hypersensitivity; therapy; dog; antisense; immunomodulation.
XX

OS Canis familiaris.
XX

EH Key Location/Qualifiers
XX

FT Misc-difference 55 /note= "encoded by ACC"
XX

FT Misc-difference 56 /note= "encoded by TAC"
XX

FT Misc-difference 67 /note= "encoded by GCC"
XX

FT Misc-difference 83 /note= "encoded by NNT"
XX

FT Misc-difference 174 /note= "encoded by GGN"
XX

FT Misc-difference 175 /note= "encoded by NNG"
XX

FT Misc-difference 176 /note= "encoded by TGN"
XX

FT Misc-difference 203 /note= "encoded by TCC"
XX

FT Misc-difference 204 /note= "encoded by GAC"
XX

PN WO9730156-A2.
XX

PD 21-AUG-1997.
XX

PF 14-FEB-1997; 97WO-US002322.
XX

PR 14-FEB-1996; 96US-00601197.
XX

PA (IDEX-) IDEXX LAB INC.
XX

PI Wermer B, Harris RA, Steifring AE;
XX

XX WPI; 1997-425031/39.
XX

DR N-PSDB; AAT79278.
XX

PT Isolated canine IgE heavy chain constant region DNA - useful to develop
PT products for treatment of canine allergies and for immunomodulation in
PT dogs.
XX

PS Disclosure; Page 35-39; 59pp; English.
XX

XX This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IgE
CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,
CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant
CC peptides encoded by exons 1-6 can be produced in eukaryotic or
CC prokaryotic cells. Such peptides, and antibodies raised against them, are
CC used in methods to treat the manifestation of allergy in dogs, e.g. to
CC treat type I immediate hypersensitivity, and for immunomodulation

CC Revised record issued on 30-JUN-2005 : Typo in comments
XX
SQ Sequence 417 AA;

SQ Sequence 417 AA;

Query Match	100.0%	Score 97	DB 2:	Length 417
Best Local Similarity	100.0%	Pred. No.	1.7e-07	
Matches 18	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```
QY      1 VDGQKATNIFPYTAPGK 18
          |||||
Db      141 VDGQKATNIFPYTAPGK 158
```

RESULT 4
AAR97753
ID AAR97753 standard; protein; 426 AA
vv

AC AAR97753 ;

DT 28-AUG-1996 (first entry)

DE Canine IgE.

KW IGE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.

OS **Canis familiaris.**

PN WO9614867-A1.

PD 23-MAY-1996.

PF 03-NOV-1995; 95WO-US013795.

PR 09-NOV-1994; 94US-00336583.

XXXX

PA (MERI) MERCK & CO INC.

PI Hollis GF, Patel M

DR WPI; 1996-277321/28.

DR N-PSDB; AAT29824.

PT New DNA encoding canine IGE and IGA - useful in vaccines, anti-sense therapy, assays, drug screening, etc.

PS Claim 11; Page 29-30; 49pp; English.

CC The canine IgE amino acid sequence (AA9397753) was deduced from an
CC isolated gene (AA292824) obtd. from a canine liver DNA library. The
CC cloning of the IgE gene allows prodn. of large quantities of recombinant
CC IgE using bacterial, yeast, mammalian, insect or viral systems. The IgE
CC can be used in drug development (e.g. small molecule screening, assay
CC development and anti-IgE antibody generation). Fragments of IgE can
CC be used in vaccines or to prevent IgE-mediated hypersensitivity. The new
CC sequence information permits targeted modulation of IgE-mediated immune
CC responses

SQ Sequence 426 AA;

Query Match	100.0%	Score 97	DB 2	Length 426
Best Local Similarity	100.0%	Pred. NO. 1.7e-07		
Matches 18	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```

OY      1 VDGKATNIFPYTAGTK 18
         |||||
Db      146 VDGKATNIFPYTAGTK 163

```

RESULT 5
ABP96583
ID ABP96583 standard; protein; 426 AA

AC ABP96583 ;

DT 28-MAY-2003 (first entry)

Dog IgE heavy chain amino acid sequence SEQ ID NO:28.

KW Immunoglobulin E; vaccine; IgE-cytotoxic T lymphocyte response;
 KW immune response; major histocompatibility complex; MHC; immunogenic;
 KW anti-allergic; antihistaminic; immunosuppressive; vasotropic; cytostatic
 KW dermatological; antiinflammatory; IgE-mediated condition; food allergy
 KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
 KW allergic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
 KW ulceraria hives.

OS Canis familiaris

PN WO2003015716-A2.

PD 27-FEB-2003

PF 08-AUG-2002; 2002WO-US026986.

PR 13-AUG-2001; 2001US-0312120P.

PA (IGET-) IGE THERAPEUTICS INC.

PI Chen SA, Yang Y, Barankiewicz T, Chen Z; PI

WPI; 2003-268242/26.

PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
PT against IGE, by identifying peptide eliciting CTL response to IGE
PT peptides naturally presented by major histocompatibility complex class I
PT protein.

PS Example 7; Page 152-154; 187pp; English

The present invention describes a method (M1) for identifying peptide that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin E (IgE), comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to naturally processed and presented IGE peptides, where a peptide that induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (M1), (C2) comprising at least one isolated polynucleotide encoding (I); and (C3) comprising antigen-presenting cells that recognise at least one (I). Where C1-3 are able to bind to at least one MHC class I molecule and to elicit in a mammal a CTL response to naturally processed and presented IGE peptides, C1-3 have antiallergic, antiasthmatic, immunosuppressive, vasotropic, dermatological, antiinflammatory and cytostatic activities, and can be used as inducers of a CTL response against IGE, and in vaccines. C1-3 can be used for modulating an IGE-mediated condition in a mammal. C1-3 are useful for modulating an IGE-mediated condition such as IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are useful for treating atopic hypersensitivity conditions (such as allergic rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-atopic hypersensitivity conditions (such as anaphylaxis, and urticaria hives). The present sequence represents an IGE heavy chain amino acid sequence, which is given in an example from the present invention

SQ Sequence 426 AA;

Query Match	100.0%	Score 97;	DB 6;	Length 426;
Best Local Similarity	100.0%;	Pred. No. 1.7e-07;		
Matches 18; Conservative	0;	Mismatches	0;	Gaps 0

OY		1	V	D	G	K	A	T	N	I	F	P	Y	A	P	G	T	K	18
Db		146	V	D	G	K	A	T	N	I	F	P	Y	A	P	G	T	K	163

```

RESULT 6
ADRI0610
ID   ADRI0610 standard; peptide; 18 AA.
XX
XX
AC   ADRI0610;
XX
DT   21-OCT-2004 (first entry)
XX
DE   Cat IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.
XX
XX   Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KM   anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX   cat.
XX   Felis catus.
OS   WO2004065936-A2.
XX
XX   05-AUG-2004.
XX
XX   15-JAN-2004; 2004WO-US003566.
XX
XX   16-JAN-2003; 2003US-0440472P.
XX
XX   (UYNC-) UNIV NORTH CAROLINA STATE.
XX
XX   Hammerberg B;
XX
XX   WPI; 2004-593545/57.
XX
XX   Novel antibody that specifically binds to mammalian IGE epitope, useful
PT   for testing an allergen reactivity of IGE sample, detecting mammalian IGE
XX   or treating asthma or anaphylactic shock.
XX
XX   Example 6; Page 9; 14pp; English.
XX
XX   The present invention relates to a novel monoclonal antibody (I) that
CC   specifically binds to a mammalian IGE epitope, where the epitope is
CC   between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC   (I) is useful for testing an allergen reactivity of an IGE sample. The
CC   allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC   and corn allergens. The sample is a biological sample collected from a
CC   dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC   treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC   antibodies recognise epitopes on canine IGE corresponding to amino acid
CC   residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC   canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
CC   cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC   3.76 were observed to have good cross-reactivity with the epsilon-chain
CC   of IGE from cat and horse, but did not exhibit cross-reactivity with
CC   either pig or human epsilon-chains of IGE. The present sequence is the
CC   cat IGE 3.76 recognition site.
XX
XX
SQ   Sequence 18 AA;
XX
XX
Query Match      89.7%; Score 87; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY   1 VDGOKATNIFPYTPAG 16
    1 VDGOKATNIFPYTPAG 16
DB   1 VDGOKATNIFPYTPAG 16
XX
XX
RESULT 7
ADG73237
ID   ADG73237 standard; protein; 431 AA.
XX
XX
AC   ADG73237;
XX
XX
DT   11-MAR-2004 (first entry)
XX
XX
DE   Cat immunoglobulin E (IGE) constant region.
XX

```

```

XX
XX   antiAllergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;
KM   immune response; IGE-mediated response; allergy; cat; constant region.
XX
XX   Felis catus.
OS   US2003216565-A1.
XX
XX   20-NOV-2003.
XX
XX   07-APR-2003; 2003US-00409772.
XX
XX   07-JAN-1999; 99US-0115033P.
XX
XX   07-JAN-2000; 2000US-00479614.
XX
XX   (MCCA/) MCCAL, C.
PA   (WEBER/) WEBER E.
XX
XX   Mccall C, Weber E;
XX
XX   WPI; 2004-010802/01.
XX
XX   N-PSDB; ADG73236.
XX
XX   New isolated nucleic acid molecule encoding a portion of a feline IGE
PT   heavy chain protein, useful for treating and/or eliciting feline immune
XX   responses for IGE-mediated responses, such as allergies.
XX
XX   Claim 12; SEQ ID NO 14; 44pp; English.
XX
XX
CC   The invention describes an isolated nucleic acid molecule (II) encoding a
CC   portion of a feline IGE heavy chain protein. The methods and compositions
CC   of the present invention are useful for eliciting feline immune responses
CC   for and/or treating IGE-mediated responses, such as allergies. This is
CC   the amino acid sequence of a cat immunoglobulin E (IGE) constant region.
XX
XX
SQ   Sequence 431 AA;
XX
XX
Query Match      89.7%; Score 87; DB 8; Length 431;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY   1 VDGOKATNIFPYTPAG 16
    1 VDGOKATNIFPYTPAG 16
DB   151 VDGOKATNIFPYTPAG 166
XX
XX
RESULT 8
ABP96580
ID   ABP96580 standard; protein; 496 AA.
XX
XX
AC   ABP96580;
XX
XX
DT   28-MAY-2003 (first entry)
XX
XX
DE   Cat IGE heavy chain amino acid sequence SEQ ID NO:25.
XX
XX   Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
KM   immune response; major histocompatibility complex; MHC; immunogenic;
KM   antiAllergic; antiasthmatic; immunosuppressive; vasodilator; cytostatic;
KM   dermatological; antiinflammatory; IGE-mediated condition; food allergy;
KM   atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KM   atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
XX   urticaria hives.
XX
XX   Felis catus.
OS   WO2003015716-A2.
XX
XX   27-FEB-2003.
XX
XX   08-AUG-2002; 2002WO-US026986.
XX
XX   13-AUG-2001; 2001US-0312120P.
XX

```

[illegible][illegible]

PA (MCCA/) MCCA.L. C.
PA (WEBE/) WEBER E.
XX
XX Mccall C, Weber E;
XX
DR WPI; 2003-391997/37.
DR N-PSDB; ABX95713.
XX
XX
PT New nucleic acid molecule encoding feline immunoglobulin E (IgE) heavy or
PT light chain protein, useful for treating feline IGE-mediated responses
PT e.g. allergies, parasitic infections or neoplasia.
XX
PS Claim 1; Page 24-25; 45pp; English.
XX
XX The present invention relates to the isolation of feline immunoglobulin E
CC (1GE) kappa light chain and IGE epsilon heavy chain proteins, and the
CC polynucleotide sequences encoding them. The sequences of the invention
CC are useful for treating feline IGE-mediated immune responses (e.g.
CC allergies, parasitic infections or neoplasia), in vaccine technology,
CC small molecule/antibody technology, molecular biology, and various
CC immunological techniques related to feline IGE and its functions. The
CC present sequence represents feline IGE epsilon heavy chain #1
XX
SQ Sequence 496 AA;
XX
Query Match 89.7%; Score 87; DB 6; Length 496;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VDGQKATNIFPYTAPG 16
Db 216 VDGQKATNIFPYTAPG 231
XX
RESULT 11
ADG73251
ID ADG73251 standard; protein; 496 AA.
XX
AC ADG73251;
XX
DT 11-MAR-2004 (first entry)
XX
DE Cat partial immunoglobulin E (IGE) heavy chain #2.
XX
KM antiallergic; IGE-modulator; vaccine; feline; IGF; immunoglobulin E;
KM immune response; IGE-mediated response; allergy; cat; heavy chain.
XX
OS Felis catus.
XX
PN US2003216565-A1.
PD 20-NOV-2003.
XX
PF 07-APR-2003; 2003US-00409772.
XX
PR 07-JAN-1999; 99US-0115033P.
PR 07-JAN-2000; 2000US-00479614.
XX
PA (MCCA/) MCCA.L. C.
PA (WEBE/) WEBER E.
XX
XX Mccall C, Weber E;
XX
XX WPI; 2004-010802/01.
DR N-PSDB; ADG73250.
XX
XX New isolated nucleic acid molecule encoding a portion of a feline IGE
PT heavy chain protein, useful for treating and/or eliciting feline immune
PT responses for IGE-mediated responses, such as allergies.
PS Claim 8; SEQ ID NO 29; 44pp; English.
XX
XX The invention describes an isolated nucleic acid molecule (I) encoding a

CC portion of a feline IGE heavy chain protein. The methods and compositions
CC of the present invention are useful for eliciting feline immune responses
CC for and/or treating IGE-mediated responses, such as allergies. This is
CC the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy
CC chain.
XX
SQ Sequence 496 AA;
XX
Query Match 89.7%; Score 87; DB 8; Length 496;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VDGQKATNIFPYTAPG 16
Db 216 VDGQKATNIFPYTAPG 231
XX
RESULT 12
ADG73225
ID ADG73225 standard; protein; 496 AA.
XX
AC ADG73225;
XX
DT 11-MAR-2004 (first entry)
XX
DE Cat partial immunoglobulin E (IGE) heavy chain #1.
XX
KM antiallergic; IGE-modulator; vaccine; feline; IGF; immunoglobulin E;
KM immune response; IGE-mediated response; allergy; cat; heavy chain.
XX
OS Felis catus.
XX
PN US2003216565-A1.
PD 20-NOV-2003.
XX
PF 07-APR-2003; 2003US-00409772.
XX
PR 07-JAN-1999; 99US-0115033P.
PR 07-JAN-2000; 2000US-00479614.
XX
PA (MCCA/) MCCA.L. C.
PA (WEBE/) WEBER E.
XX
XX Mccall C, Weber E;
XX
XX WPI; 2004-010802/01.
DR N-PSDB; ADG73224.
XX
XX New isolated nucleic acid molecule encoding a portion of a feline IGE
PT heavy chain protein, useful for treating and/or eliciting feline immune
PT responses for IGE-mediated responses, such as allergies.
XX
PS Claim 8; SEQ ID NO 2; 44pp; English.
XX
XX The invention describes an isolated nucleic acid molecule (I) encoding a
CC portion of a feline IGE heavy chain protein. The methods and compositions
CC of the present invention are useful for eliciting feline immune responses
CC for and/or treating IGE-mediated responses, such as allergies. This is
CC the amino acid sequence of a partial cat immunoglobulin E (IGE) heavy
CC chain.
XX
SQ Sequence 496 AA;
XX
Query Match 89.7%; Score 87; DB 8; Length 496;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VDGQKATNIFPYTAPG 16
Db 216 VDGQKATNIFPYTAPG 231

RESULT 13
ABP96584
ID ABB96584 standard; protein; 577 AA.
XX
AC ABB96584;
XX
DT 28-MAY-2003 (first entry)
XX
DE Duckbilled platypus IGE heavy chain amino acid sequence SEQ ID NO:29.
XX
KW Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
KW immune response; major histocompatibility complex; MHC; immunogenic;
KW antiallergic; antiallergic; immunosuppressive; vasotropic; cytostatic;
KW dermatological; antiinflammatory; IGE-mediated condition; food allergy;
KW atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KW atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
KW urticaria hives.
XX
OS Ornithorhynchus anatinus.
XX
PN MO2003015716-A2.
XX
PD 27-FEB-2003.
XX
PF 08-AUG-2002; 2002MO-US026986.
XX
PR 13-AUG-2001; 2001US-0312120P.
XX
PA (IGET-) IGE THERAPEUTICS INC.
XX
PI Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX
DR WPI; 2003-268242/26.
XX
PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
PT against IGE, by identifying peptide eliciting CTL response to IGE
PT peptides naturally presented by major histocompatibility complex class I
PT protein.
XX
PS Example 7; Page 154-157; 187pp; English.
XX
CC The present invention describes a method (M1) for identifying peptides
CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
CC E (IGE), comprising providing a test peptide (T) suspected of being able
CC to bind to major histocompatibility complex (MHC) class I molecule, and
CC evaluating (T) for ability to elicit in a mammal a CTL response to
CC naturally processed and presented IGE peptides, where a peptide that
CC induces such a response is identified. Also described are compositions:
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
CC (C2) comprising at least one isolated polynucleotide encoding (I); and
CC (C3) comprising antigen-presenting cells that recognise at least one (I).
CC Where C1-3 are able to bind to at least one MHC class I molecule and to
CC elicit in a mammal a CTL response to naturally processed and presented
CC IGE peptides. C1-3 have antiallergic, antiallergic, immunosuppressive,
CC vasotropic, dermatological, antiinflammatory and cytostatic activities,
CC and can be used as inducers of a CTL response against IGE, and in
CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a
CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as
CC IGE-mediated atopic hypersensitivity condition. IGE-mediated non-atopic
CC hypersensitivity condition. IGE myeloma in a mammal. Preferably, C1-3 are
CC useful for treating atopic hypersensitivity conditions (such as allergic
CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
CC hives). The present sequence represents an IGE heavy chain amino acid
CC sequence, which is given in an example from the present invention
XX
SQ Sequence 577 AA;
XX
Query Match 75.3%; Score 73; DB 6; Length 577;
Best Local Similarity 86.7%; Pred. No. 0.0025;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VDGKATNIPFYTAP 15

DB 295 VDGKATNIPFYTAP 309
||||| :|||||
RESULT 14
AAB06204
ID AAB06204 standard; protein; 343 AA.
XX
AC AAB06204;
XX
DT 22-NOV-2000 (first entry)
XX
DE Platypus IGE heavy chain constant regions 2, 3 and 4.
XX
KW Platypus; immunoglobulin E; IGE; vaccination; infection; allergy; asthma;
KW eczema; immunogenic peptide.
XX
OS Ornithorhynchus anatinus.
XX
PN Key Location/Qualifiers
XX
FT Misc-difference 1..343
FT /label= OTHER
FT /note= "Xaa=unknown"
XX
PD WO200025722-A2.
XX
PF 11-MAY-2000.
XX
PR 21-OCT-1999; 99WO-SE001896.
XX
PR 02-NOV-1998; 98US-0106652P.
XX
PR 22-SEP-1999; 99US-00401636.
XX
PA (RESI-) RESISTENTIA PHARM AB.
XX
PI Hellman LT;
XX
DR WPI; 2000-365342/31.
XX
PT Immunogenic polypeptides useful for preventing the harmful effects of
PT Immunoglobulin E in mammals.
XX
PS Disclosure; Fig 2; 50pp; English.
XX
CC The present sequence is an immunogenic peptide consisting of the heavy
CC chain constant regions 2, 3 and 4 of the platypus IGE. It was used to
CC construct a number of immunogenic peptides which consisted of regions of
CC IGE from different mammals, which appear to cause a stronger polyclonal
CC anti-self IGE response than peptides consisting of the same regions from
CC one mammal. Immunogenic peptides, particularly those consisting of
CC different heavy chain constant regions, can be used for vaccination in
CC humans, against bacterial and viral infections and allergies, such as
CC asthma, fur, pollen and food allergies and eczema
XX
SQ Sequence 343 AA;
XX
Query Match 70.1%; Score 68; DB 3; Length 343;
Best Local Similarity 80.0%; Pred. No. 0.0099;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 VDGKATNIPFYTAP 15
||||| :|||||
DB 61 VDGKATNIPFYTAP 75
RESULT 15
ADF90022
ID ADF90022 standard; protein; 337 AA.
XX
AC ADF90022;
XX
DT 26-FEB-2004 (first entry)
XX

DE Opossum-rat chimeric IgE polypeptide.
 KW IgE; immunoglobulin; antibody; opossum; rat; vaccine; antiallergic;
 KW antiasthmatic; dermatological.
 XX
 OS Chimeric.
 OS Didelphis virginiana.
 OS Ratus ep.
 XX WO2003096966-A2.
 XX
 XX 27-NOV-2003.
 PD
 PF 15-MAY-2003; 2003WO-IB002503.
 XX
 XX 21-MAY-2002; 2002US-0382552P.
 PR
 XX
 XX (RESI-) RESISTENTIA PHARM AB.
 PA
 PI Lundgren M, Fuentes A, Magnusson A;
 PI
 XX
 XX WPI; 2004-042496/04.
 DR N-PSDB; ADF90020, ADF90021.
 DR
 XX
 PT New host cell comprising a nucleic acid vector comprising a
 PT cytomagalovirus promoter, an Ig leader sequence, an insert sequence or
 PT SV40 late polyadenylation sequence, useful in producing a chimeric IgE
 PT polypeptide.
 XX
 XX
 PS Claim 3; SEQ ID NO 3; 23pp; English.
 XX
 CC The present sequence is the protein sequence of an opossum CH2-rat CH3-
 CC opossum CH4 (ORO) chimeric IgE polypeptide. A vector comprising a nucleic
 CC acid encoding ORO can be used for recombinant production of this chimeric
 CC IgE in host, e.g. CHO, cells. The invention provides methods and
 CC materials related to expressing chimeric IgE proteins. Nucleic acid
 CC vectors, host cells, and methods for producing chimeric IgE polypeptides
 CC are provided. When administered to a mammal, the chimeric polypeptides
 CC can reduce the IgE antibody effects of IgE-related diseases such as
 CC asthma, allergies and eczema.
 CC
 XX
 SQ Sequence 337 AA;

Query Match 59.8%; Score 58; DB 8; Length 337;
 Best Local Similarity 76.9%; Pred. No. 0.46;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VDGOKATNIRPYT 13
 |||||:|:|||||
 Db 56 VDGQEAENLPPYT 68

Search completed: December 12, 2005, 20:30:29
 Job time : 97.6034 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:23:41 ; Search time 24.5172 Seconds
(without alignments)
60.699 Million cell updates/sec

Title: US-10-758-165A-9
Perfect score: 97
Sequence: 1 VDCGKATNIPFYTAGTK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	108	2	US-09-281-760E-35
2	97	100.0	312	2	US-09-701-623C-2
3	97	100.0	426	1	US-08-336-583-2
4	97	100.0	426	4	PCT-US95-13795-2
5	87	89.7	431	2	US-09-479-614-14
6	87	89.7	496	2	US-09-479-614-2
7	87	89.7	496	2	US-09-479-614-29
8	73	75.3	436	2	US-09-401-636-7
9	58	59.8	341	2	US-09-401-636-3
10	58	59.8	341	2	US-09-401-636-4
11	58	59.8	341	2	US-09-401-636-6
12	58	59.8	341	2	US-09-401-636-9
13	58	59.8	341	2	US-09-401-636-11
14	58	59.8	342	2	US-09-401-636-5
15	58	59.8	342	2	US-09-401-636-8
16	58	59.8	345	2	US-09-401-636-10
17	46	47.4	135	2	US-09-252-991A-10004
18	46	47.4	497	2	US-10-077-699C-5
19	45	46.4	350	2	US-09-094-103-6
20	45	46.4	350	2	US-09-080-963-2
21	45	46.4	350	2	US-08-947-251-2
22	45	46.4	350	2	US-09-769-787-89
23	45	46.4	358	2	US-09-583-110-5009
24	45	46.4	358	2	US-09-107-433-2360
25	45	46.4	583	6	5256558-4
26	44	45.4	121	2	US-09-710-279-2524
27	44	45.4	132	2	US-09-134-001C-4212

28	43	44.3	475	2	US-08-840-767-10	Sequence 10, Appl
29	43	44.3	586	6	5256558-2	Patent No. 5256558
30	42	43.3	557	2	US-09-902-540-12884	Sequence 12884, A
31	42	43.3	985	2	US-09-993-777-6	Sequence 6, Appl
32	42	43.3	985	2	US-09-993-777-66	Sequence 66, Appl
33	42	43.3	985	4	PCT-US96-03916-6	Sequence 6, Appl
34	42	43.3	985	4	PCT-US96-03916-66	Sequence 66, Appl
35	41	42.3	232	2	US-09-489-039A-8106	Sequence 8106, Ap
36	41	42.3	570	1	US-08-967-364-1	Sequence 1, Appl
37	41	42.3	570	1	US-08-967-364-7	Sequence 7, Appl
38	41	42.3	570	2	US-09-368-408-1	Sequence 1, Appl
39	41	42.3	570	2	US-09-368-408-7	Sequence 7, Appl
40	41	42.3	1364	2	US-09-252-991A-26880	Sequence 26880, A
41	40.5	41.8	464	2	US-09-543-681A-4924	Sequence 4924, Ap
42	40.5	41.8	608	2	US-09-252-991A-27624	Sequence 27624, A
43	40	41.2	63	2	US-09-612-402B-29	Sequence 29, Appl
44	40	41.2	63	2	US-09-542-520-29	Sequence 29, Appl
45	40	41.2	284	2	US-09-248-796A-20559	Sequence 20559, A

ALIGNMENTS

RESULT 1
US-09-281-760E-35
Sequence 35, Application US/09281760E
Patent No. 6734287
GENERAL INFORMATION:
APPLICANT: Lawton, Robert
APPLICANT: Mettner, Brian
APPLICANT: Francoeur, Greg
TITLE OF INVENTION: Specific Binding Protein for Treating
TITLE OF INVENTION: Canine Allergy
FILE REFERENCE: 01-1275A
CURRENT APPLICATION NUMBER: US/09/281,760E
CURRENT FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 09/058,331
PRIOR FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatsSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 108
TYPE: PRT
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: misc feature
LOCATION: (81)..(81)
OTHER INFORMATION: The 'Xaa' at location 81 stands for Lys, Arg, Thr, Met, Glu, Gly,
OTHER INFORMATION: Ala, Val, Gln, Pro, Leu, a stop codon, Trp, or Ser.
FEATURE:
NAME/KEY: misc feature
LOCATION: (82)..(82)
OTHER INFORMATION: The 'Xaa' at location 82 stands for a stop codon, Trp, or Cys.
FEATURE:
NAME/KEY: misc feature
LOCATION: (136)..(136)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (451)..(451)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (460)..(462)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (500)..(500)
OTHER INFORMATION: "n" stands for any nucleic acid

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FEATURE:
NAME/KEY: misc feature
LOCATION: (530)..(530)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (847)..(849)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (853)..(853)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (1382)..(1382)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (1832)..(1832)
OTHER INFORMATION: "n" stands for any nucleic acid
US-09-281-760E-35
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Query Match 100.0%; Score 97; DB 2; Length 108;

Best Local Similarity 100.0%; Pred. No. 3.2e-08;

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Qy 1 VDGOKATNIPPTAPGK 18
Db 47 VDGOKATNIPPTAPGK 64
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RESULT 2

US-09-701-623C-2

Sequence 2, Application US/09701623C

Patent No. 6811782

GENERAL INFORMATION:

APPLICANT: Wang Ph.D., Chang Yi

TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

FILE REFERENCE: 1151413US1

CURRENT APPLICATION NUMBER: US/09/701.623C

PRIOR FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: PCT/US99/13959

PRIOR FILING DATE: 1999-06-21

PRIOR APPLICATION NUMBER: 08/100,287

PRIOR FILING DATE: 1998-06-20

NUMBER OF SEQ ID NOS: 91

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 312

TYPE: PRT

ORGANISM: Dog

FEATURE:

OTHER INFORMATION: CH2CH3n of dog IgE

PUBLICATION INFORMATION:

AUTHORS: Patel,

JOURNAL: Immunogenetics

VOLUME: 41

PAGES: 282-286

DATE: 1995

US-09-701-623C-2

Query Match 100.0%; Score 97; DB 2; Length 312;

Best Local Similarity 100.0%; Pred. No. 1e-07;

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VDGOKATNIPPTAPGK 18
Db 48 VDGOKATNIPPTAPGK 65
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RESULT 3

US-08-336-583-2

Sequence 2, Application US/08336583

Patent No. 5629415

GENERAL INFORMATION:

APPLICANT: HOLDIS, GREGORY F.

APPLICANT: PATEL, MAYUR D.

TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHRISTINE E. CARTY

STREET: 126 E. LINCOLN AVENUE

CITY: RAHWAY

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/336,583

FILING DATE: 09-NOV-1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: CARTY, CHRISTINE E.

REGISTRATION NUMBER: 36,099

REFERENCE/DOCKET NUMBER: 19211

TELEPHONE: (908) 594-6734

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 426 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-336-583-2

Query Match 100.0%; Score 97; DB 1; Length 426;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VDGOKATNIPPTAPGK 18
Db 146 VDGOKATNIPPTAPGK 163
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RESULT 4

PCT-US95-13795-2

Sequence 2, Application PC/TUS9513795

GENERAL INFORMATION:

APPLICANT: HOLDIS, GREGORY F.

APPLICANT: PATEL, MAYUR D.

TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHRISTINE E. CARTY

STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000

CITY: RAHWAY

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: PCT/US95/13795
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CARY, CHRISTINE E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19211Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-13795-2

Query Match          100.0%; Score 97; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAG 18
Db      146 VDGQKATNIPFYTAG 163

RESULT 5
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
; US-09-479-614-14

Query Match          89.7%; Score 87; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAG 16
Db      151 VDGQKATNIPFYTAG 166

RESULT 6
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
; US-09-479-614-2

Query Match          89.7%; Score 87; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAG 16
Db      216 VDGQKATNIPFYTAG 231

RESULT 7
US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
; US-09-479-614-29

Query Match          89.7%; Score 87; DB 2; Length 496;
Best Local Similarity 100.0%; Pred. No. 6.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAG 16
Db      216 VDGQKATNIPFYTAG 231

RESULT 8
US-09-401-636-7
; Sequence 7, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-7

Query Match          75.3%; Score 73; DB 2; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.00079;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYTAG 15
Db      111 VDGQKATNIPFYTAG 15
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Db      61 VDGQKATNIPFYP 75

RESULT 9
US-09-401-636-3
; Sequence 3, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-3

Query Match      59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYP 13
      |||||:|:||||
Db      62 VDGQEAENLPFYP 74

RESULT 10
US-09-401-636-4
; Sequence 4, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-4

Query Match      59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYP 13
      |||||:|:||||
Db      62 VDGQEAENLPFYP 74

RESULT 11
US-09-401-636-6
; Sequence 6, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
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; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-6

Query Match      59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYP 13
      |||||:|:||||
Db      62 VDGQEAENLPFYP 74

RESULT 12
US-09-401-636-9
; Sequence 9, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9

Query Match      59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPFYP 13
      |||||:|:||||
Db      62 VDGQEAENLPFYP 74

RESULT 13
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

Query Match 59.8%; Score 58; DB 2; Length 341;
Best Local Similarity 76.9%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYT 13
|||:|:|:|
Db 62 VDGQEAENLFPYT 74

RESULT 14

US-09-401-636-5
; Sequence 5, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-5

Query Match 59.8%; Score 58; DB 2; Length 342;
Best Local Similarity 76.9%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYT 13
|||:|:|:|
Db 62 VDGQEAENLFPYT 74

RESULT 15

US-09-401-636-8
; Sequence 8, Application US/09401636
; Patent No. 6913749
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-8

Query Match 59.8%; Score 58; DB 2; Length 342;
Best Local Similarity 76.9%; Pred. No. 0.2;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VDGQKATNIFPYT 13
|||:|:|:|
Db 62 VDGQEAENLFPYT 74

Search completed: December 12, 2005, 19:37:05
Job time : 24.5172 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:33:42 ; Search time 80.3793 Seconds
(without alignments)
93.568 Million cell updates/sec

Title: US-10-758-165A-9

Perfect score: 97
Sequence: 1 VDGQKATNIFPYTAPGTR 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA_Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	US-10-758-165-9	Sequence 9, Appli
2	97	100.0	426	US-10-214-524-28	Sequence 28, Appl
3	87	89.7	18	US-10-758-165-10	Sequence 10, Appl
4	87	89.7	431	US-09-479-614-14	Sequence 14, Appl
5	87	89.7	431	US-10-409-772-14	Sequence 14, Appl
6	87	89.7	496	US-09-479-614-2	Sequence 2, Appli
7	87	89.7	496	US-09-479-614-29	Sequence 29, Appl
8	87	89.7	496	US-10-214-524-25	Sequence 25, Appl
9	87	89.7	496	US-10-409-772-2	Sequence 29, Appl
10	87	89.7	496	US-10-409-772-29	Sequence 29, Appl
11	73	75.3	343	US-09-401-636-7	Sequence 7, Appli
12	73	75.3	343	US-10-176-664-7	Sequence 7, Appli
13	73	75.3	343	US-10-673-594-7	Sequence 7, Appli
14	73	75.3	577	US-10-214-524-29	Sequence 29, Appl
15	58	59.8	337	US-10-438-794-3	Sequence 3, Appli
16	58	59.8	337	US-10-453-915-3	Sequence 3, Appli
17	58	59.8	338	US-10-438-794-6	Sequence 6, Appli
18	58	59.8	338	US-10-453-915-6	Sequence 6, Appli
19	58	59.8	341	US-09-401-636-3	Sequence 6, Appli
20	58	59.8	341	US-09-401-636-4	Sequence 3, Appli
21	58	59.8	341	US-09-401-636-6	Sequence 6, Appli
22	58	59.8	341	US-09-401-636-9	Sequence 6, Appli
23	58	59.8	341	US-09-401-636-11	Sequence 11, Appl
24	58	59.8	341	US-10-176-664-3	Sequence 3, Appli
25	58	59.8	341	US-10-176-664-4	Sequence 4, Appli
26	58	59.8	341	US-10-176-664-6	Sequence 6, Appli
27	58	59.8	341	US-10-176-664-9	Sequence 9, Appli

	28	58	59.8	341	4	US-10-176-664-11	Sequence 11, Appl
	29	58	59.8	341	4 <td>US-10-673-594-3<td>Sequence 3, Appli</td></td>	US-10-673-594-3 <td>Sequence 3, Appli</td>	Sequence 3, Appli
	30	58	59.8	341	4 <td>US-10-673-594-4<td>Sequence 4, Appli</td></td>	US-10-673-594-4 <td>Sequence 4, Appli</td>	Sequence 4, Appli
	31	58	59.8	341	4 <td>US-10-673-594-6<td>Sequence 6, Appli</td></td>	US-10-673-594-6 <td>Sequence 6, Appli</td>	Sequence 6, Appli
	32	58	59.8	341	4 <td>US-10-673-594-9<td>Sequence 9, Appli</td></td>	US-10-673-594-9 <td>Sequence 9, Appli</td>	Sequence 9, Appli
	33	58	59.8	341	4 <td>US-10-673-594-11<td>Sequence 11, Appli</td></td>	US-10-673-594-11 <td>Sequence 11, Appli</td>	Sequence 11, Appli
	34	58	59.8	342	3 <td>US-09-401-636-5<td>Sequence 5, Appli</td></td>	US-09-401-636-5 <td>Sequence 5, Appli</td>	Sequence 5, Appli
	35	58	59.8	342	3 <td>US-09-401-636-8<td>Sequence 8, Appli</td></td>	US-09-401-636-8 <td>Sequence 8, Appli</td>	Sequence 8, Appli
	36	58	59.8	342	4 <td>US-10-176-664-5<td>Sequence 5, Appli</td></td>	US-10-176-664-5 <td>Sequence 5, Appli</td>	Sequence 5, Appli
	37	58	59.8	342	4 <td>US-10-176-664-8<td>Sequence 8, Appli</td></td>	US-10-176-664-8 <td>Sequence 8, Appli</td>	Sequence 8, Appli
	38	58	59.8	342	4 <td>US-10-673-594-5<td>Sequence 5, Appli</td></td>	US-10-673-594-5 <td>Sequence 5, Appli</td>	Sequence 5, Appli
	39	58	59.8	342	4 <td>US-10-673-594-8<td>Sequence 8, Appli</td></td>	US-10-673-594-8 <td>Sequence 8, Appli</td>	Sequence 8, Appli
	40	58	59.8	345	3 <td>US-09-401-636-10<td>Sequence 10, Appl</td></td>	US-09-401-636-10 <td>Sequence 10, Appl</td>	Sequence 10, Appl
	41	58	59.8	345	4 <td>US-10-176-664-10<td>Sequence 10, Appl</td></td>	US-10-176-664-10 <td>Sequence 10, Appl</td>	Sequence 10, Appl
	42	58	59.8	345	4 <td>US-10-673-594-10<td>Sequence 10, Appl</td></td>	US-10-673-594-10 <td>Sequence 10, Appl</td>	Sequence 10, Appl
	43	58	59.8	347	4 <td>US-10-438-794-14<td>Sequence 14, Appl</td></td>	US-10-438-794-14 <td>Sequence 14, Appl</td>	Sequence 14, Appl
	44	58	59.8	347	4 <td>US-10-453-915-14<td>Sequence 14, Appl</td></td>	US-10-453-915-14 <td>Sequence 14, Appl</td>	Sequence 14, Appl
	45	58	59.8	353	4 <td>US-10-453-915-21<td>Sequence 21, Appl</td></td>	US-10-453-915-21 <td>Sequence 21, Appl</td>	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-9

Query Match 100.0%; Score 97; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 9; ie-09; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPGTR 18
|||
Db 1 VDGQKATNIFPYTAPGTR 18

RESULT 2
US-10-214-524-28
; Sequence 28, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: ICG-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Dog (Canis familiaris)

US-10-214-524-28

Query Match 100.0%; Score 97; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIPFYTAG 18
DB 146 VDGOKATNIPFYTAG 163

RESULT 3

US-10-758-165-10
; Sequence 10, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammetberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-10

Query Match 89.7%; Score 87; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIPFYTAG 16
DB 1 VDGOKATNIPFYTAG 16

RESULT 4

US-09-479-614-14
; Sequence 14, Application US/09479614
; Publication No. US2003003183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

Query Match 89.7%; Score 87; DB 3; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIPFYTAG 16
DB 151 VDGOKATNIPFYTAG 166

RESULT 5

US-10-409-772-14
; Sequence 14, Application US/10409772

; Publication No. US20030216565A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/10/409,772
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US/09/479,614
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-14

Query Match 89.7%; Score 87; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIPFYTAG 16
DB 151 VDGOKATNIPFYTAG 166

RESULT 6

US-09-479-614-2
; Sequence 2, Application US/09479614
; Publication No. US2003003183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

Query Match 89.7%; Score 87; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIPFYTAG 16
DB 216 VDGOKATNIPFYTAG 231

RESULT 7

US-09-479-614-29
; Sequence 29, Application US/09479614
; Publication No. US2003003183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29

LENGTH: 496
TYPE: PRT
ORGANISM: Felis catus
US-09-479-614-29

Query Match 89.7% Score 87; DB 3; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAG 16
|||
Db 216 VDGQKATNIPFYTAG 231

RESULT 8
US-10-214-524-25
Sequence 25, Application US/10214524
Publication No. US20030073142A1
GENERAL INFORMATION:
APPLICANT: Chen, Swei-Shen Alex
APPLICANT: Yang, Yong-Min
APPLICANT: Barankiewicz, Theresa J.
APPLICANT: Chen, Zhong
TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
FILE REFERENCE: IGE-00101.P.1.1
CURRENT APPLICATION NUMBER: US/10/214,524
CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: 60/312,120
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 496
TYPE: PRT
ORGANISM: Cat (Felis catus)
US-10-214-524-25

Query Match 89.7% Score 87; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAG 16
|||
Db 216 VDGQKATNIPFYTAG 231

RESULT 9
US-10-409-772-2
Sequence 2, Application US/10409772
Publication No. US20030216565A1
GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/10/409,772
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US/09/479,614
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 496
TYPE: PRT
ORGANISM: Felis catus
US-10-409-772-2

Query Match 89.7% Score 87; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAG 16
|||

Db 216 VDGQKATNIPFYTAG 231

RESULT 10
US-10-409-772-29
Sequence 29, Application US/10409772
Publication No. US20030216565A1
GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/10/409,772
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US/09/479,614
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 496
TYPE: PRT
ORGANISM: Felis catus
US-10-409-772-29

Query Match 89.7% Score 87; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAG 16
|||
Db 216 VDGQKATNIPFYTAG 231

RESULT 11
US-09-401-636-7
Sequence 7, Application US/09401636
Patent No. US2001003843A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 343
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-7

Query Match 75.3% Score 73; DB 3; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.0019;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VDGQKATNIPFYTAG 15
|||
Db 61 VDGQKATNIPFYTAG 75

RESULT 12
US-10-176-664-7
Sequence 7, Application US/10176664
Publication No. US20030031663A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/10/176,664

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; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-7

Query Match      75.3%; Score 73; DB 4; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.0019;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPYPYAP 15
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Db      61 VDGQKAKENLPYPYAP 75

RESULT 13
US-10-673-594-7
; Sequence 7, Application US/10673594
; Publication No. US2004007625A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-7

Query Match      75.3%; Score 73; DB 4; Length 343;
Best Local Similarity 86.7%; Pred. No. 0.0019;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPYPYAP 15
        ||||| : |||||
Db      61 VDGQKAKENLPYPYAP 75

RESULT 14
US-10-214-524-29
; Sequence 29, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Yang, Yong-Min
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Duckbilled platypus (Ornithorhynchus anatinus)
US-10-214-524-29

Query Match      75.3%; Score 73; DB 4; Length 577;
Best Local Similarity 86.7%; Pred. No. 0.0034;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPYPYAP 15
        ||||| : |||||
Db      295 VDGQKAKENLPYPYAP 309

RESULT 15
US-10-438-794-3
; Sequence 3, Application US/10438794
; Publication No. US20040038395A1
; GENERAL INFORMATION:
; APPLICANT: LUNDGREN, Mats
; APPLICANT: FUENTES, Alexis
; APPLICANT: MAGNUSSON, Ann-Christin
; TITLE OF INVENTION: Chimeric IGE Polypeptides and Host Cells
; FILE REFERENCE: 10223-017001
; CURRENT APPLICATION NUMBER: US/10/438,794
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US 60/382,552
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polypeptide designated ORO
US-10-438-794-3

Query Match      59.8%; Score 58; DB 4; Length 337;
Best Local Similarity 76.9%; Pred. No. 0.055;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VDGQKATNIPYPY 13
        ||||| : |||||
Db      56 VDGQKAKENLPYPY 68

Search completed: December 12, 2005, 20:19:25
Job time : 81.3793 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 12, 2005, 19:34:33 ; Search time 2.94828 Seconds
(without alignments)
34.094 Million cell updates/sec

Title: US-10-758-165A-9
Perfect score: 97
Sequence: 1 VDGQKATNIPFYTA PGTK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 32527 seqs, 5584426 residues
Total number of hits satisfying chosen parameters: 32527

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:
1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/PC1_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	312	6 US-10-723-207-2	Sequence 2, Appli
2	46	47.4	497	6 US-10-763-712A-24	Sequence 24, Appl
3	46	47.4	497	6 US-10-763-712A-91	Sequence 91, Appl
4	44	45.4	121	6 US-10-793-626-2524	Sequence 2524, Ap
5	43	44.3	102	6 US-10-821-234-1457	Sequence 1457, Ap
6	43	44.3	254	6 US-10-485-517-168	Sequence 188, App
7	40	41.2	430	6 US-10-467-657-2346	Sequence 2346, Ap
8	38	39.2	241	6 US-10-485-517-189	Sequence 189, App
9	38	39.2	530	6 US-10-131-826A-130	Sequence 130, App
10	37	38.1	32	6 US-10-467-657-8080	Sequence 8080, Ap
11	37	38.1	345	6 US-10-793-626-3168	Sequence 3168, Ap
12	37	38.1	468	6 US-10-957-566-28	Sequence 28, Appl
13	36	37.1	375	6 US-10-793-626-2172	Sequence 2172, Ap
14	36	37.1	532	7 US-11-184-380-6	Sequence 6, Appli
15	36	37.1	588	7 US-11-184-380-5	Sequence 5, Appli
16	36	37.1	724	7 US-11-184-380-4	Sequence 4, Appli
17	35.5	36.6	811	7 US-11-055-822-1142	Sequence 1142, Ap
18	35.5	36.6	811	7 US-11-055-822-1144	Sequence 1144, Ap
19	35.5	36.6	811	7 US-11-124-291-4	Sequence 4, Appli
20	35.5	36.6	1045	7 US-11-113-424-54	Sequence 54, Appl
21	35.5	36.6	1094	6 US-10-821-234-1097	Sequence 1097, Ap
22	35.5	36.6	2376	7 US-11-096-051-4	Sequence 4, Appli
23	35.5	36.6	2715	7 US-11-096-051-2	Sequence 2, Appli
24	35.5	36.6	2715	7 US-11-113-424-51	Sequence 51, Appl
25	35.5	36.6	2721	7 US-11-096-051-10	Sequence 10, Appl

26	35.5	36.6	2725	7 US-11-096-051-8	Sequence 8, Appli
27	35	36.1	288	6 US-10-467-657-1682	Sequence 1682, Ap
28	35	36.1	433	6 US-10-131-826A-6	Sequence 6, Appli
29	35	36.1	517	6 US-10-485-517-310	Sequence 310, App
30	35	36.1	605	6 US-10-821-234-1207	Sequence 1207, Ap
31	35	36.1	805	6 US-10-518-559-4	Sequence 4, Appli
32	35	36.1	805	6 US-10-518-559-24	Sequence 24, Appl
33	35	36.1	826	6 US-10-793-626-1066	Sequence 1066, Ap
34	35	36.1	853	6 US-10-821-234-1110	Sequence 1110, Ap
35	35	36.1	901	6 US-10-793-626-342	Sequence 342, App
36	35	36.1	1006	6 US-10-467-657-8400	Sequence 8400, Ap
37	35	36.1	2335	6 US-10-821-234-1610	Sequence 1610, Ap
38	34.5	35.6	2011	7 US-11-080-991-56	Sequence 56, Appl
39	34	35.1	119	6 US-10-763-712A-63	Sequence 63, Appl
40	34	35.1	124	6 US-10-467-657-2914	Sequence 2914, Ap
41	34	35.1	146	7 US-11-000-463-881	Sequence 881, App
42	34	35.1	232	6 US-10-510-386-116	Sequence 116, App
43	34	35.1	240	7 US-11-054-515-1989	Sequence 1989, Ap
44	34	35.1	409	6 US-10-793-626-2002	Sequence 2002, Ap
45	34	35.1	409	6 US-10-793-626-2306	Sequence 2306, Ap

ALIGNMENTS

RESULT 1
US-10-723-207-2
Sequence 2, Application US/10723207
Publication No. US20050250934A1
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
TITLE OF INVENTION: ALLERGY
FILE REFERENCE: 1151-4153US2
CURRENT APPLICATION NUMBER: US/10/723, 207
PRIOR FILING DATE: 2003-11-24
PRIOR APPLICATION NUMBER: 09/701, 623
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US99/13959
PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 09/100, 287
PRIOR FILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 312
TYPE: PRT
ORGANISM: Dog
FEATURE:
OTHER INFORMATION: CH2CH3n of dog Ige
PUBLICATION INFORMATION:
AUTHORS: Patel,
JOURNAL: Immunogenetics
VOLUME: 41
PAGES: 282-286
DATE: 1995
US-10-723-207-2
Query Match 100.0%; Score 97; DB 6; Length 312;
Best Local Similarity 100.0%; Pred. No. 9.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VDGQKATNIPFYTA PGTK 18
DB 48 VDGQKATNIPFYTA PGTK 65
RESULT 2
US-10-763-712A-24
Sequence 24, Application US/10763712A
Publication No. US20050266541A1
GENERAL INFORMATION:

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; APPLICANT: Solazyme, Inc.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-10-763-712A-24
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Query Match      47.4%; Score 46; DB 6; Length 497;
Best Local Similarity 55.6%; Pred. No. 0.81;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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QY      1 VDGKATNIFPYTAPGK 18
Db      324 MDGIKETNITWVPAPGSK 341
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RESULT 3
US-10-763-712A-91
; Sequence 91, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 497
; TYPE: PRT
; ORGANISM: C. reinhardtii
US-10-763-712A-91
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Query Match      47.4%; Score 46; DB 6; Length 497;
Best Local Similarity 55.6%; Pred. No. 0.81;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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QY      1 VDGKATNIFPYTAPGK 18
Db      324 MDGIKETNITWVPAPGSK 341
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RESULT 4
US-10-793-626-2524
; Sequence 2524, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
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; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2524
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2524
```

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Query Match      45.4%; Score 44; DB 6; Length 121;
Best Local Similarity 60.0%; Pred. No. 0.38;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      3 GQKATNIFPYTAPGT 17
Db      44 GKTATNIEKXTSQGT 58
```

```
RESULT 5
US-10-821-234-1457
; Sequence 1457, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Strache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc seq_genes Version 1.0
; SEQ ID NO 1457
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1457
```

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Query Match      44.3%; Score 43; DB 6; Length 102;
Best Local Similarity 46.7%; Pred. No. 0.47;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
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```
QY      2 DQKATNIFPYTAPG 16
Db      14 DQGEAPDVVAFAVPG 28
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RESULT 6
US-10-485-517-188
; Sequence 188, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
```

NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
SEQ ID NO 188
LENGTH: 254
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-485-517-188

Query Match 44.3%; Score 43; DB 6; Length 254;
Best Local Similarity 88.9%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KATNIFPYT 13
DB 58 KDTNIFPYT 66

RESULT 7
US-10-467-657-2346
Sequence 2346, Application US/10467657
Publication No. US20050260581a1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 2346
LENGTH: 430
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2346

Query Match 41.2%; Score 40; DB 6; Length 430;
Best Local Similarity 46.7%; Pred. No. 7.4;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 VDSOKATNIFPYTAP 15
DB 127 LDGDDITKLAPYDRP 141

RESULT 8
US-10-485-517-189
Sequence 189, Application US/10485517
Publication No. US20050256299a1
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynex Incorporated
APPLICANT: Foster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629WO
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
SEQ ID NO 189
LENGTH: 241
TYPE: PRT
ORGANISM: Staphylococcus aureus

US-10-485-517-189

Query Match 39.2%; Score 38; DB 6; Length 241;
Best Local Similarity 87.5%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KATNIFPY 12
DB 46 KDTNIFPY 53

RESULT 9
US-10-131-826A-130
Sequence 130, Application US/10131826A
Publication No. US20050245730a1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Deenoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.

US-10-131-826A-130
SEQUENCE: Homo Sapien
LENGTH: 530
TYPE: PRT
ORGANISM: Homo Sapien

Query Match 39.2%; Score 38; DB 6; Length 530;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 6 ATNIFPYTAPGT 17
DB 242 STNIEHSPGCT 253

RESULT 10
US-10-467-657-8080
; Sequence 8080, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8080
; LENGTH: 32
; TYPE: PR1
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8080

Query Match 38.1%; Score 37; DB 6; Length 32;
Best Local Similarity 56.2%; Pred. No. 1.4;
Matches 9; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 3 GQKATNIPPTAPGK 18
Db 8 GRRTNT--ATVPGT 21

RESULT 11
US-10-793-626-3168
; Sequence 3168, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 3168
; LENGTH: 345
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3168

Query Match 38.1%; Score 37; DB 6; Length 345;
Best Local Similarity 63.6%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGKATNIP 11
Db 223 LDGKATNIP 233

RESULT 12
US-10-957-569-28
; Sequence 28, Application US/10957569
; Publication No. US20050246785A1
; GENERAL INFORMATION:
; APPLICANT: COOK, Zhifeng et al.

; TITLE OF INVENTION: PROMOTER, PROMOTER CONTROL ELEMENTS, AND COMBINATIONS, AND USES
; FILE REFERENCE: THEREOP
; CURRENT APPLICATION NUMBER: US/10/957,569
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: US 10/950,321
; PRIOR FILING DATE: 2004-09-23
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patent version 3.3
; SEQ ID NO 28
; LENGTH: 468
; TYPE: PR1
; ORGANISM: Arabidopsis thaliana
US-10-957-569-28

Query Match 38.1%; Score 37; DB 6; Length 468;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 KATNIPPTAPGT 17
Db 203 KGNSTPMSLPGT 215

RESULT 13
US-10-793-626-2172
; Sequence 2172, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 2172
; LENGTH: 375
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2172

Query Match 37.1%; Score 36; DB 6; Length 375;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 VDGKATNIPPTAPGK 18
Db 114 VDTTKTENTEQYIKPETK 131

RESULT 14
US-11-184-380-6
; Sequence 6, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Chioirini, John
; APPLICANT: Kotin, Robert M.
; TITLE OF INVENTION: AAVS NUCLEIC ACIDS
; FILE REFERENCE: 14014.032303
; CURRENT APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 6
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: Synthetic construct
US-11-184-380-6

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```

Query March 37.1%; Score 36; DB 7; Length 532;
Best Local Similarity 46.7%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 1 VDGOKATNIPPYTAP 15
    ||| | | | |
Db 63 VDGSNANAYFGYSTP 77

```

```

RESULT 15
US-11-184-380-5
; Sequence 5, Application US/11184380
; Publication No. US20050255089A1
; GENERAL INFORMATION:
; APPLICANT: Chiorini, John
; APPLICANT: Kocin, Robert M.
; TITLE OF INVENTION: AAV5 NUCLEIC ACIDS
; FILE REFERENCE: 14014.0323U3
; CURRENT APPLICATION NUMBER: US/11/184,380
; CURRENT FILING DATE: 2005-07-19
; PRIOR APPLICATION NUMBER: PCT/US99/11958
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,029
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; Note =
; OTHER INFORMATION: Synthetic construct
US-11-184-380-5

```

```

Query March 37.1%; Score 36; DB 7; Length 588;
Best Local Similarity 46.7%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

```

```

QY 1 VDGOKATNIPPYTAP 15
    ||| | | | |
Db 119 VDGSNANAYFGYSTP 133

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Search completed: December 12, 2005, 20:19:49
 Job time : 3.94828 secs

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OM protein - protein search, using sw model

Run on: December 12, 2005, 20:10:49 ; Search time 15.2069 Seconds
(without alignments)
113.889 Million cell updates/sec

Title: US-10-758-165A-9
Perfect score: 97
Sequence: 1 VDGOKATNIFPYTAPGTR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.5	270	2 T16880	hypothetical prote
2	46	47.4	579	2 JMW0071	asparagine synthas
3	46	47.4	586	2 S69183	asparagine synthas
4	45	47.4	658	2 AH0110	probable surface p
5	45	46.4	350	2 G95009	sensor histidine k
6	45	46.4	350	2 E97881	histidine kinase (
7	45	46.4	583	1 AJPMM2	asparagine synthas
8	44	45.4	511	2 T16279	hypothetical prote
9	43	44.3	322	2 AD3488	transporter BME118
10	43	44.3	586	1 AJPMM1	putative trans-acon
11	42	43.3	258	2 AF0306	asparagine synthas
12	42	43.3	381	2 AD2436	ATP-binding protei
13	42	43.3	476	2 AC2465	6-phosphogluconate
14	42	43.3	623	2 T22177	hypothetical prote
15	42	43.3	683	2 B71325	conserved hypotet
16	42	43.3	1686	2 A87692	conserved hypotet
17	41	42.3	241	2 T17798	hypothetical prote
18	41	42.3	272	2 H87075	probable conserved
19	41	42.3	359	2 G83039	probable conserved
20	41	42.3	570	2 JCS722	vacuolar protein s
21	41	42.3	619	2 H84416	hypothetical prote
22	41	42.3	643	1 S15623	hypothetical prote
23	41	42.3	713	2 J50230	EL protein - human
24	41	42.3	859	2 A82217	NADPH-cytochrome P
25	41	42.3	909	2 T06246	hypothetical prote
26	41	42.3	916	2 T06246	aspartate kinase (
27	41	42.3	1032	2 S74487	aspartate kinase (
28	41	42.3	1055	2 C82600	multitrug-efflux t
29	40.5	41.8	795	2 B83608	hypothetical prote

30	40	41.2	101	2 G69203	conserved hypotet
31	40	41.2	109	2 F89886	hypothetical prote
32	40	41.2	137	2 A83751	hypothetical prote
33	40	41.2	179	2 D90167	conserved hypotet
34	40	41.2	189	2 S49846	asparagine synthas
35	40	41.2	217	1 GMBPT4	gene 59 protein -
36	40	41.2	227	2 C7582	conserved hypotet
37	40	41.2	240	2 C89967	serine proteinase
38	40	41.2	302	2 T03109	probable membrane
39	40	41.2	327	2 S40753	hypothetical prote
40	40	41.2	357	1 A48511	protein-glutamate
41	40	41.2	374	2 G81926	probable polyamine
42	40	41.2	419	2 C81179	spermidine/putresc
43	40	41.2	454	2 AH2821	conserved hypotet
44	40	41.2	470	2 H97599	BH0982 hypothetical
45	40	41.2	584	2 T12989	asparagine synthas

ALIGNMENTS

RESULT 1

T16880
hypothetical protein T14G12.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-Oct-2004
C:Accession: T16880
R:Milcox, L.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid T14G12.
A:Reference number: Z18596
A:Accession: T16880
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-270 <Nil>
A:Cross-references: UNIPROT:Q22510; UNIPARC:UPI0000075025; EMBL:U41268; NID:G1086843; PI
C:Gene: CESP:T14G12.4
A:Introns: 37/1; 72/3; 164/1
F:93-185/Domain: fork head DNA-binding domain homology <FHD>

Query Match 49.5%; Score 48; DB 2; Length 270;
Best Local Similarity 57.1%; Pred. No. 2;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Cy 3 GOKATNIFPYTAPG 16
Db 205 GAAGANLFPYFSPG 218

RESULT 2

JMW071
asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) - soybean
C:Species: *Glycine max* (soybean)
C:Date: 13-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 09-Jul-2004
C:Accession: JMW071
R:Yamagata, H.; Nakajima, A.; Bowler, C.; Iwasaki, T.
Biotech. Biochemol. Biochem. 62, 148-150, 1998
A>Title: Molecular cloning and characterization of a cDNA encoding asparagine synthetase
A:Reference number: JMW071; MUID:98162148; PMID:9501527
A:Accession: JMW071
A:Molecule type: mRNA
A:Residues: 1-579 <YAM>
A:Cross-references: UNIPROT:Q42792; UNIPARC:UPI00000A958C; GB:U55874; NID:G1305548; PIDN
C:Superfamily: asparagine synthase (glutamine-hydrolysing)
C:Keywords: asparagine biosynthesis; ligase
F:2-579/Product: asparagine synthase (glutamine-hydrolysing) #status predicted <DUM>
F:2/Active site: Cys #status predicted

Query Match 47.4%; Score 46; DB 2; Length 579;
Best Local Similarity 34.4%; Pred. No. 10;
Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

QY 1 VDGQK-----ATNIPYTAAGTK 18
:|||||:
Db 462 IDG|KAHAEKVTDRMMLANANIPFPTTK 493

RESULT 3
S69183
asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - Lotus japonicus
C:Species: Lotus japonicus
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S69183; S57932
R:Waterhouse, R.N.; Smyth, A.J.; Massemeau, A.; Proseer, I.M.; Clarkson, D.T.
Plant Mol. Biol. 30, 883-897, 1996
A:Title: Molecular cloning and characterisation of asparagine synthetase from Lotus japonicus
A:Reference number: S69182; MUID:96270369; PMID:8639748
A:Accession: S69183
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-586 <WAT>
A:Cross-references: UNIPROT:P49093; UNIPARC:UPI000016DE2B; EMBL:X89410; NID:G897772; PID
A:Experimental source: strain B-129
C:Genetics:
A:Gene: AS2
C:Superfamily: asparagine synthase (glutamine-hydrolyzing)
C:Keywords: asparagine biosynthesis; ligase
F:2-586/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <DUM>
F:2/Active site: Cys #status predicted

Query Match 47.4%; Score 46; DB 2; Length 586;
Best Local Similarity 31.2%; Pred. No. 10;
Matches 10; Conservative 4; Mismatches 4; Indels 14; Gaps 1;

QY 1 VDGQK-----ATNIPYTAAGTK 18
:|||||:
Db 462 IDG|KAHAEKVTDRMMLANANIPFPTTK 493

RESULT 4
AH0110
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH0110
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-658 <KUR>
A:Cross-references: UNIPROT:Q8ZHJ0; UNIPARC:UPI000000CD765; GB:AL590842; PIDN:CAC89747.1;
A:Genetics:
A:Gene: YPO0902

Query Match 47.4%; Score 46; DB 2; Length 658;
Best Local Similarity 52.9%; Pred. No. 12;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGQKATNIPYTAAGT 17
:|||||:
Db 99 LINGQKATNLAPATISST 115

RESULT 5
G95009
sensor histidine kinase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: G95009
R:Teitelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I.
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95009
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <KUR>
A:Cross-references: UNIPROT:Q9SLJ1; UNIPROT:Q8DRK0; UNIPARC:UPI0000051BF0; GB:AE005672; I
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP0084

Query Match 46.4%; Score 45; DB 2; Length 350;
Best Local Similarity 72.7%; Pred. No. 8.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 NIPYTAAGTK 18
:|||||:
Db 248 NAFKYSAPGTK 258

RESULT 6
E97881
histidine kinase (EC 2.7.3.-) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: E97881
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: E97881
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <KUR>
A:Cross-references: UNIPROT:Q9SLJ1; UNIPROT:Q8DRK0; UNIPARC:UPI0000051BF0; GB:AB007317; I
A:Genetics:
A:Gene: hk08
C:Keywords: phosphotransferase

Query Match 46.4%; Score 45; DB 2; Length 350;
Best Local Similarity 72.7%; Pred. No. 8.6;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 NIPYTAAGTK 18
:|||||:
Db 248 NAFKYSAPGTK 258

RESULT 7
AJPMN2
asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) [similarity] - garden pea
N:Alternate names: asparagine synthetase (glutamine-hydrolyzing)
C:Species: Pisum sativum (garden pea)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: S11443
R:Teal, F.Y.; Coruzzi, G.M.
EMBO J. 9, 323-332, 1990
A:Title: Dark-induced and organ-specific expression of two asparagine synthetase genes in
A:Reference number: S11443; MUID:90151604; PMID:1968003
A:Accession: S11443
A:Molecule type: DNA
A:Residues: 1-583 <TSA>
A:Cross-references: UNIPROT:P19252; UNIPARC:UPI000016DF0B; EMBL:X52180; NID:G20651; PIDN
C:Genetics:
A:Gene: AS2
C:Superfamily: asparagine synthase (glutamine-hydrolyzing)

RESULT 10

R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchitani, S.; Nakazaki, N.; Shingo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AD2436
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-381 <KUR>
A/Cross-references: UNIPROT:Q8YLM2; UNIPARC:UPI00000CED3F; GB:BA000019; P1DN:BA876743.1;
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: all5044

Query Match 43.3%; Score 42; DB 2; Length 381;
Best Local Similarity 53.3%; Pred. No. 31;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 VDGKATNIFPYTAP 15
DB 80 IQGQPMNTNIPYRPP 94

RESULT 13
AC2465
6-phosphogluconate dehydrogenase [imported] - Nostoc sp. (strain PCC 7120)
C/Species: Nostoc sp. PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AC2465

R/Kaneke T.; Nakamura, Y.; Wolk, C.P.; Kurlitz, T.; Sasamoto, S.; Watanabe, A.; Iriuchihara, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AC2465
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-476 <KUR>
A/Cross-references: UNIPROT:Q8YLM3; UNIPARC:UPI00000CEB0D; GB:BA000019; P1DN:BA876974.1;
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: all5275

C/Superfamily: phosphogluconate dehydrogenase (decarboxylating); 3-hydroxyisobutyrate dehydrogenase
Query Match 43.3%; Score 42; DB 2; Length 476;
Best Local Similarity 72.7%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 NIFPYTAPGTX 18
DB 238 NIFPYTIDPXTK 248

RESULT 14
T22177
hypothetical protein F44FL.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T22177

R/Dobson, R.
submitted to the EMBL Data Library, October 1996
A/Reference number: Z19527
A/Accession: T22177
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-623 <WIL>
A/Cross-references: UNIPROT:O02260; UNIPARC:UPI000017B9C4; EMBL:Z81083; P1DN:CAB03101.1;
A/Experimental source: clone F44FL
C/Genetics:
A/Gene: CESP:F44FL.3
A/Map position: 1
A/Intons: 43/2; 69/3; 181/3; 241/2; 493/3; 526/2; 548/3

Query Match 43.3%; Score 42; DB 2; Length 623;

Best Local Similarity 50.0%; Pred. No. 53;
Matches 11; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
QY 1 VDGKATNIFPYTAPGTX 18
DB 152 VDGQMKTIIDDFPTTDDIR 173

RESULT 15
B71325
conserved hypothetical protein TP0421 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: B71325
R/Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinther, J.; Khatala, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetzerback, T.; McDorthe, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; MUID:98332770; PMID:9665876
A/Accession: B71325
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-683 <COL>
A/Cross-references: UNIPROT:O83436; UNIPARC:UPI00000C0A71; GB:AE01220; GB:AE000520; NID:
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0421

Query Match 43.3%; Score 42; DB 2; Length 683;
Best Local Similarity 50.0%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 3 GOKATNIFPYTAPG 16
DB 278 GOKSARFFGTSARG 291

Search completed: December 12, 2005, 20:42:50
Job time : 17.2069 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: December 12, 2005, 20:10:41 ; Search time 97.7586 Seconds
(without alignments)
129.907 Million cell updates/sec

Title: US-10-758-165A-9
Perfect score: 97
Sequence: 1 VDCGKATNIFPYTAPGTR 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	52.6	382	2	Q7PSV1_FUSNV
2	51	52.6	382	2	Q8R6B3_FUSNM
3	48	49.5	168	2	Q950A8_CAEEL
4	48	49.5	270	2	Q22510_CAEEL
5	47	48.5	1054	2	Q608X6_METCA
6	47	48.5	1538	2	Q94H26_ORYSA
7	46	47.4	497	2	Q9FYU1_CHLRE
8	46	47.4	579	2	P93168_SOYBN
9	46	47.4	579	2	Q42792_SOYBN
10	46	47.4	579	2	Q9SM55_PHAVU
11	46	47.4	585	1	ASNS2_LOTJA
12	46	47.4	641	2	Q8CKM1_YERPE
13	46	47.4	658	2	Q8ZHJ0_YERPE
14	45	46.4	190	2	Q68E47_ABRPU
15	45	46.4	279	2	Q619H6_CABBR
16	45	46.4	350	2	Q8DRK0_STRRP
17	45	46.4	350	2	Q9S1J1_STRRP
18	45	46.4	445	1	ALN_SPRCO
19	45	46.4	582	1	ASNS2_PEA
20	45	46.4	583	2	Q8RVLD_9PABA
21	44	45.4	131	1	S58_STAEP
22	44	45.4	131	2	Q5HMC5_STAEP
23	44	45.4	340	2	Q9AYAO_ORYSA
24	44	45.4	395	2	Q9ZHQ4_STRFR
25	44	45.4	511	1	U171_CAEEL
26	44	45.4	525	2	Q6AL11_DESPS
27	44	45.4	584	2	Q9WB61_ASTSI
28	44	45.4	586	2	Q84X69_9PABA
29	44	45.4	589	2	Q53Q04_ORYSA
30	44	45.4	760	2	Q6UDM4_ORYSA
31	44	45.4	875	2	Q7FAL9_ORYSA

32	44	45.4	884	2	Q53JX1_ORYSA	Q53JX1 oryza sativ
33	44	45.4	1436	2	Q7FAL2_ORYSA	Q7FAL2 oryza sativ
34	44	45.4	1685	2	Q7XSP1_ORYSA	Q7XSP1 oryza sativ
35	44	45.4	1829	2	Q70XV6_AMBTC	Q70XV6 amborella t
36	43.5	44.8	1335	2	Q91A54_9CAUD	Q91A54 bacterioph
37	43.5	44.8	1335	2	Q91A58_9CAUD	Q91A58 prophage p-
38	43	44.3	52	2	Q7WYM4_BACSH	Q7WYM4 bacillus sp
39	43	44.3	102	1	GAGC1_HUMAN	GAGC1 homo sapien
40	43	44.3	102	2	Q61B11_HUMAN	Q61B11 homo sapien
41	43	44.3	120	2	Q52EG8_MAGGR	Q52EG8 magnaporthe
42	43	44.3	127	1	CRCB_NITRU	CRCB09 nitrosomon
43	43	44.3	166	2	Q6GCH5_STRAS	Q6GCH5 staphylococ
44	43	44.3	166	2	Q8NYE3_STRAM	Q8NYE3 staphylococ
45	43	44.3	240	2	Q9KH50_STRAM	Q9KH50 staphylococ

ALIGNMENTS

RESULT 1
Q7PSV1_FUSNV PRELIMINARY; PRT; 382 AA.
ID Q7PSV1_FUSNV
AC Q7PSV1
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.-).
GN Name=FV1343;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteriia; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=209882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 49256;
RA Kaprethel V., Ivanova N., Anderson I., Reznik G., Bhattacharya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haselkorn R., Overbeek R., Kyriades N.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAF0100055; EAA24105.1; -; Genomic_DNA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR010327; HGD-D.
DR Pfam; PF06050; HGD-D; 1.
KW Lyase.
SQ SEQUENCE 382 AA; 43893 MW; 441C738161C761E CRC64;
Query Match 52.6%; Score 51; DB 2; Length 382;
Best Local Similarity 64.3%; Pred. No. 7.8;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 2 DGOKATNIFPYTAP 15
Db 28 EGKAVGIFPYAP 41
RESULT 2
Q8R6B3_FUSNM PRELIMINARY; PRT; 382 AA.
ID Q8R6B3_FUSNM
AC Q8R6B3
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE (R)-2-hydroxyglutaryl-CoA dehydratase beta-subunit (EC 4.2.1.-).
GN OrderedLocustName=FNO208;
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteriia; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RX DOI=10.1128/JB.184.7.2005-2018.2002;
RA Kapatalay V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goldsman E., Bernal A.,
RA Larsen N., D'Souza M., Malinas T., Pusch G., Haselkorn R.,
RA Fornslein M., Kyriplides N.C., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586."
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL: AE009951.1: AAL94414.1: -; Genomic_DNA.
DR InterPro: IPR010327; HGD-D.
DR Pfam: PF06050; HGD-D; 1.
KW Complete proteome; Lyase.
SQ SEQUENCE 382 AA; 43923 MW; 93038D4296AE34CD CRC64;

Query Match 52.6%; Score 51; DB 2; Length 382;
Best Local Similarity 64.3%; Pred. No. 7.8;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DQKATNIPPTAP 15
Db 28 EGKKAAGIFPYAP 41

RESULT 3
Q95QA9 CAEBL PRELIMINARY; PRT; 168 AA.
ID Q95QA9 CAEBL PRELIMINARY; PRT; 168 AA.
AC Q95QA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Forkhead transcription factor family protein 2, isoform b.
GN Name=fkh-2; ORFNames=TI4G12.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC EMBL: U41268; AAL02521.1; -; Genomic_DNA.
DR HSSP: Q99958; 1D5V.
DR SMR: Q95QA9; 2-68.
DR Ensemble: T14G12.4; Caenorhabditis elegans.
DR WormBase: WBGene0001434; fkh-2.
DR WormPep: T14G12.4b; CE29342.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription; DNA-dependent; IEA.
DR GO: GO:0006350; P:transcription; IEA.
DR InterPro: IPR001766; TF_Fork_head.
DR InterPro: IPR011991; Wing_hlx_DNA_bd.
DR Pfam: PF00250; Fork_head_1.
DR PRINTS: PR00053; FORKHEAD.
DR PRODOM: PD000425; TF_Fork_head_1.
DR SMART: SM00339; FH; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS50039; FORK_HEAD_3; 1.
KW Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 168 AA; 19239 MW; 8E01AC4B6968572 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 168;
Best Local Similarity 57.1%; Pred. No. 11;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy 3 GQKATNIPPTAPG 16
Db 103 GAAANLFPYFSPG 116

RESULT 4
Q22510 CAEBL PRELIMINARY; PRT; 270 AA.
ID Q22510 CAEBL PRELIMINARY; PRT; 270 AA.
AC Q22510;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Forkhead transcription factor family protein 2, isoform a.
GN Name=fkh-2; ORFNames=TI4G12.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
CC -1- INTERACTION:
CC Q21648:R02F2.5; NBExp=1; IntAct=EBI-327741, EBI-314179;
CC Q9XW88:Y75B8A.1; NBExp=1; IntAct=EBI-327741, EBI-316766;
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL: U41268; AAL82436.1; -; Genomic_DNA.
DR PIR: T16880; T16880.
DR HSSP: Q99958; 1D5V.
DR SMR: Q22510; 93-170.
DR InterPro: IPR011991; Wing_hlx_DNA_bd.
DR Pfam: PF00250; Fork_head_1.
DR PRINTS: PR00053; FORKHEAD.
DR PRODOM: PD000425; TF_Fork_head_1.
DR SMART: SM00339; FH; 1.
DR PROSITE: PS00657; FORK_HEAD_1; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS50039; FORK_HEAD_3; 1.
KW Complete proteome; DNA-binding; Nuclear protein; Transcription;
KW Transcription regulation.
SQ SEQUENCE 270 AA; 30491 MW; 7C4911655EC76175 CRC64;

Query Match 49.5%; Score 48; DB 2; Length 270;
Best Local Similarity 57.1%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GQKATNIPPTAPG 16
Db 205 GAAANLFPYFSPG 218

RESULT 5
Q608X6 METCA PRELIMINARY; PRT; 1054 AA.
ID Q608X6 METCA PRELIMINARY; PRT; 1054 AA.
AC Q608X6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hydrophobe/ampiphile Efflux-1 (HAE1) family protein.

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GN OrderedLocustNames=MCA1360;
OS Methylococcus capsulatus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
OC Methylococcaceae; Methylococcus.
OX NCBI_TaxID=414;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Bath / NCIMB 11132;
RX PubMed=1538340; DOI=10.1371/journal.pbio.0020303;
RA Ward N.L., Larsen O., Sakwa J., Bruneeth L., Khouri H.M., Durkin A.S.,
RA Dimetrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E.,
RA Mehe B.A., Wu M., Heideberg J.F., Paulsen I.T., Fouts D.E.,
RA Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R.,
RA Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,
RA Grindberg S.H., Holt I.E., Eidhammer I., Jonassen I., Vanaken S.,
RA Uterbeck T.R., Feldblyum T.V., Fraser C.M., Lilienhaug J.R.,
RA Eiken J.A.,
RT "Genomic insights into methanotrophy: the complete genome sequence of
RT Methylococcus capsulatus (Bath).";
RL PLOS Biol. 2:1616-1628(2004).
DR EMBL; AE017282; AA092574.1; -; Genomic_DNA.
DR TIGR; MCA1360; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001036; Acrflavin_res.
DR InterPro; IPR004764; HAE1.
DR Pfam; PF00873; ACR_tran_1.
DR PRINTS; PR00702; ACRIPLAVINRP.
DR TIGRFAMs; TIGR00915; 2A0602; 1.
DR Complete proteome.
SQ SEQUENCE 1054 AA; 115004 MW; BB032CB91B38D1A8 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 1054;
Best Local Similarity 56.2%; Pred. No. 1.1e+02;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGGKATNIPFYTAG 16
   |||:|:|:|:|:|
Db 294 VNGHKSTQIVVYTLPG 309

RESULT 6
094H26 ORYSA
ID 094H26 ORYSA PRELIMINARY; PRT; 1538 AA.
AC 094H26
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative gag-pol polyprotein.
GN Name=OSJNBa0077622.13;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Buell C.R., Yuan Q., Ouyang S., Mo'fat K.S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Telserin T.,
RA Riggs F., Hsiao J., Ziemann V., Blunt S., Pai G., Vanken S.E.,
RA Uterbeck T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Fraser C.M.;
RA Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC Buell R.;
RA Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC094831; AAK52152.1; -; Genomic_DNA.
DR Gramene; O94H26; -;
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.

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DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR GO; GO:0006278; P:DNA-dependent DNA replication; IEA.
DR InterPro; IPR005162; Retrotrans_gag.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR001584; Rve.
DR Pfam; PF03732; Retrotrans_gag; 1.
DR Pfam; PF00075; RNaseH; 1.
DR Pfam; PF00665; rve; 1.
DR PROSITE; PS50879; RNaseH_H; 1.
DR Polypeptide.
SQ SEQUENCE 1538 AA; 174627 MW; 5E7A521B398BC776 CRC64;

Query Match 48.5%; Score 47; DB 2; Length 1538;
Best Local Similarity 61.5%; Pred. No. 1.6e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGGKATNIPFYT 13
   |||:|:|:|
Db 740 VDGRAAVNLMPYT 752

RESULT 7
09FYU1 CHURE
ID 09FYU1 CHURE PRELIMINARY; PRT; 497 AA.
AC 09FYU1
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
DE Fe-hydrogenase precursor (BC 1.18.99.1) (Iron-hydrogenase HydA1).
GN Name=hyd1; Synonyms=hydA, hydA1;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
OC Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C9;
RA Metz L.J.;
RT "The iron hydrogenase of Chlamydomonas reinhardtii has a single
RT folding domain containing an H-cluster catalytic center and lacking
RT bound electron carriers.";
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=21gr;
RA Forestier M., Zhang L., Plummer S., Ahmann D., Seibert M.,
RA Ghirardi M.L.;
RT "Two putative Fe-only hydrogenases cloned from Chlamydomonas
RT reinhardtii are coexpressed in cells undergoing anaerobiosis.";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Kaminski A.U., Happe T.;
RT "Isolation and characterization of the hydA gene encoding the Fe-
RT hydrogenase of Chlamydomonas reinhardtii.";
RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC Happe T., Kaminski A.;
RA "Isolation and characterization of the hydA gene encoding the Fe-
RT hydrogenase of Chlamydomonas reinhardtii.";
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF289201; AAG00591.1; -; mRNA.
DR EMBL; AY055755; AAL23572.1; -; mRNA.
DR EMBL; AJ012098; CAC80065.1; -; mRNA.
DR EMBL; AJ08413; CAC83731.1; -; Genomic_DNA.
DR HSP; P07598; IHFE.
DR GO; GO:0005449; F:electron transporter activity; IEA.
DR GO; GO:0008901; F:ferredoxin hydrogenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR004108; Fe_hyd_1g_C.

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DR Pfam; PF00733; Asn_synthase; 1.
 DR Pfam; PF00310; GATase_2; 1.
 DR TIGRFAMs; TIGR01536; asn_synth_AEB; 1.
 DR PROSITE; PS00443; GATASE_TYPE_II; UNKNOWN_1.
 KW Ligase.
 SQ SEQUENCE 579 AA; 65265 MW; 7A74F5A8B52CE2E6 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 579;
 Best Local Similarity 34.4%; Pred. No. 85;
 Matches 11; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

OY 1 VDQOK-----ATNIPPYAPGK 18
 :|||:||||:
 Db 462 IDGLKHAKEKVTDRMLNANIPFPNTPTK 493

RESULT 11
 ASNS2_LOTUA STANDARD; PRT; 585 AA.
 ID ASNS2_LOTUA
 AC P49093;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Asparagine synthetase [glutamine-hydrolyzing] 2 (EC 6.3.5.4)
 DE (Glutamine-dependent asparagine synthetase 2).
 GN Name=AS2;
 OS Lotus japonicus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.
 OX NCBI_TaxID=34305;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=cv Gifu / B-129;
 RX MEDLINE=36270368; PubMed=8639748;
 RA Waterhouse R.N., Smyth A.J., Massonau A., Proesser I.M.,
 RA Clarkson D.T.;
 RT "Molecular cloning and characterisation of asparagine synthetase from
 Lotus japonicus: dynamics of asparagine synthesis in N-sufficient
 conditions."
 RT Plant Mol. Biol. 30:883-897 (1996).
 RL -1- CATALYTIC ACTIVITY: ATP + L-aspartate + L-glutamine = AMP +
 CC -1- diphosphate + L-asparagine + L-glutamate.
 CC -1- PATHWAY: Asparagine biosynthesis.
 CC -1- SIMILARITY: Contains 1 asparagine synthetase domain.
 CC -1- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; X89410; CAA61590.1; -; mRNA.
 DR PIR; S69183; S69183.
 DR HSSP; P22106; 1CT9.
 DR InterPro; IPR006426; Asn_synth_AEB.
 DR InterPro; IPR001962; Asn_synthase.
 DR InterPro; IPR000583; GATase_2.
 DR Pfam; PF00733; Asn_synthase; 1.
 DR Pfam; PF00310; GATase_2; 1.
 DR TIGRFAMs; TIGR01536; asn_synth_AEB; 1.
 DR PROSITE; PS00443; GATASE_TYPE_II; 1.
 KW amino-acid biosynthesis; Asparagine biosynthesis;
 KW Glutamine amidotransferase; Ligase; Multigene family.
 FT INTR MET 0
 FT DOMAIN 192 515 Asparagine synthetase.
 FT REGION 1 107 Glutamine amidotransferase.
 FT ACT_SITE 1 1 GATase (by similarity).
 SQ SEQUENCE 585 AA; 65839 MW; F56DCA2015F73451 CRC64;

Query Match 47.4%; Score 46; DB 1; Length 585;
 Best Local Similarity 31.2%; Pred. No. 86;

Matches 10; Conservative 4; Mismatches 4; Indels 14; Gaps 1;
 OY 1 VDQOK-----ATNIPPYAPGK 18
 :|||:||||:
 Db 461 IDGLKHAKEKVTDRMLNANIPFPNTPTK 492

RESULT 12
 O8CKM1_YERPE PRELIMINARY; PRT; 641 AA.
 ID O8CKM1_YERPE
 AC O8CKM1_YERPE
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Hypothetical.
 GN OrderedLocustNames=yj3288;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=KIMS / Biovar Mediavalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RX DOI=10.1128/JB.184.16.4601-4611.2002;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Staley S.C., McDonough K.A., Niles M.W., Mason J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM."
 RL J. Bacteriol. 184:4601-4611 (2002).
 DR EMBL; AE013929; AAM86837.1; -; Genomic DNA.
 DR GO; GO:0019867; C:outer membrane; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008640; Hep_Hag.
 DR InterPro; IPR008635; HIM.
 DR InterPro; IPR005594; Yada_C.
 DR Pfam; PF05658; Hep_Hag; 7.
 DR Pfam; PF05662; HIM; 4.
 DR Pfam; PF03895; Yada; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 641 AA; 62093 MW; A5951553FEA5162 CRC64;

Query Match 47.4%; Score 46; DB 2; Length 641;
 Best Local Similarity 52.9%; Pred. No. 94;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 VDQKATNIPFYAPGT 17
 :|||:||||:
 Db 82 LMGKATVLAATISST 98

RESULT 13
 O8ZHJ0_YERPE PRELIMINARY; PRT; 658 AA.
 ID O8ZHJ0_YERPE
 AC O8ZHJ0_YERPE
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Putative surface protein (Fragment).
 GN OrderedLocustNames=YPO0902;
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
 RX Parkhill J., Wren B.W., Thomson N.R., Tlball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,

RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Kariyshev A.V.,
 RA Leather S., Mole S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.,
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."
 RL Nature 413:523-527(2001).
 DR EMBL: AJ314145; CAC89747.1; -; Genomic_DNA.
 DR PIR: AH0110; AH0110.
 DR GO: GO:0019867; C:outer membrane; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR008640; Hep_Hag.
 DR InterPro: IPR005594; HIM_
 DR InterPro: IPR005594; Yada_C.
 DR Pfam: PF05658; Hep_Hag; 7.
 DR Pfam: PF05662; HIM; 4.
 DR Pfam: PF03895; Yada; 1.
 KM Complete proteome.
 FT NON TER 1
 SQ SEQUENCE 658 AA; 63875 MW; FC20411944FPEZPF CRC64;

Query Match 47.4%; Score 46; DB 2; Length 658;
 Best Local Similarity 52.9%; Pred. No. 97;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDQKATNIPFYTAGT 17
 Db 99 LINGOKATNIPATIST 115

RESULT 14

Q68E47_AERPU PRELIMINARY; PRT; 190 AA.
 ID Q68E47;
 AC Q68E47;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE Hypothetical protein.
 GN ORFNames=PFBA076.62;
 OS Aeromonas punctata (Aeromonas caviae).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
 OC Aeromonadaceae; Aeromonas.
 OX NCBI_TaxID=648;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HGB5;
 RA Rhodes G., Parkhill J., Bird C., Ambrose K., Jones M., Huys G.,
 RA Swings J., Pickup R.W.;
 RT "The complete nucleotide sequence of the conjugative tetracycline
 RT resistance plasmid pFBA076, a member of a group of Incu plasmids with
 RT global ubiquity."
 RL Appl. Environ. Microbiol. 70:7497-7510(2004).
 DR EMBL: CR376602; CAG15109.1; -; Genomic_DNA.
 KM Hypothetical protein.
 SQ SEQUENCE 190 AA; 21295 MW; 4790837FF3CFEB54 CRC64;

Query Match 46.4%; Score 45; DB 2; Length 190;
 Best Local Similarity 47.1%; Pred. No. 38;
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 DQKATNIPFYTAGT 18
 Db 58 DGEDASNTVATDPATE 74

RESULT 15

O619H6_CAEPR PRELIMINARY; PRT; 279 AA.
 ID O619H6;
 AC O619H6;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE Hypothetical protein CBG14280.
 GN Name=CBG14280;

OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6238;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RG The C.briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL: CAAC0100068; CAC68479.1; -; Genomic_DNA.
 DR SMR: O619H6; 101-178.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001766; TF_Fork_head.
 DR InterPro: IPR011991; Wing_hlx_DNA_bd.
 DR Pfam: PF00250; Fork_head; 1.
 DR PRINTS: PR00053; FORKHEAD.
 DR PRODOM: PD000425; TF_Fork_head; 1.
 DR SMART: SM00339; FH; 1.
 DR PROSITE: PS00657; FORK_HEAD_1; 1.
 DR PROSITE: PS00658; FORK_HEAD_2; 1.
 DR PROSITE: PS50039; FORK_HEAD_3; 1.
 KM DNA-binding; Hypothetical protein; Nuclear protein; Transcription;
 KM Transcription regulation.
 SQ SEQUENCE 279 AA; 31322 MW; 0C926B95AD122D9B CRC64;

Query Match 46.4%; Score 45; DB 2; Length 279;
 Best Local Similarity 57.1%; Pred. No. 58;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 GQKATNIPFYTAG 16
 Db 213 GAATAATPFYFNG 226

Search completed: December 12, 2005, 20:41:10
 Job time : 100.759 secs